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(54) Title: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

(57) Abstract: The present invention provides novel nucleic acids, novel polypeptide sequences encoded by these nucleic acids and uses thereof.



For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

1. TECHNICAL FIELD

The present invention provides novel polynucleotides and proteins encoded by such polynucleotides, along with uses for these polynucleotides and proteins, for example in therapeutic, diagnostic and research methods.

2. BACKGROUND

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Technology aimed at the discovery of protein factors (including e.g., cytokines, such as lymphokines, interferons, CSFs, chemokines, and interleukins) has matured rapidly over the past decade. The now routine hybridization cloning and expression cloning techniques clone novel polynucleotides "directly" in the sense that they rely on information directly related to the discovered protein (i.e., partial DNA/amino acid sequence of the protein in the case of hybridization cloning; activity of the protein in the case of expression cloning). More recent "indirect" cloning techniques such as signal sequence cloning, which isolates DNA sequences based on the presence of a now well-recognized secretory leader sequence motif, as well as various PCR-based or low stringency hybridization-based cloning techniques, have advanced the state of the art by making available large numbers of DNA/amino acid sequences for proteins that are known to have biological activity, for example, by virtue of their secreted nature in the 20 case of leader sequence cloning, by virtue of their cell or tissue source in the case of PCR-based techniques, or by virtue of structural similarity to other genes of known biological activity.

Identified polynucleotide and polypeptide sequences have numerous applications in, ferexample, diagnostics, forensics, gene mapping; identification of mutations responsible for genetic disorders or other traits, to assess biodiversity, and to produce many other types of data and products dependent on DNA and amino acid sequences.

3. SUMMARY OF THE INVENTION

The compositions of the present invention include novel isolated polypeptides, novel isolated polynucleotides encoding such polypeptides, including recombinant DNA molecules, cloned genes or degenerate variants thereof, especially naturally occurring variants such as allelic variants, antisense polynucleotide molecules, and antibodies that specifically recognize one or more epitopes present on such polypeptides, as well as hybridomas producing such antibodies.

The compositions of the present invention additionally include vectors, including expression vectors, containing the polynucleotides of the invention, cells genetically engineered to contain such polynucleotides and cells genetically engineered to express such polynucleotides.



The present invention relates to a collection or library of at least one novel nucleic acid sequence assembled from expressed sequence tags (ESTs) isolated mainly by sequencing by hybridization (SBH), and in some cases, sequences obtained from one or more public databases. The invention relates also to the proteins encoded by such polynucleotides, along with therapeutic, diagnostic and research utilities for these polynucleotides and proteins. These nucleic acid sequences are designated as SEQ ID NO: 1-1786 and 3573-5358. The polypeptides sequences are designated SEQ ID NO: 2n (wherein n = 1 to 20). The nucleic acids and polypeptides are provided in the Sequence Listing. In the nucleic acids provided in the Sequence Listing, A is adenosine; C is cytosine; G is guanine; T is thymine; and N is any of the four bases. In the amino acids provided in the Sequence Listing, * corresponds to the stop codon.

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The nucleic acid sequences of the present invention also include, nucleic acid sequences that hybridize to the complement of SEQ ID NO:1-1786 and 3573-5358 under stringent hybridization conditions; nucleic acid sequences which are allelic variants or species homologues of any of the nucleic acid sequences recited above, or nucleic acid sequences that encode a peptide comprising a specific domain or truncation of the peptides encoded by SEQ ID NO:1-1786 and 3573-5358. A polynucleotide comprising a nucleotide sequence having at least 90% identity to an identifying sequence of SEQ ID NO:1-1786 and 3573-5358 or a degenerate variant or fragment thereof. The identifying sequence can be 100 base pairs in length.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO:1-1786 and 3573-5358. The sequence information can be a segment of any one of SEQ ID NO:1-1786 and 3573-5358 that uniquely identifies or represents the sequence information of SEQ ID NO:1-1786 and 3573-5358.

A collection as used in this application can be a collection of only one polynucleotide. The collection of sequence information or identifying information of each sequence can be provided on a nucleic acid array. In one embodiment, segments of sequence information is provided on a nucleic acid array to detect the polynucleotide that contains the segment. The array can be designed to detect full-match or mismatch to the polynucleotide that contains the segment. The collection can also be provided in a computer-readable format.

This invention also includes the reverse or direct complement of any of the nucleic acid sequences recited above; cloning or expression vectors containing the nucleic acid sequences; and host cells or organisms transformed with these expression vectors. Nucleic acid sequences (or their reverse or direct complements) according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology, such as use as hybridization probes, use as primers for PCR, use in an array, use in computer-readablemedia, use in sequencing

2

full-length genes, use for chromosome and gene mapping, use in the recombinant production of protein, and use in the generation of anti-sense DNA or RNA, their chemical analogs and the like.

In a preferred embodiment, the nucleic acid sequences of SEQ ID NO:1-1786 and 3573-5358 or novel segments or parts of the nucleic acids of the invention are used as primers in expression assays that are well known in the art. In a particularly preferred embodiment, the nucleic acid sequences of SEQ ID NO:1-1786 and 3573-5358 or novel segments or parts of the nucleic acids provided herein are used in diagnostics for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., Science 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

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The isolated polynucleotides of the invention include, but are not limited to, a polynucleotide comprising any one of the nucleotide sequences set forth in SEQ ID NO:1-1786 and 3573-5358; a polynucleotide comprising any of the full length protein coding sequences of SEQ ID NO:1-1786 and 3573-5358; and a polynucleotide comprising any of the nucleotide sequences of the mature protein coding sequences of SEQ ID NO:1-1786 and 3573-5358. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent hybridization conditions to (a) the complement of any one of the nucleotide sequences set forth in SEQ ID NO:1-1786 and 3573-5358; (b) a nucleotide sequence encoding any one of the amino acid sequences set forth in the Sequence Listing; (c) a polynucleotide which is an allelic variant of any polynucleotides recited above; (d) a polynucleotide which encodes a species homolog (e.g. orthologs) of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of any of the polypeptides comprising an amino acid sequence set forth in the Sequence Listing.

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising any of the amino acid sequences set forth in the Sequence Listing; or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides with biological activity that are encoded by (a) any of the polynucleotides having a nucleotide sequence set forth in SEQ ID NO:1-1786 and 3573-5358; or (b) polynucleotides that hybridize to the complement of the polynucleotides of (a) under stringent hybridization conditions. Biologically or immunologically active variants of any of the polypeptide sequences in the Sequence Listing, and "substantial equivalents" thereof (e.g., with at least about 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98% or 99% amino acid sequence identity) that preferably retain biological activity are also contemplated. The polypeptides of the invention may be wholly or partially chemically synthesized but are preferably produced by recombinant means using the genetically engineered cells (e.g. host cells) of the invention.

The invention also provides compositions comprising a polypeptide of the invention. Polypeptide compositions of the invention may further comprise an acceptable carrier, such as a hydrophilic, e.g., pharmaceutically acceptable, carrier.

The invention also provides host cells transformed or transfected with a polynucleotide of the invention.

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The invention also relates to methods for producing a polypeptide of the invention comprising growing a culture of the host cells of the invention in a suitable culture medium under conditions permitting expression of the desired polypeptide, and purifying the polypeptide from the culture or from the host cells. Preferred embodiments include those in which the protein produced by such process is a mature form of the protein.

Polynucleotides according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology. These techniques include use as hybridization probes, use as oligomers, or primers, for PCR, use for chromosome and gene mapping, use in the recombinant production of protein, and use in generation of anti-sense DNA or RNA, their chemical analogs and the like. For example, when the expression of an mRNA is largely restricted to a particular cell or tissue type, polynucleotides of the invention can be used as hybridization probes to detect the presence of the particular cell or tissue mRNA in a sample using, e.g., in situ hybridization.

In other exemplary embodiments, the polynucleotides are used in diagnostics as expressed sequence tags for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., Science 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The polypeptides according to the invention can be used in a variety of conventional procedures and methods that are currently applied to other proteins. For example, a polypeptide of the invention can be used to generate an antibody that specifically binds the polypeptide. Such antibodies, particularly monoclonal antibodies, are useful for detecting or quantitating the polypeptide in tissue. The polypeptides of the invention can also be used as molecular weight markers, and as a food supplement.

Methods are also provided for preventing, treating, or ameliorating a medical condition which comprises the step of administering to a mammalian subject a therapeutically effective amount of a composition comprising a polypeptide of the present invention and a pharmaceutically acceptable carrier.

In particular, the polypeptides and polynucleotides of the invention can be utilized, for example, in methods for the prevention and/or treatment of disorders involving aberrant protein expression or biological activity.

4

The present invention further relates to methods for detecting the presence of the polynucleotides or polypeptides of the invention in a sample. Such methods can, for example, be utilized as part of prognostic and diagnostic evaluation of disorders as recited herein and for the identification of subjects exhibiting a predisposition to such conditions. The invention provides a method for detecting the polynucleotides of the invention in a sample, comprising contacting the sample with a compound that binds to and forms a complex with the polynucleotide of interest for a period sufficient to form the complex and under conditions sufficient to form a complex and detecting the complex such that if a complex is detected, the polynucleotide of interest is detected. The invention also provides a method for detecting the polypeptides of the invention in a sample comprising contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex and detecting the formation of the complex such that if a complex is formed, the polypeptide is detected.

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The invention also provides kits comprising polynucleotide probes and/or monoclonal antibodies, and optionally quantitative standards, for carrying out methods of the invention. Furthermore, the invention provides methods for evaluating the efficacy of drugs, and monitoring the progress of patients, involved in clinical trials for the treatment of disorders as recited above.

The invention also provides methods for the identification of compounds that modulate (i.e., increase or decrease) the expression or activity of the polynucleotides and/or polypeptides of the invention. Such methods can be utilized, for example, for the identification of compounds that can ameliorate symptoms of disorders as recited herein. Such methods can include, but are not limited to, assays for identifying compounds and other substances that interact with (e.g., bind to) the polypeptides of the invention. The invention provides a method for identifying a compound that binds to the polypeptides of the invention comprising contacting the compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and detecting the complex by detecting the reporter gene sequence expression such that if expression of the reporter gene is detected the compound the binds to a polypeptide of the invention is identified.

The methods of the invention also provides methods for treatment which involve the administration of the polynucleotides or polypeptides of the invention to individuals exhibiting symptoms or tendencies. In addition, the invention encompasses methods for treating diseases or disorders as recited herein comprising administering compounds and other substances that modulate the overall activity of the target gene products. Compounds and other substances can

effect such modulation either on the level of target gene/protein expression or target protein activity.

The polypeptides of the present invention and the polynucleotides encoding them are also useful for the same functions known to one of skill in the art as the polypeptides and polynucleotides to which they have homology (set forth in Table 2); for which they have a signature region (as set forth in Table 3); or for which they have homology to a gene family (as set forth in Table 4). If no homology is set forth for a sequence, then the polypeptides and polynucleotides of the present invention are useful for a variety of applications, as described herein, including use in arrays for detection.

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4. DETAILED DESCRIPTION OF THE INVENTION

4.1 DEFINITIONS

It must be noted that as used herein and in the appended claims, the singular forms "a", "an" and "the" include plural references unless the context clearly dictates otherwise.

The term "active" refers to those forms of the polypeptide which retain the biologic and/or immunologic activities of any naturally occurring polypeptide. According to the invention, the terms "biologically active" or "biological activity" refer to a protein or peptide having structural, regulatory or biochemical functions of a naturally occurring molecule. Likewise "immunologically active" or "immunological activity" refers to the capability of the natural, recombinant or synthetic polypeptide to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies.

The term "activated cells" as used in this application are those cells which are engaged in extracellular or intracellular membrane trafficking, including the export of secretory or enzymatic molecules as part of a normal or disease process.

The terms "complementary" or "complementarity" refer to the natural binding of polynucleotides by base pairing. For example, the sequence 5'-AGT-3' binds to the complementary sequence 3'-TCA-5'. Complementarity between two single-stranded molecules may be "partial" such that only some of the nucleic acids bind or it may be "complete" such that total complementarity exists between the single stranded molecules. The degree of complementarity between the nucleic acid strands has significant effects on the efficiency and strength of the hybridization between the nucleic acid strands.

The term "embryonic stem cells (ES)" refers to a cell that can give rise to many differentiated cell types in an embryo or an adult, including the germ cells. The term "germ line stem cells (GSCs)" refers to stem cells derived from primordial stem cells that provide a steady

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and continuous source of germ cells for the production of gametes. The term "primordial germ cells (PGCs)" refers to a small population of cells set aside from other cell lineages particularly from the yolk sac, mesenteries, or gonadal ridges during embryogenesis that have the potential to differentiate into germ cells and other cells. PGCs are the source from which GSCs and ES cells are derived The PGCs, the GSCs and the ES cells are capable of self-renewal. Thus these cells not only populate the germ line and give rise to a plurality of terminally differentiated cells that comprise the adult specialized organs, but are able to regenerate themselves.

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The term "expression modulating fragment," EMF, means a series of nucleotides which modulates the expression of an operably linked ORF or another EMF.

As used herein, a sequence is said to "modulate the expression of an operably linked sequence" when the expression of the sequence is altered by the presence of the EMF. EMFs include, but are not limited to, promoters, and promoter modulating sequences (inducible elements). One class of EMFs are nucleic acid fragments which induce the expression of an operably linked ORF in response to a specific regulatory factor or physiological event.

The terms "nucleotide sequence" or "nucleic acid" or "polynucleotide" or "oligonculeotide" are used interchangeably and refer to a heteropolymer of nucleotides or the sequence of these nucleotides. These phrases also refer to DNA or RNA of genomic or synthetic origin which may be single-stranded or double-stranded and may represent the sense or the antisense strand, to peptide nucleic acid (PNA) or to any DNA-like or RNA-like material. In the sequences herein A is adenine, C is cytosine, T is thymine, G is guanine and N is A, C, G or T (U). It is contemplated that where the polynucleotide is RNA, the T (thymine) in the sequences provided herein is substituted with U (uracil). Generally, nucleic acid segments provided by this invention may be assembled from fragments of the genome and short oligonucleotide linkers, or from a series of oligonucleotides, or from individual nucleotides, to provide a synthetic nucleic acid which is capable of being expressed in a recombinant transcriptional unit comprising regulatory elements derived from a microbial or viral operon, or a eukaryotic gene.

The terms "oligonucleotide fragment" or a "polynucleotide fragment", "portion," or "segment" or "probe" or "primer" are used interchangeably and refer to a sequence of nucleotide residues which are at least about 5 nucleotides, more preferably at least about 7 nucleotides, more preferably at least about 9 nucleotides, more preferably at least about 11 nucleotides and most preferably at least about 17 nucleotides. The fragment is preferably less than about 500 nucleotides, preferably less than about 200 nucleotides, more preferably less than about 100 nucleotides, more preferably less than about 50 nucleotides and most preferably less than 30 nucleotides. Preferably the probe is from about 6 nucleotides to about 200 nucleotides,

preferably from about 15 to about 50 nucleotides, more preferably from about 17 to 30

nucleotides and most preferably from about 20 to 25 nucleotides. Preferably the fragments can be used in polymerase chain reaction (PCR), various hybridization procedures or microarray procedures to identify or amplify identical or related parts of mRNA or DNA molecules. A fragment or segment may uniquely identify each polynucleotide sequence of the present invention. Preferably the fragment comprises a sequence substantially similar to any one of SEQ ID NOs:1-20.

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Probes may, for example, be used to determine whether specific mRNA molecules are present in a cell or tissue or to isolate similar nucleic acid sequences from chromosomal DNA as described by Walsh et al. (Walsh, P.S. et al., 1992, PCR Methods Appl 1:241-250). They may be labeled by nick translation, Klenow fill-in reaction, PCR, or other methods well known in the art. Probes of the present invention, their preparation and/or labeling are elaborated in Sambrook, J. et al., 1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY; or Ausubel, F.M. et al., 1989, Current Protocols in Molecular Biology, John Wiley & Sons, New York NY, both of which are incorporated herein by reference in their entirety.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO:1-1786 and 3573-5358. The sequence information can be a segment of any one of SEQ ID NO:1-1786 and 3573-5358 that uniquely identifies or represents the sequence information of that sequence of SEQ ID NO:1-1786 and 3573-5358. One such segment can be a twenty-mer nucleic acid sequence because the probability that a twenty-mer is fully matched in the human genome is 1 in 300. In the human genome, there are three billion base pairs in one set of chromosomes. Because 4²⁰ possible twenty-mers exist, there are 300 times more twenty-mers than there are base pairs in a set of human chromosomes. Using the same analysis, the probability for a seventeen-mer to be fully matched in the human genome is approximately 1 in 5. When these segments are used in arrays for expression studies, fifteen-mer segments can be used. The probability that the fifteen-mer is fully matched in the expressed sequences is also approximately one in five because expressed sequences comprise less than approximately 5% of the entire genome sequence.

Similarly, when using sequence information for detecting a single mismatch, a segment can be a twenty-five mer. The probability that the twenty-five mer would appear in a human genome with a single mismatch is calculated by multiplying the probability for a full match $(1 \div 4^{25})$ times the increased probability for mismatch at each nucleotide position (3×25) . The probability that an eighteen mer with a single mismatch can be detected in an array for expression studies is approximately one in five. The probability that a twenty-mer with a single mismatch can be detected in a human genome is approximately one in five.

The term "open reading frame," ORF, means a series of nucleotide triplets coding for amino acids without any termination codons and is a sequence translatable into protein.

The terms "operably linked" or "operably associated" refer to functionally related nucleic acid sequences. For example, a promoter is operably associated or operably linked with a coding sequence if the promoter controls the transcription of the coding sequence. While operably linked nucleic acid sequences can be contiguous and in the same reading frame, certain genetic elements e.g. repressor genes are not contiguously linked to the coding sequence but still control transcription/translation of the coding sequence.

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The term "pluripotent" refers to the capability of a cell to differentiate into a number of differentiated cell types that are present in an adult organism. A pluripotent cell is restricted in its differentiation capability in comparison to a totipotent cell.

The terms "polypeptide" or "peptide" or "amino acid sequence" refer to an oligopeptide, peptide, polypeptide or protein sequence or fragment thereof and to naturally occurring or synthetic molecules. A polypeptide "fragment," "portion," or "segment" is a stretch of amino acid residues of at least about 5 amino acids, preferably at least about 7 amino acids, more preferably at least about 9 amino acids and most preferably at least about 17 or more amino acids. The peptide preferably is not greater than about 200 amino acids, more preferably less than 150 amino acids and most preferably less than 100 amino acids. Preferably the peptide is from about 5 to about 200 amino acids. To be active, any polypeptide must have sufficient length to display biological and/or immunological activity.

The term "naturally occurring polypeptide" refers to polypeptides produced by cells that have not been genetically engineered and specifically contemplates various polypeptides arising from post-translational modifications of the polypeptide including, but not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation and acylation.

The term "translated protein coding portion" means a sequence which encodes for the full length protein which may include any leader sequence or any processing sequence.

The term "mature protein coding sequence" means a sequence which encodes a peptide or protein without a signal or leader sequence. The "mature protein portion" means that portion of the protein which does not include a signal or leader sequence. The peptide may have been produced by processing in the cell which removes any leader/signal sequence. The mature protein portion may or may not include the initial methionine residue. The methionine residue may be removed from the protein during processing in the cell. The peptide may be produced synthetically or the protein may have been produced using a polynucleotide only encoding for the mature protein coding sequence.

The term "derivative" refers to polypeptides chemically modified by such techniques as ubiquitination, labeling (e.g., with radionuclides or various enzymes), covalent polymer attachment such as pegylation (derivatization with polyethylene glycol) and insertion or substitution by chemical synthesis of amino acids such as ornithine, which do not normally occur in human proteins.

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The term "variant" (or "analog") refers to any polypeptide differing from naturally occurring polypeptides by amino acid insertions, deletions, and substitutions, created using, e.g., recombinant DNA techniques. Guidance in determining which amino acid residues may be replaced, added or deleted without abolishing activities of interest, may be found by comparing the sequence of the particular polypeptide with that of homologous peptides and minimizing the number of amino acid sequence changes made in regions of high homology (conserved regions) or by replacing amino acids with consensus sequence.

Alternatively, recombinant variants encoding these same or similar polypeptides may be synthesized or selected by making use of the "redundancy" in the genetic code. Various codon substitutions, such as the silent changes which produce various restriction sites, may be introduced to optimize cloning into a plasmid or viral vector or expression in a particular prokaryotic or eukaryotic system. Mutations in the polynucleotide sequence may be reflected in the polypeptide or domains of other peptides added to the polypeptide to modify the properties of any part of the polypeptide, to change characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate.

Preferably, amino acid "substitutions" are the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, i.e., conservative amino acid replacements. "Conservative" amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues involved. For example, nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine; polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine; positively charged (basic) amino acids include arginine, lysine, and histidine; and negatively charged (acidic) amino acids include aspartic acid and glutamic acid. "Insertions" or "deletions" are preferably in the range of about 1 to 20 amino acids, more preferably 1 to 10 amino acids. The variation allowed may be experimentally determined by systematically making insertions, deletions, or substitutions of amino acids in a polypeptide molecule using recombinant DNA techniques and assaying the resulting recombinant variants for activity.

Alternatively, where alteration of function is desired, insertions, deletions or non-conservative alterations can be engineered to produce altered polypeptides. Such alterations

can, for example, alter one or more of the biological functions or biochemical characteristics of the polypeptides of the invention. For example, such alterations may change polypeptide characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate. Further, such alterations can be selected so as to generate polypeptides that are better suited for expression, scale up and the like in the host cells chosen for expression. For example, cysteine residues can be deleted or substituted with another amino acid residue in order to eliminate disulfide bridges.

The terms "purified" or "substantially purified" as used herein denotes that the indicated nucleic acid or polypeptide is present in the substantial absence of other biological macromolecules, e.g., polynucleotides, proteins, and the like. In one embodiment, the polynucleotide or polypeptide is purified such that it constitutes at least 95% by weight, more preferably at least 99% by weight, of the indicated biological macromolecules present (but water, buffers, and other small molecules, especially molecules having a molecular weight of less than 1000 daltons, can be present).

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The term "isolated" as used herein refers to a nucleic acid or polypeptide separated from at least one other component (e.g., nucleic acid or polypeptide) present with the nucleic acid or polypeptide in its natural source. In one embodiment, the nucleic acid or polypeptide is found in the presence of (if anything) only a solvent, buffer, ion, or other component normally present in a solution of the same. The terms "isolated" and "purified" do not encompass nucleic acids or polypeptides present in their natural source.

The term "recombinant," when used herein to refer to a polypeptide or protein, means that a polypeptide or protein is derived from recombinant (e.g., microbial, insect, or mammalian) expression systems. "Microbial" refers to recombinant polypeptides or proteins made in bacterial or fungal (e.g., yeast) expression systems. As a product, "recombinant microbial" defines a polypeptide or protein essentially free of native endogenous substances and unaccompanied by associated native glycosylation. Polypeptides or proteins expressed in most bacterial cultures, e.g., E. coli, will be free of glycosylation modifications; polypeptides or proteins expressed in yeast will have a glycosylation pattern in general different from those expressed in mammalian cells.

The term "recombinant expression vehicle or vector" refers to a plasmid or phage or virus or vector, for expressing a polypeptide from a DNA (RNA) sequence. An expression vehicle can comprise a transcriptional unit comprising an assembly of (1) a genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers, (2) a structural or coding sequence which is transcribed into mRNA and translated into protein, and (3) appropriate transcription initiation and termination sequences. Structural units intended for use

in yeast or eukaryotic expression systems preferably include a leader sequence enabling extracellular secretion of translated protein by a host cell. Alternatively, where recombinant protein is expressed without a leader or transport sequence, it may include an amino terminal methionine residue. This residue may or may not be subsequently cleaved from the expressed recombinant protein to provide a final product.

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The term "recombinant expression system" means host cells which have stably integrated a recombinant transcriptional unit into chromosomal DNA or carry the recombinant transcriptional unit extrachromosomally. Recombinant expression systems as defined herein will express heterologous polypeptides or proteins upon induction of the regulatory elements linked to the DNA segment or synthetic gene to be expressed. This term also means host cells which have stably integrated a recombinant genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers. Recombinant expression systems as defined herein will express polypeptides or proteins endogenous to the cell upon induction of the regulatory elements linked to the endogenous DNA segment or gene to be expressed. The cells can be prokaryotic or eukaryotic.

The term "secreted" includes a protein that is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence when it is expressed in a suitable host cell. "Secreted" proteins include without limitation proteins secreted wholly (e.g., soluble proteins) or partially (e.g., receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins that are transported across the membrane of the endoplasmic reticulum. "Secreted" proteins are also intended to include proteins containing non-typical signal sequences (e.g. Interleukin-1 Beta, see Krasney, P.A. and Young, P.R. (1992) Cytokine 4(2):134 -143) and factors released from damaged cells (e.g. Interleukin-1 Receptor Antagonist, see Arend, W.P. et. al. (1998) Annu. Rev. Immunol. 16:27-55)

Where desired, an expression vector may be designed to contain a "signal or leader sequence" which will direct the polypeptide through the membrane of a cell. Such a sequence may be naturally present on the polypeptides of the present invention or provided from heterologous protein sources by recombinant DNA techniques.

The term "stringent" is used to refer to conditions that are commonly understood in the art as stringent. Stringent conditions can include highly stringent conditions (i.e., hybridization to filter-bound DNA in 0.5 M NaHPO₄, 7% sodium dodecyl sulfate (SDS), 1 mM EDTA at 65°C, and washing in 0.1X SSC/0.1% SDS at 68°C), and moderately stringent conditions (i.e., washing in 0.2X SSC/0.1% SDS at 42°C). Other exemplary hybridization conditions are described herein in the examples.

In instances of hybridization of deoxyoligonucleotides, additional exemplary stringent hybridization conditions include washing in 6X SSC/0.05% sodium pyrophosphate at 37°C (for 14-base oligonucleotides), 48°C (for 17-base oligos), 55°C (for 20-base oligonucleotides), and 60°C (for 23-base oligonucleotides).

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As used herein, "substantially equivalent" can refer both to nucleotide and amino acid sequences, for example a mutant sequence, that varies from a reference sequence by one or more substitutions, deletions, or additions, the net effect of which does not result in an adverse functional dissimilarity between the reference and subject sequences. Typically, such a substantially equivalent sequence varies from one of those listed herein by no more than about 35% (i.e., the number of individual residue substitutions, additions, and/or deletions in a substantially equivalent sequence, as compared to the corresponding reference sequence, divided by the total number of residues in the substantially equivalent sequence is about 0.35 or less). Such a sequence is said to have 65% sequence identity to the listed sequence. In one embodiment, a substantially equivalent, e.g., mutant, sequence of the invention varies from a listed sequence by no more than 30% (70% sequence identity); in a variation of this embodiment, by no more than 25% (75% sequence identity); and in a further variation of this embodiment, by no more than 20% (80% sequence identity) and in a further variation of this embodiment, by no more than 10% (90% sequence identity) and in a further variation of this embodiment, by no more that 5% (95% sequence identity). Substantially equivalent, e.g., mutant, amino acid sequences according to the invention preferably have at least 80% sequence identity with a listed amino acid sequence, more preferably at least 90% sequence identity. Substantially equivalent nucleotide sequences of the invention can have lower percent sequence identities, taking into account, for example, the redundancy or degeneracy of the genetic code. Preferably, nucleotide sequence has at least about 65% identity, more preferably at least about 75% identity, and most preferably at least about 95% identity. For the purposes of the present invention, sequences having substantially equivalent biological activity and substantially equivalent expression characteristics are considered substantially equivalent. For the purposes of determining equivalence, truncation of the mature sequence (e.g., via a mutation which creates a spurious stop codon) should be disregarded. Sequence identity may be determined, e.g., using the Jotun Hein method (Hein, J. (1990) Methods Enzymol. 183:626-645). Identity between sequences can also be determined by other methods known in the art, e.g. by varying hybridization conditions.

The term "totipotent" refers to the capability of a cell to differentiate into all of the cell types of an adult organism.

The term "transformation" means introducing DNA into a suitable host cell so that the DNA is replicable, either as an extrachromosomal element, or by chromosomal integration. The

term "transfection" refers to the taking up of an expression vector by a suitable host cell, whether or not any coding sequences are in fact expressed. The term "infection" refers to the introduction of nucleic acids into a suitable host cell by use of a virus or viral vector.

As used herein, an "uptake modulating fragment," UMF, means a series of nucleotides which mediate the uptake of a linked DNA fragment into a cell. UMFs can be readily identified using known UMFs as a target sequence or target motif with the computer-based systems described below. The presence and activity of a UMF can be confirmed by attaching the suspected UMF to a marker sequence. The resulting nucleic acid molecule is then incubated with an appropriate host under appropriate conditions and the uptake of the marker sequence is determined. As described above, a UMF will increase the frequency of uptake of a linked marker sequence.

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Each of the above terms is meant to encompass all that is described for each, unless the context dictates otherwise.

4.2 NUCLEIC ACIDS OF THE INVENTION

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Nucleotide sequences of the invention are set forth in the Sequence Listing.

The isolated polynucleotides of the invention include a polynucleotide comprising the nucleotide sequences of SEQ ID NO:1-1786 and 3573-5358; a polynucleotide encoding any one of the peptide sequences of SEQ ID NO:1787-3572 and 5359-7144; and a polynucleotide comprising the nucleotide sequence encoding the mature protein coding sequence of the polypeptides of any one of SEQ ID NO:1787-3572 and 5359-7144. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent conditions to (a) the complement of any of the nucleotides sequences of SEQ ID NO:1-1786 and 3573-5358; (b) nucleotide sequences encoding any one of the amino acid sequences set forth in the Sequence Listing; (c) a polynucleotide which is an allelic variant of any polynucleotide recited above; (d) a polynucleotide which encodes a species homolog of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of the polypeptides of SEQ ID NO:1787-3572 and 5359-7144. Domains of interest may depend on the nature of the encoded polypeptide; e.g., domains in receptor-like polypeptides include ligand-binding, extracellular, transmembrane, or cytoplasmic domains, or combinations thereof; domains in immunoglobulin-like proteins include the variable immunoglobulin-like domains; domains in enzyme-like polypeptides include catalytic and substrate binding domains; and domains in ligand polypeptides include receptor-binding domains.

The polynucleotides of the invention include naturally occurring or wholly or partially synthetic DNA, e.g., cDNA and genomic DNA, and RNA, e.g., mRNA. The polynucleotides may include all of the coding region of the cDNA or may represent a portion of the coding region of the cDNA.

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The present invention also provides genes corresponding to the cDNA sequences disclosed herein. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. Further 5' and 3' sequence can be obtained using methods known in the art. For example, full length cDNA or genomic DNA that corresponds to any of the polynucleotides of SEQ ID NO:1-1786 and 3573-5358 can be obtained by screening appropriate cDNA or genomic DNA libraries under suitable hybridization conditions using any of the polynucleotides of SEQ ID NO:1-1786 and 3573-5358 or a portion thereof as a probe. Alternatively, the polynucleotides of SEQ ID NO:1-1786 and 3573-5358 may be used as the basis for suitable primer(s) that allow identification and/or amplification of genes in appropriate genomic DNA or cDNA libraries.

The nucleic acid sequences of the invention can be assembled from ESTs and sequences (including cDNA and genomic sequences) obtained from one or more public databases, such as dbEST, gbpri, and UniGene. The EST sequences can provide identifying sequence information, representative fragment or segment information, or novel segment information for the full-length gene.

The polynucleotides of the invention also provide polynucleotides including nucleotide sequences that are substantially equivalent to the polynucleotides recited above. Polynucleotides according to the invention can have, e.g., at least about 65%, at least about 70%, at least about 75%, at least about 80%, more typically at least about 90%, and even more typically at least about 95%, sequence identity to a polynucleotide recited above.

Included within the scope of the nucleic acid sequences of the invention are nucleic acid sequence fragments that hybridize under stringent conditions to any of the nucleotide sequences of SEQ ID NO:1-1786 and 3573-5358, or complements thereof, which fragment is greater than about 5 nucleotides, preferably 7 nucleotides, more preferably greater than 9 nucleotides and most preferably greater than 17 nucleotides. Fragments of, e.g. 15, 17, or 20 nucleotides or more that are selective for (i.e. specifically hybridize to any one of the polynucleotides of the invention) are contemplated. Probes capable of specifically hybridizing to a polynucleotide can differentiate polynucleotide sequences of the invention from other polynucleotide sequences in

the same family of genes or can differentiate human genes from genes of other species, and are preferably based on unique nucleotide sequences.

The sequences falling within the scope of the present invention are not limited to these specific sequences, but also include allelic and species variations thereof. Allelic and species variations can be routinely determined by comparing the sequence provided SEQ ID NO:1-1786 and 3573-5358, a representative fragment thereof, or a nucleotide sequence at least 90% identical, preferably 95% identical, to SEQ ID NO:1-1786 and 3573-5358 with a sequence from another isolate of the same species. Furthermore, to accommodate codon variability, the invention includes nucleic acid molecules coding for the same amino acid sequences as do the specific ORFs disclosed herein. In other words, in the coding region of an ORF, substitution of one codon for another codon that encodes the same amino acid is expressly contemplated.

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The nearest neighbor or homology result for the nucleic acids of the present invention, including SEQ ID NO:1-1786 and 3573-5358, can be obtained by searching a database using an algorithm or a program. Preferably, a BLAST which stands for Basic Local Alignment Search Tool is used to search for local sequence alignments (Altshul, S.F. J Mol. Evol. 36 290-300 (1993) and Altschul S.F. et al. J. Mol. Biol. 21:403-410 (1990)). Alternatively a FASTA version 3 search against Genpept, using Fastxy algorithm.

Species homologs (or orthologs) of the disclosed polynucleotides and proteins are also provided by the present invention. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous or related to that encoded by the polynucleotides.

The nucleic acid sequences of the invention are further directed to sequences which encode variants of the described nucleic acids. These amino acid sequence variants may be prepared by methods known in the art by introducing appropriate nucleotide changes into a native or variant polynucleotide. There are two variables in the construction of amino acid sequence variants: the location of the mutation and the nature of the mutation. Nucleic acids encoding the amino acid sequence variants are preferably constructed by mutating the polynucleotide to encode an amino acid sequence that does not occur in nature. These nucleic acid alterations can be made at sites that differ in the nucleic acids from different species (variable positions) or in highly conserved regions (constant regions). Sites at such locations will typically be modified in series, e.g., by substituting first with conservative choices (e.g.,

hydrophobic amino acid to a different hydrophobic amino acid) and then with more distant choices (e.g., hydrophobic amino acid to a charged amino acid), and then deletions or insertions may be made at the target site. Amino acid sequence deletions generally range from about 1 to 30 residues, preferably about 1 to 10 residues, and are typically contiguous. Amino acid insertions include amino- and/or carboxyl-terminal fusions ranging in length from one to one hundred or more residues, as well as intrasequence insertions of single or multiple amino acid residues. Intrasequence insertions may range generally from about 1 to 10 amino residues, preferably from 1 to 5 residues. Examples of terminal insertions include the heterologous signal sequences necessary for secretion or for intracellular targeting in different host cells and sequences such as FLAG or poly-histidine sequences useful for purifying the expressed protein.

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In a preferred method, polynucleotides encoding the novel amino acid sequences are changed via site-directed mutagenesis. This method uses oligonucleotide sequences to alter a polynucleotide to encode the desired amino acid variant, as well as sufficient adjacent nucleotides on both sides of the changed amino acid to form a stable duplex on either side of the site of being changed. In general, the techniques of site-directed mutagenesis are well known to those of skill in the art and this technique is exemplified by publications such as, Edelman et al., DNA 2:183 (1983). A versatile and efficient method for producing site-specific changes in a polynucleotide sequence was published by Zoller and Smith, Nucleic Acids Res. 10:6487-6500 (1982). PCR may also be used to create amino acid sequence variants of the novel nucleic acids. When small amounts of template DNA are used as starting material, primer(s) that differs slightly in sequence from the corresponding region in the template DNA can generate the desired amino acid variant. PCR amplification results in a population of product DNA fragments that differ from the polynucleotide template encoding the polypeptide at the position specified by the primer. The product DNA fragments replace the corresponding region in the plasmid and this gives a polynucleotide encoding the desired amino acid variant.

A further technique for generating amino acid variants is the cassette mutagenesis technique described in Wells et al., *Gene* 34:315 (1985); and other mutagenesis techniques well known in the art, such as, for example, the techniques in Sambrook et al., supra, and *Current Protocols in Molecular Biology*, Ausubel et al. Due to the inherent degeneracy of the genetic code, other DNA sequences which encode substantially the same or a functionally equivalent amino acid sequence may be used in the practice of the invention for the cloning and expression of these novel nucleic acids. Such DNA sequences include those which are capable of hybridizing to the appropriate novel nucleic acid sequence under stringent conditions.

Polynucleotides encoding preferred polypeptide truncations of the invention can be used to generate polynucleotides encoding chimeric or fusion proteins comprising one or more domains of the invention and heterologous protein sequences.

The polynucleotides of the invention additionally include the complement of any of the polynucleotides recited above. The polynucleotide can be DNA (genomic, cDNA, amplified, or synthetic) or RNA. Methods and algorithms for obtaining such polynucleotides are well known to those of skill in the art and can include, for example, methods for determining hybridization conditions that can routinely isolate polynucleotides of the desired sequence identities.

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In accordance with the invention, polynucleotide sequences comprising the mature protein coding sequences corresponding to any one of SEQ ID NO:1-1786 and 3573-5358, or functional equivalents thereof, may be used to generate recombinant DNA molecules that direct the expression of that nucleic acid, or a functional equivalent thereof, in appropriate host cells. Also included are the cDNA inserts of any of the clones identified herein.

A polynucleotide according to the invention can be joined to any of a variety of other 15 nucleotide sequences by well-established recombinant DNA techniques (see Sambrook J et al. (1989) Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY). Useful nucleotide sequences for joining to polynucleotides include an assortment of vectors, e.g., plasmids, cosmids, lambda phage derivatives, phagemids, and the like, that are well known in the art. Accordingly, the invention also provides a vector including a polynucleotide of the 20 invention and a host cell containing the polynucleotide. In general, the vector contains an origin of replication functional in at least one organism, convenient restriction endonuclease sites, and a selectable marker for the host cell. Vectors according to the invention include expression vectors, replication vectors, probe generation vectors, and sequencing vectors. A host cell according to the invention can be a prokaryotic or eukaryotic cell and can be a unicellular organism or part of a multicellular organism.

The present invention further provides recombinant constructs comprising a nucleic acid having any of the nucleotide sequences of SEQ ID NO:1-1786 and 3573-5358 or a fragment thereof or any other polynucleotides of the invention. In one embodiment, the recombinant constructs of the present invention comprise a vector, such as a plasmid or viral vector, into which a nucleic acid having any of the nucleotide sequences of SEQ ID NO:1-1786 and 3573-5358 or a fragment thereof is inserted, in a forward or reverse orientation. In the case of a vector comprising one of the ORFs of the present invention, the vector may further comprise regulatory sequences, including for example, a promoter, operably linked to the ORF. Large numbers of suitable vectors and promoters are known to those of skill in the art and are commercially available for generating the recombinant constructs of the present invention. The following

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vectors are provided by way of example. Bacterial: pBs, phagescript, PsiX174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene); pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia). Eukaryotic: pWLneo, pSV2cat, pOG44, PXTI, pSG (Stratagene) pSVK3, pBPV, pMSG, pSVL (Pharmacia).

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The isolated polynucleotide of the invention may be operably linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman et al., Nucleic Acids Res. 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, Methods in Enzymology 185, 537-566 (1990). As defined herein "operably linked" means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. Two appropriate vectors are pKK232-8 and pCM7. Particular named bacterial promoters include lacI, lacZ, T3, T7, gpt, lambda PR, and trc. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art. Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, e.g., the ampicillin resistance gene of E. coli and S. cerevisiae TRP1 gene, and a promoter derived from a highly-expressed gene to direct transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK), a-factor, acid phosphatase, or heat shock proteins, among others. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an amino terminal identification peptide imparting desired characteristics, e.g., stabilization or simplified purification of expressed recombinant product. 30 Useful expression vectors for bacterial use are constructed by inserting a structural DNA sequence encoding a desired protein together with suitable translation initiation and termination signals in operable reading phase with a functional promoter. The vector will comprise one or more phenotypic selectable markers and an origin of replication to ensure maintenance of the vector and to, if desirable, provide amplification within the host. Suitable prokaryotic hosts for 35

transformation include *E. coli*, *Bacillus subtilis*, *Salmonella typhimurium* and various species within the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*, although others may also be employed as a matter of choice.

As a representative but non-limiting example, useful expression vectors for bacterial use can comprise a selectable marker and bacterial origin of replication derived from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example, pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and GEM 1 (Promega Biotech, Madison, WI, USA). These pBR322 "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed. Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter is induced or derepressed by appropriate means (e.g., temperature shift or chemical induction) and cells are cultured for an additional period. Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification.

Polynucleotides of the invention can also be used to induce immune responses. For example, as described in Fan et al., *Nat. Biotech.* 17:870-872 (1999), incorporated herein by reference, nucleic acid sequences encoding a polypeptide may be used to generate antibodies against the encoded polypeptide following topical administration of naked plasmid DNA or following injection, and preferably intramuscular injection of the DNA. The nucleic acid sequences are preferably inserted in a recombinant expression vector and may be in the form of naked DNA.

4.3 ANTISENSE

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Another aspect of the invention pertains to isolated antisense nucleic acid molecules that are hybridizable to or complementary to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:1-1786 and 3573-5358, or fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein, e.g., complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. In specific aspects, antisense nucleic acid molecules are provided that comprise a sequence complementary to at least about 10, 25, 50, 100, 250 or 500 nucleotides or an entire coding strand, or to only a portion thereof. Nucleic acid molecules encoding fragments, homologs, derivatives and analogs of a protein of any of SEQ ID NO:1787-3572 and 5359-7144 or antisense nucleic acids complementary to a nucleic acid sequence of SEQ ID NO:1-1786 and 3573-5358 are additionally provided.

In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence of the invention. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues. In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence of the invention. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (i.e., also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding a nucleic acid disclosed herein (e.g., SEQ ID NO:1-1786 and 3573-5358, antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick or Hoogsteen base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of a mRNA, but more preferably is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of a mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of a mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis or enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (e.g., an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, e.g., phosphorothioate derivatives and acridine substituted nucleotides can be used.

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Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxylmethyl) uracil, 5-carboxymethylaminomethyl-25 2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, 30 queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (i.e., RNA transcribed from the 35

inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

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The antisense nucleic acid molecules of the invention are typically administered to a subject or generated in situ such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a protein according to the invention to thereby inhibit expression of the protein, e.g., by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule that binds to DNA duplexes, through specific interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface, e.g., by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an α-anomeric nucleic acid molecule. An α-anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β-units, the strands run parallel to each other (Gaultier et al. (1987) Nucleic Acids Res 15: 6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue et al. (1987) Nucleic Acids Res 15: 6131-6148) or a chimeric RNA -DNA analogue (Inoue et al. (1987) FEBS Lett 215: 327-330).

4.4 RIBOZYMES AND PNA MOIETIES

In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity that are capable of cleaving a single-stranded nucleic acid, such as a mRNA, to which they have a complementary region. Thus, ribozymes (e.g., hammerhead ribozymes (described in Haselhoff and Gerlach (1988) Nature 334:585-591)) can be used to catalytically cleave a mRNA transcripts to thereby inhibit translation of a mRNA. A ribozyme having specificity for a nucleic acid of the invention can be designed based upon the nucleotide sequence of a DNA disclosed herein (i.e., SEQ ID NO:1-1786 and 3573-5358). For example, a derivative of a Tetrahymena L-19 IVS RNA can be

constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in a SECX-encoding mRNA. See, e.g., Cech et al. U.S. Pat. No. 4,987,071; and Cech et al. U.S. Pat. No. 5,116,742. Alternatively, SECX mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, e.g., Bartel et al., (1993) Science 261:1411-1418.

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Alternatively, gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region (e.g., promoter and/or enhancers) to form triple helical structures that prevent transcription of the gene in target cells. See generally, Helene. (1991) Anticancer Drug Des. 6: 569-84; Helene. et al. (1992) Ann. N.Y. Acad. Sci. 660:27-36; and Maher (1992) Bioassays 14: 807-15.

In various embodiments, the nucleic acids of the invention can be modified at the base moiety, sugar moiety or phosphate backbone to improve, e.g., the stability, hybridization, or solubility of the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids (see Hyrup et al. (1996) Bioorg Med Chem 4: 5-23). As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics, e.g., DNA mimics, in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of PNAs has been shown to allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid phase peptide synthesis protocols as described in Hyrup et al. (1996) above, Perry-O'Keefe et al. (1996) PNAS 93: 14670-675.

PNAs of the invention can be used in therapeutic and diagnostic applications. For example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, e.g., inducing transcription or translation arrest or inhibiting replication. PNAs of the invention can also be used, e.g., in the analysis of single base pair mutations in a gene by, e.g., PNA directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, e.g., S1 nucleases (Hyrup B. (1996) above); or as probes or primers for DNA sequence and hybridization (Hyrup et al. (1996), above; Perry-O'Keefe (1996), above).

In another embodiment, PNAs of the invention can be modified, e.g., to enhance their stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by the formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug delivery known in the art. For example, PNA-DNA chimeras can be generated that may combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes, e.g., RNase H and DNA polymerases, to interact with the DNA portion while the PNA

portion would provide high binding affinity and specificity. PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleobases, and orientation (Hyrup (1996) above). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup (1996) above and Finn et al. (1996) Nucl Acids Res 24: 3357-63. For example, a DNA chain can be synthesized on a solid support using standard phosphoramidite coupling chemistry, and modified nucleoside analogs, e.g., 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite, can be used between the PNA and the 5' end of DNA (Mag et al. (1989) Nucl Acid Res 17: 5973-88). PNA monomers are then coupled in a stepwise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment (Finn et al. (1996) above). Alternatively, chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment. See, Petersen et al. (1975) Bioorg Med Chem Lett 5: 1119-11124.

In other embodiments, the oligonucleotide may include other appended groups such as peptides (e.g., for targeting host cell receptors in vivo), or agents facilitating transport across the cell membrane (see, e.g., Letsinger et al., 1989, Proc. Natl. Acad. Sci. U.S.A. 86:6553-6556; Lemaitre et al., 1987, Proc. Natl. Acad. Sci. 84:648-652; PCT Publication No. W088/09810) or the blood-brain barrier (see, e.g., PCT Publication No. W089/10134). In addition, oligonucleotides can be modified with hybridization triggered cleavage agents (See, e.g., Krol et al., 1988, BioTechniques 6:958-976) or intercalating agents. (See, e.g., Zon, 1988, Pharm. Res. 5: 539-549). To this end, the oligonucleotide may be conjugated to another molecule, e.g., a peptide, a hybridization triggered cross-linking agent, a transport agent, a hybridization-triggered cleavage agent, etc.

4.5 HOSTS

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The present invention further provides host cells genetically engineered to contain the polynucleotides of the invention. For example, such host cells may contain nucleic acids of the invention introduced into the host cell using known transformation, transfection or infection methods. The present invention still further provides host cells genetically engineered to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in the cell.

Knowledge of nucleic acid sequences allows for modification of cells to permit, or increase, expression of endogenous polypeptide. Cells can be modified (e.g., by homologous recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express

the polypeptide at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the encoding sequences. See, for example, PCT International Publication No. WO94/12650, PCT International Publication No. WO92/20808, and PCT International Publication No. WO91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (e.g., ada, dhfr, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the coding sequence, amplification of the marker DNA by standard selection methods results in coamplification of the desired protein coding sequences in the cells.

The host cell can be a higher eukaryotic host cell, such as a mammalian cell, a lower eukaryotic host cell, such as a yeast cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Introduction of the recombinant construct into the host cell can be effected by calcium phosphate transfection, DEAE, dextran mediated transfection, or electroporation (Davis, L. et al., Basic Methods in Molecular Biology (1986)). The host cells containing one of the polynucleotides of the invention, can be used in conventional manners to produce the gene product encoded by the isolated fragment (in the case of an ORF) or can be used to produce a heterologous protein under the control of the EMF.

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Any host/vector system can be used to express one or more of the ORFs of the present invention. These include, but are not limited to, eukaryotic hosts such as HeLa cells, Cv-1 cell, COS cells, 293 cells, and Sf9 cells, as well as prokaryotic host such as E. coli and B. subtilis. The most preferred cells are those which do not normally express the particular polypeptide or protein or which expresses the polypeptide or protein at low natural level. Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook, et al., in Molecular Cloning: A Laboratory Manual, Second Edition, Cold Spring Harbor, New York (1989), the disclosure of which is hereby incorporated by reference.

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney 30 fibroblasts, described by Gluzman, Cell 23:175 (1981). Other cell lines capable of expressing a compatible vector are, for example, the C127, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3 cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from in vitro culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK,

HL-60, U937, HaK or Jurkat cells. Mammalian expression vectors will comprise an origin of replication, a suitable promoter and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking nontranscribed sequences. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early promoter, enhancer, splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements. Recombinant polypeptides and proteins produced in bacterial culture are usually isolated by initial extraction from cell pellets, followed by one or more salting-out, aqueous ion exchange or size exclusion chromatography steps. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps. Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents.

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Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or insects or in prokaryotes such as bacteria. Potentially suitable yeast strains include Saccharomyces cerevisiae, Schizosaccharomyces pombe, Kluyveromyces strains, Candida, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include Escherichia coli, Bacillus subtilis, Salmonella typhimurium, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequence include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the

protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

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herein in its entirety.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, e.g., inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the host cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference

4.6 POLYPEPTIDES OF THE INVENTION

The isolated polypeptides of the invention include, but are not limited to, a polypeptide

comprising: the amino acid sequences set forth as any one of SEQ ID NO:1787-3572 and 5359
7144 or an amino acid sequence encoded by any one of the nucleotide sequences SEQ ID NO:1
1786 and 3573-5358 or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides preferably with biological or immunological activity that are encoded by: (a) a polynucleotide having any one of the nucleotide sequences set forth in SEQ ID

NO:1-1786 and 3573-5358 or (b) polynucleotides encoding any one of the amino acid sequences

set forth as SEQ ID NO:1787-3572 and 5359-7144 or (c) polynucleotides that hybridize to the complement of the polynucleotides of either (a) or (b) under stringent hybridization conditions. The invention also provides biologically active or immunologically active variants of any of the amino acid sequences set forth as SEQ ID NO:1787-3572 and 5359-7144 or the corresponding full length or mature protein; and "substantial equivalents" thereof (e.g., with at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, typically at least about 95%, more typically at least about 98%, or most typically at least about 99% amino acid identity) that retain biological activity. Polypeptides encoded by allelic variants may have a similar, increased, or decreased activity compared to polypeptides comprising SEQ ID NO:1787-3572 and 5359-7144.

Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, as described in H. U. Saragovi, et al., Bio/Technology 10, 773-778 (1992) and in R. S. McDowell, et al., J. Amer. Chem. Soc. 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites.

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The present invention also provides both full-length and mature forms (for example, without a signal sequence or precursor sequence) of the disclosed proteins. The protein coding sequence is identified in the sequence listing by translation of the disclosed nucleotide sequences. The mature form of such protein may be obtained by expression of a full-length polynucleotide in a suitable mammalian cell or other host cell. The sequence of the mature form of the protein is also determinable from the amino acid sequence of the full-length form. Where proteins of the present invention are membrane bound, soluble forms of the proteins are also provided. In such forms, part or all of the regions causing the proteins to be membrane bound are deleted so that the proteins are fully secreted from the cell in which they are expressed.

Protein compositions of the present invention may further comprise an acceptable carrier, such as a hydrophilic, e.g., pharmaceutically acceptable, carrier.

The present invention further provides isolated polypeptides encoded by the nucleic acid fragments of the present invention or by degenerate variants of the nucleic acid fragments of the present invention. By "degenerate variant" is intended nucleotide fragments which differ from a nucleic acid fragment of the present invention (e.g., an ORF) by nucleotide sequence but, due to the degeneracy of the genetic code, encode an identical polypeptide sequence. Preferred nucleic acid fragments of the present invention are the ORFs that encode proteins.

A variety of methodologies known in the art can be utilized to obtain any one of the isolated polypeptides or proteins of the present invention. At the simplest level, the amino acid sequence can be synthesized using commercially available peptide synthesizers. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. This technique is particularly useful in producing small peptides and fragments of larger polypeptides. Fragments are useful, for example, in generating antibodies against the native polypeptide. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

The polypeptides and proteins of the present invention can alternatively be purified from cells which have been altered to express the desired polypeptide or protein. As used herein, a cell is said to be altered to express a desired polypeptide or protein when the cell, through genetic manipulation, is made to produce a polypeptide or protein which it normally does not produce or which the cell normally produces at a lower level. One skilled in the art can readily adapt procedures for introducing and expressing either recombinant or synthetic sequences into eukaryotic or prokaryotic cells in order to generate a cell which produces one of the polypeptides or proteins of the present invention.

The invention also relates to methods for producing a polypeptide comprising growing a culture of host cells of the invention in a suitable culture medium, and purifying the protein from the cells or the culture in which the cells are grown. For example, the methods of the invention include a process for producing a polypeptide in which a host cell containing a suitable expression vector that includes a polynucleotide of the invention is cultured under conditions that allow expression of the encoded polypeptide. The polypeptide can be recovered from the culture, conveniently from the culture medium, or from a lysate prepared from the host cells and further purified. Preferred embodiments include those in which the protein produced by such process is a full length or mature form of the protein.

In an alternative method, the polypeptide or protein is purified from bacterial cells which naturally produce the polypeptide or protein. One skilled in the art can readily follow known methods for isolating polypeptides and proteins in order to obtain one of the isolated polypeptides or proteins of the present invention. These include, but are not limited to, immunochromatography, HPLC, size-exclusion chromatography, ion-exchange chromatography, and immuno-affinity chromatography. See, e.g., Scopes, Protein Purification: Principles and Practice, Springer-Verlag (1994); Sambrook, et al., in Molecular Cloning: A Laboratory Manual; Ausubel et al., Current Protocols in Molecular Biology. Polypeptide fragments that

retain biological/immunological activity include fragments comprising greater than about 100 amino acids, or greater than about 200 amino acids, and fragments that encode specific protein domains.

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The purified polypeptides can be used in *in vitro* binding assays which are well known in the art to identify molecules which bind to the polypeptides. These molecules include but are not limited to, for e.g., small molecules, molecules from combinatorial libraries, antibodies or other proteins. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

In addition, the peptides of the invention or molecules capable of binding to the peptides may be complexed with toxins, e.g., ricin or cholera, or with other compounds that are toxic to cells. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for SEQ ID NO:1787-3572 and 5359-7144.

The protein of the invention may also be expressed as a product of transgenic animals, e.g., as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications, in the peptide or DNA sequence, can be made by those skilled in the art using known techniques. Modifications of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, e.g., U.S. Pat. No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein. Regions of the protein that are important for the protein function can be determined by various methods known in the art including the alanine-scanning method which involved systematic substitution of single or strings of amino acids with alanine, followed by testing the resulting alanine-containing variant for biological activity. This type of analysis determines the importance of the substituted amino acid(s) in biological activity. Regions of the protein that are important for protein function may be determined by the eMATRIX program.

Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and are useful for screening or other immunological

methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are encompassed by the present invention.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, e.g., Invitrogen, San Diego, Calif., U.S.A. (the MaxBatTM kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

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The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (i.e., from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearlTM or Cibacrom blue 3GA SepharoseTM; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX), or as a His tag. Kits for expression and purification of such fusion proteins are commercially available from New England BioLab (Beverly, Mass.), Pharmacia (Piscataway, N.J.) and Invitrogen, respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("FLAG®") is commercially available from Kodak (New Haven, Conn.).

Finally, one or more reverse-phase high performance liquid chromatography (RP-HPLC) steps employing hydrophobic RP-HPLC media, e.g., silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

The polypeptides of the invention include analogs (variants). This embraces fragments, as well as peptides in which one or more amino acids has been deleted, inserted, or substituted. Also, analogs of the polypeptides of the invention embrace fusions of the polypeptides or modifications of the polypeptides of the invention, wherein the polypeptide or analog is fused to another moiety or moieties, e.g., targeting moiety or another therapeutic agent. Such analogs may exhibit improved properties such as activity and/or stability. Examples of moieties which may be fused to the polypeptide or an analog include, for example, targeting moieties which provide for the delivery of polypeptide to pancreatic cells, e.g., antibodies to pancreatic cells, antibodies to immune cells such as T-cells, monocytes, dendritic cells, granulocytes, etc., as well as receptor and ligands expressed on pancreatic or immune cells. Other moieties which may be fused to the polypeptide include therapeutic agents which are used for treatment, for example, immunosuppressive drugs such as cyclosporin, SK506, azathioprine, CD3 antibodies and steroids. Also, polypeptides may be fused to immune modulators, and other cytokines such as alpha or beta interferon.

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4.6.1 DETERMINING POLYPEPTIDE AND POLYNUCLEOTIDE IDENTITY AND SIMILARITY

Preferred identity and/or similarity are designed to give the largest match between the sequences tested. Methods to determine identity and similarity are codified in computer programs including, but are not limited to, the GCG program package, including GAP 20 (Devereux, J., et al., Nucleic Acids Research 12(1):387 (1984); Genetics Computer Group, University of Wisconsin, Madison, WI), BLASTP, BLASTN, BLASTX, FASTA (Altschul, S.F. et al., J. Molec. Biol. 215:403-410 (1990), PSI-BLAST (Altschul S.F. et al., Nucleic Acids Res. vol. 25, pp. 3389-3402, herein incorporated by reference), eMatrix software (Wu et al., J. Comp. Biol., Vol. 6, pp. 219-235 (1999), herein incorporated by reference), eMotif software (Nevill-25 Manning et al, ISMB-97, Vol. 4, pp. 202-209, herein incorporated by reference), pFam software (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1), pp. 320-322 (1998), herein incorporated by reference) and the Kyte-Doolittle hydrophobocity prediction algorithm (J. Mol Biol, 157, pp. 105-31 (1982), incorporated herein by reference). The BLAST programs are publicly available from the National Center for Biotechnology Information (NCBI) and other sources (BLAST Manual, Altschul, S., et al. NCB NLM NIH Bethesda, MD 20894; Altschul, S., et al., J. Mol. Biol. 215:403-410 (1990).

4.7 CHIMERIC AND FUSION PROTEINS

The invention also provides chimeric or fusion proteins. As used herein, a "chimeric protein" or "fusion protein" comprises a polypeptide of the invention operatively linked to

another polypeptide. Within a fusion protein the polypeptide according to the invention can correspond to all or a portion of a protein according to the invention. In one embodiment, a fusion protein comprises at least one biologically active portion of a protein according to the invention. In another embodiment, a fusion protein comprises at least two biologically active portions of a protein according to the invention. Within the fusion protein, the term "operatively linked" is intended to indicate that the polypeptide according to the invention and the other polypeptide are fused in-frame to each other. The polypeptide can be fused to the N-terminus or C-terminus.

For example, in one embodiment a fusion protein comprises a polypeptide according to the invention operably linked to the extracellular domain of a second protein.

In another embodiment, the fusion protein is a GST-fusion protein in which the polypeptide sequences of the invention are fused to the C-terminus of the GST (i.e., glutathione S-transferase) sequences.

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In another embodiment, the fusion protein is an immunoglobulin fusion protein in which
the polypeptide sequences according to the invention comprises one or more domains are fused
to sequences derived from a member of the immunoglobulin protein family. The
immunoglobulin fusion proteins of the invention can be incorporated into pharmaceutical
compositions and administered to a subject to inhibit an interaction between a ligand and a
protein of the invention on the surface of a cell, to thereby suppress signal transduction in vivo.

The immunoglobulin fusion proteins can be used to affect the bioavailability of a cognate ligand.
Inhibition of the ligand/protein interaction may be useful therapeutically for both the treatment of
proliferative and differentiative disorders, e,g., cancer as well as modulating (e.g., promoting or
inhibiting) cell survival. Moreover, the immunoglobulin fusion proteins of the invention can be
used as immunogens to produce antibodies in a subject, to purify ligands, and in screening assays
to identify molecules that inhibit the interaction of a polypeptide of the invention with a ligand.

A chimeric or fusion protein of the invention can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, e.g., by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers that give rise to complementary overhangs between two consecutive gene fragments that can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for

example, Ausubel et al. (eds.) CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (e.g., a GST polypeptide). A nucleic acid encoding a polypeptide of the invention can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the protein of the invention.

4.8 GENE THERAPY

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Mutations in the polynucleotides of the invention gene may result in loss of normal function of the encoded protein. The invention thus provides gene therapy to restore normal activity of the polypeptides of the invention; or to treat disease states involving polypeptides of the invention. Delivery of a functional gene encoding polypeptides of the invention to appropriate cells is effected ex vivo, in situ, or in vivo by use of vectors, and more particularly viral vectors (e.g., adenovirus, adeno-associated virus, or a retrovirus), or ex vivo by use of physical DNA transfer methods (e.g., liposomes or chemical treatments). See, for example, Anderson, Nature, supplement to vol. 392, no. 6679, pp.25-20 (1998). For additional reviews of gene therapy technology see Friedmann, Science, 244: 1275-1281 (1989); Verma, Scientific American: 68-84 (1990); and Miller, Nature, 357: 455-460 (1992). Introduction of any one of the nucleotides of the present invention or a gene encoding the polypeptides of the present invention can also be accomplished with extrachromosomal substrates (transient expression) or artificial chromosomes (stable expression). Cells may also be cultured ex vivo in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced in vivo for therapeutic purposes. Alternatively, it is contemplated that in other human disease states, preventing the expression of or inhibiting the activity of polypeptides of the invention will be useful in treating the disease states. It is contemplated that antisense therapy or gene therapy could be applied to negatively regulate the expression of polypeptides of the invention.

Other methods inhibiting expression of a protein include the introduction of antisense molecules to the nucleic acids of the present invention, their complements, or their translated RNA sequences, by methods known in the art. Further, the polypeptides of the present invention can be inhibited by using targeted deletion methods, or the insertion of a negative regulatory element such as a silencer, which is tissue specific.

The present invention still further provides cells genetically engineered in vivo to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in

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the cell. These methods can be used to increase or decrease the expression of the polynucleotides of the present invention.

Knowledge of DNA sequences provided by the invention allows for modification of cells to permit, increase, or decrease, expression of endogenous polypeptide. Cells can be modified (e.g., by homologous recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the protein at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the desired protein encoding sequences. See, for example, PCT International Publication No. WO 94/12650, PCT International Publication No. WO 92/20808, and PCT International Publication No. WO 91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (e.g., ada, dhfr, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the desired protein coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequences include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, e.g., inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are

added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

4.9 TRANSGENIC ANIMALS

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In preferred methods to determine biological functions of the polypeptides of the invention in vivo, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of a promoter of the polynucleotides of the invention is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The homologous

promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

The polynucleotides of the present invention also make possible the development, through, e.g., homologous recombination or knock out strategies, of animals that fail to express polypeptides of the invention or that express a variant polypeptide. Such animals are useful as models for studying the *in vivo* activities of polypeptide as well as for studying modulators of the polypeptides of the invention.

In preferred methods to determine biological functions of the polypeptides of the invention *in vivo*, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of the polynucleotides of the invention promoter is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The homologous promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

4.10 USES AND BIOLOGICAL ACTIVITY

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The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified herein. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA). The mechanism underlying the particular condition or pathology will dictate whether the

polypeptides of the invention, the polynucleotides of the invention or modulators (activators or inhibitors) thereof would be beneficial to the subject in need of treatment. Thus, "therapeutic compositions of the invention" include compositions comprising isolated polynucleotides (including recombinant DNA molecules, cloned genes and degenerate variants thereof) or polypeptides of the invention (including full length protein, mature protein and truncations or domains thereof), or compounds and other substances that modulate the overall activity of the target gene products, either at the level of target gene/protein expression or target protein activity. Such modulators include polypeptides, analogs, (variants), including fragments and fusion proteins, antibodies and other binding proteins; chemical compounds that directly or indirectly activate or inhibit the polypeptides of the invention (identified, e.g., via drug screening assays as described herein); antisense polynucleotides and polynucleotides suitable for triple helix formation; and in particular antibodies or other binding partners that specifically recognize one or more epitopes of the polypeptides of the invention.

The polypeptides of the present invention may likewise be involved in cellular activation or in one of the other physiological pathways described herein.

4.10.1 RESEARCH USES AND UTILITIES

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The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell 75:791-803 (1993)) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The polypeptides provided by the present invention can similarly be used in assays to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding polypeptide is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E. F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S. L. and A. R. Kimmel eds., 1987.

4.10.2 NUTRITIONAL USES

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Polynucleotides and polypeptides of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the polypeptide or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the polypeptide or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

4.10.3 CYTOKINE AND CELL PROLIFERATION/DIFFERENTIATION ACTIVITY

A polypeptide of the present invention may exhibit activity relating to cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor-dependent cell proliferation assays, and hence the assays serve as a convenient

confirmation of cytokine activity. The activity of therapeutic compositions of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+(preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e, CMK,

HUVEC, and Caco. Therapeutic compositions of the invention can be used in the following:

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Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Bertagnolli et al., J. Immunol. 145:1706-1712, 1990; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Bertagnolli, et al., I. Immunol. 149:3778-3783, 1992; Bowman et al., I. Immunol. 152:1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A. M. and Shevach, E. M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human interleukin-γ, Schreiber, R. D. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 20 and Interleukin 4, Bottomly, K., Davis, L. S. and Lipsky, P. E. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; dcVries et al., J. Exp. Med. 173:1205-1211, 1991; Moreau et al., Nature 336:690-692, 1988; Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse 25 and human interleukin 6--Nordan, R. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., Proc. Natl. Aced. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11--Bennett, F., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 30 9--Ciarletta, A., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W Strober,

Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

4.10.4 STEM CELL GROWTH FACTOR ACTIVITY

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A polypeptide of the present invention may exhibit stem cell growth factor activity and be involved in the proliferation, differentiation and survival of pluripotent and totipotent stem cells including primordial germ cells, embryonic stem cells, hematopoietic stem cells and/or germ line stem cells. Administration of the polypeptide of the invention to stem cells in vivo or ex vivo is expected to maintain and expand cell populations in a totipotential or pluripotential state which would be useful for re-engineering damaged or diseased tissues, transplantation, manufacture of bio-pharmaceuticals and the development of bio-sensors. The ability to produce large quantities of human cells has important working applications for the production of human proteins which currently must be obtained from non-human sources or donors, implantation of cells to treat diseases such as Parkinson's, Alzheimer's and other neurodegenerative diseases; tissues for grafting such as bone marrow, skin, cartilage, tendons, bone, muscle (including cardiac muscle), blood vessels, cornea, neural cells, gastrointestinal cells and others; and organs for transplantation such as kidney, liver, pancreas (including islet cells), heart and lung.

It is contemplated that multiple different exogenous growth factors and/or cytokines may be administered in combination with the polypeptide of the invention to achieve the desired effect, including any of the growth factors listed herein, other stem cell maintenance factors, and specifically including stem cell factor (SCF), leukemia inhibitory factor (LIF), Flt-3 ligand (Flt-3L), any of the interleukins, recombinant soluble IL-6 receptor fused to IL-6, macrophage inflammatory protein 1-alpha (MIP-1-alpha), G-CSF, GM-CSF, thrombopoietin (TPO), platelet factor 4 (PF-4), platelet-derived growth factor (PDGF), neural growth factors and basic fibroblast growth factor (bFGF).

Since totipotent stem cells can give rise to virtually any mature cell type, expansion of these cells in culture will facilitate the production of large quantities of mature cells. Techniques for culturing stem cells are known in the art and administration of polypeptides of the invention, optionally with other growth factors and/or cytokines, is expected to enhance the survival and proliferation of the stem cell populations. This can be accomplished by direct administration of the polypeptide of the invention to the culture medium. Alternatively, stroma cells transfected with a polynucleotide that encodes for the polypeptide of the invention can be used as a feeder

layer for the stem cell populations in culture or in vivo. Stromal support cells for feeder layers may include embryonic bone marrow fibroblasts, bone marrow stromal cells, fetal liver cells, or cultured embryonic fibroblasts (see U.S. Patent No. 5,690,926).

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Stem cells themselves can be transfected with a polynucleotide of the invention to induce autocrine expression of the polypeptide of the invention. This will allow for generation of undifferentiated totipotential/pluripotential stem cell lines that are useful as is or that can then be differentiated into the desired mature cell types. These stable cell lines can also serve as a source of undifferentiated totipotential/pluripotential mRNA to create cDNA libraries and templates for polymerase chain reaction experiments. These studies would allow for the isolation and identification of differentially expressed genes in stem cell populations that regulate stem cell proliferation and/or maintenance.

Expansion and maintenance of totipotent stem cell populations will be useful in the treatment of many pathological conditions. For example, polypeptides of the present invention may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease, accidental damage or genetic disorders. The polypeptide of the invention may be useful for inducing the proliferation of neural cells and for the regeneration of nerve and brain tissue, i.e. for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders which involve degeneration, death or trauma to neural cells or nerve tissue. In addition, the expanded stem cell populations can also be genetically altered for gene therapy purposes and to decrease host rejection of replacement tissues after grafting or implantation.

Expression of the polypeptide of the invention and its effect on stem cells can also be manipulated to achieve controlled differentiation of the stem cells into more differentiated cell types. A broadly applicable method of obtaining pure populations of a specific differentiated cell type from undifferentiated stem cell populations involves the use of a cell-type specific promoter driving a selectable marker. The selectable marker allows only cells of the desired type to survive. For example, stem cells can be induced to differentiate into cardiomyocytes (Wobus et al., Differentiation, 48: 173-182, (1991); Klug et al., J. Clin. Invest., 98(1): 216-224, (1998)) or skeletal muscle cells (Browder, L. W. In: *Principles of Tissue Engineering eds*. Lanza et al., Academic Press (1997)). Alternatively, directed differentiation of stem cells can be accomplished by culturing the stem cells in the presence of a differentiation factor such as retinoic acid and an antagonist of the polypeptide of the invention which would inhibit the effects of endogenous stem cell factor activity and allow differentiation to proceed.

In vitro cultures of stem cells can be used to determine if the polypeptide of the invention exhibits stem cell growth factor activity. Stem cells are isolated from any one of various cell

sources (including hematopoietic stem cells and embryonic stem cells) and cultured on a feeder layer, as described by Thompson et al. Proc. Natl. Acad. Sci, U.S.A., 92: 7844-7848 (1995), in the presence of the polypeptide of the invention alone or in combination with other growth factors or cytokines. The ability of the polypeptide of the invention to induce stem cells proliferation is determined by colony formation on semi-solid support e.g. as described by Bernstein et al., Blood, 77: 2316-2321 (1991).

4.10.5 HEMATOPOIESIS REGULATING ACTIVITY

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A polypeptide of the present invention may be involved in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell disorders. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either in-vivo or ex-vivo (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

Therapeutic compositions of the invention can be used in the following:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M. G. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, N.Y. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I. K. and Briddell, R. A. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, N.Y. 1994; Neben et al., Experimental Hematology 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R. E. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, N.Y. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, N.Y. 1994; Long term culture initiating cell assay, Sutherland, H. J. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, N.Y. 1994.

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4.10.6 TISSUE GROWTH ACTIVITY

A polypeptide of the present invention also may be involved in bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as in wound healing and tissue repair and replacement, and in healing of burns, incisions and ulcers.

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A polypeptide of the present invention which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Compositions of a polypeptide, antibody, binding partner, or other modulator of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A polypeptide of this invention may also be involved in attracting bone-forming cells, stimulating growth of bone-forming cells, or inducing differentiation of progenitors of bone-forming cells. Treatment of osteoporosis, osteoarthritis, bone degenerative disorders, or periodontal disease, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes may also be possible using the composition of the

invention.

Another category of tissue regeneration activity that may involve the polypeptide of the present invention is tendon/ligament formation. Induction of tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors ex vivo for return in vivo to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

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The compositions of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, i.e. for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a composition may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a composition of the invention.

Compositions of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

Compositions of the present invention may also be involved in the generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular

endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring may allow normal tissue to regenerate. A polypeptide of the present invention may also exhibit angiogenic activity.

A composition of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

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A composition of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

Therapeutic compositions of the invention can be used in the following:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, H. I. and Rovee, D. T., eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

4.10.7 IMMUNE STIMULATING OR SUPPRESSING ACTIVITY

A polypeptide of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A polynucleotide of the invention can encode a polypeptide exhibiting such activities. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (c.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases causes by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpes viruses, mycobacteria, Leishmania spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, proteins of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus,

rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein (or antagonists thereof, including antibodies) of the present invention may also to be useful in the treatment of allergic reactions and conditions (e.g., anaphylaxis, serum sickness, drug reactions, food allergies, insect venom allergies, mastocytosis, allergic rhinitis, hypersensitivity pneumonitis, urticaria, angioedema, eczema, atopic dermatitis, allergic contact dermatitis, erythema multiforme, Stevens-Johnson syndrome, allergic conjunctivitis, atopic keratoconjunctivitis, venereal keratoconjunctivitis, giant papillary conjunctivitis and contact allergies), such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein (or antagonists thereof) of the present invention. The therapeutic effects of the polypeptides or antagonists thereof on allergic reactions can be evaluated by in vivo animals models such as the cumulative contact enhancement test (Lastborn et al., Toxicology 125: 59-66, 1998), skin prick test (Hoffmann et al., Allergy 54: 446-54, 1999), guinea pig skin sensitization test (Vohr et al., Arch. Toxocol. 73: 501-9), and murine local lymph node assay (Kimber et al., J. Toxicol. Environ. Health 53: 563-79).

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Using the proteins of the invention it may also be possible to modulate immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as, for example, B7)), e.g., preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a therapeutic

composition of the invention may prevent cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, a lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular therapeutic compositions in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins in vivo as described in Lenschow et al., Science 257:789-792 (1992) and Turka et al., Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of therapeutic compositions of the invention on the development of that disease.

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Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block stimulation of T cells can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythmatosis in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (e.g., a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response may be useful in cases of viral infection, including systemic viral diseases such as influenza, the common cold, and encephalitis.

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Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells in vitro with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the in vitro activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells in vivo.

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A polypeptide of the present invention may provide the necessary stimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient mounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (e.g., a cytoplasmic-domain truncated portion) of an MHC class I alpha chain protein and β2 microglobulin protein or an MHC class II alpha chain protein and an MHC class II beta chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and 30 Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., I. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bowman et al., J. Virology 61:1992-1998; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: In vitro antibody production, Mond, J. J. and Brunswick, M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of Experimental Medicine 173:549-559, 1991; Macatonia et al., Journal of Immunology 154:5071-5079, 1995; Porgador et al., Journal of Experimental Medicine 182:255-260, 1995; Nair et al., Journal of Virology 67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994; Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation 94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

4.10.8 ACTIVIN/INHIBIN ACTIVITY

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A polypeptide of the present invention may also exhibit activin- or inhibin-related activities. A polynucleotide of the invention may encode a polypeptide exhibiting such characteristics. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins and are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a polypeptide of the present invention, alone or in heterodimers with a member of the inhibin family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the polypeptide of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, U.S. Pat. No. 4,798,885. A polypeptide of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as, but not limited to, cows, sheep and pigs.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods.

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., Endocrinology 91:562-572, 1972; Ling et al., Nature 321:779-782, 1986; Vale et al., Nature 321:776-779, 1986; Mason et al., Nature 318:659-663, 1985; Forage et al., Proc. Natl. Acad. Sci. USA 83:3091-3095, 1986.

4.10.9 CHEMOTACTIC/CHEMOKINETIC ACTIVITY

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A polypeptide of the present invention may be involved in chemotactic or chemokinetic activity for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Chemotactic and chemokinetic receptor activation can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic compositions (e.g. proteins, antibodies, binding partners, or modulators of the invention) provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population.

Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

Therapeutic compositions of the invention can be used in the following:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Marguiles, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25:1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153:1762-1768, 1994.

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4.10.10 HEMOSTATIC AND THROMBOLYTIC ACTIVITY

A polypeptide of the invention may also be involved in hemostatis or thrombolysis or thrombosis. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Compositions may be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A composition of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

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Therapeutic compositions of the invention can be used in the following:

Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

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4.10.11 CANCER DIAGNOSIS AND THERAPY

Polypeptides of the invention may be involved in cancer cell generation, proliferation or metastasis. Detection of the presence or amount of polynucleotides or polypeptides of the invention may be useful for the diagnosis and/or prognosis of one or more types of cancer. For example, the presence or increased expression of a polynucleotide/polypeptide of the invention

may indicate a hereditary risk of cancer, a precancerous condition, or an ongoing malignancy. Conversely, a defect in the gene or absence of the polypeptide may be associated with a cancer condition. Identification of single nucleotide polymorphisms associated with cancer or a predisposition to cancer may also be useful for diagnosis or prognosis.

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Cancer treatments promote tumor regression by inhibiting tumor cell proliferation, inhibiting angiogenesis (growth of new blood vessels that is necessary to support tumor growth) and/or prohibiting metastasis by reducing tumor cell motility or invasiveness. Therapeutic compositions of the invention may be effective in adult and pediatric oncology including in solid phase tumors/malignancies, locally advanced tumors, human soft tissue sarcomas, metastatic cancer, including lymphatic metastases, blood cell malignancies including multiple myeloma, acute and chronic leukemias, and lymphomas, head and neck cancers including mouth cancer, larynx cancer and thyroid cancer, lung cancers including small cell carcinoma and non-small cell cancers, breast cancers including small cell carcinoma and ductal carcinoma, gastrointestinal cancers including esophageal cancer, stomach cancer, colon cancer, colorectal cancer and polyps associated with colorectal neoplasia, pancreatic cancers, liver cancer, urologic cancers including bladder cancer and prostate cancer, malignancies of the female genital tract including ovarian carcinoma, uterine (including endometrial) cancers, and solid tumor in the ovarian follicle, kidney cancers including renal cell carcinoma, brain cancers including intrinsic brain tumors, neuroblastoma, astrocytic brain tumors, gliomas, metastatic tumor cell invasion in the central nervous system, bone cancers including osteomas, skin cancers including malignant melanoma, tumor progression of human skin keratinocytes, squamous cell carcinoma, basal cell carcinoma, hemangiopericytoma and Karposi's sarcoma.

Polypeptides, polynucleotides, or modulators of polypeptides of the invention (including inhibitors and stimulators of the biological activity of the polypeptide of the invention) may be administered to treat cancer. Therapeutic compositions can be administered in therapeutically effective dosages alone or in combination with adjuvant cancer therapy such as surgery, chemotherapy, radiotherapy, thermotherapy, and laser therapy, and may provide a beneficial effect, e.g. reducing tumor size, slowing rate of tumor growth, inhibiting metastasis, or otherwise improving overall clinical condition, without necessarily eradicating the cancer.

The composition can also be administered in therapeutically effective amounts as a portion of an anti-cancer cocktail. An anti-cancer cocktail is a mixture of the polypeptide or modulator of the invention with one or more anti-cancer drugs in addition to a pharmaceutically acceptable carrier for delivery. The use of anti-cancer cocktails as a cancer treatment is routine. Anti-cancer drugs that are well known in the art and can be used as a treatment in combination with the polypeptide or modulator of the invention include: Actinomycin D, Aminoglutethimide,

Asparaginase, Bleomycin, Busulfan, Carboplatin, Carmustine, Chlorambucil, Cisplatin (cis-DDP), Cyclophosphamide, Cytarabine HCl (Cytosine arabinoside), Dacarbazine, Dactinomycin, Daunorubicin HCl, Doxorubicin HCl, Estramustine phosphate sodium, Etoposide (V16-213), Floxuridine, 5-Fluorouracil (5-Fu), Flutamide, Hydroxyurea (hydroxycarbamide), Ifosfamide, Interferon Alpha-2a, Interferon Alpha-2b, Leuprolide acetate (LHRH-releasing factor analog), Lomustine, Mechlorethamine HCl (nitrogen mustard), Melphalan, Mercaptopurine, Mesna, Methotrexate (MTX), Mitomycin, Mitoxantrone HCl, Octreotide, Plicamycin, Procarbazine HCl, Streptozocin, Tamoxifen citrate, Thioguanine, Thiotepa, Vinblastine sulfate, Vincristine sulfate, Amsacrine, Azacitidine, Hexamethylmelamine, Interleukin-2, Mitoguazone, Pentostatin, Semustine, Teniposide, and Vindesine sulfate.

In addition, therapeutic compositions of the invention may be used for prophylactic treatment of cancer. There are hereditary conditions and/or environmental situations (e.g. exposure to carcinogens) known in the art that predispose an individual to developing cancers. Under these circumstances, it may be beneficial to treat these individuals with therapeutically effective doses of the polypeptide of the invention to reduce the risk of developing cancers.

In vitro models can be used to determine the effective doses of the polypeptide of the invention as a potential cancer treatment. These in vitro models include proliferation assays of cultured tumor cells, growth of cultured tumor cells in soft agar (see Freshney, (1987) Culture of Animal Cells: A Manual of Basic Technique, Wily-Liss, New York, NY Ch 18 and Ch 21), tumor systems in nude mice as described in Giovanella et al., J. Natl. Can. Inst., 52: 921-30 (1974), mobility and invasive potential of tumor cells in Boyden Chamber assays as described in Pilkington et al., Anticancer Res., 17: 4107-9 (1997), and angiogenesis assays such as induction of vascularization of the chick chorioallantoic membrane or induction of vascular endothelial cell migration as described in Ribatta et al., Intl. J. Dev. Biol., 40: 1189-97 (1999) and Li et al., Clin. Exp. Metastasis, 17:423-9 (1999), respectively. Suitable tumor cells lines are available, e.g. from American Type Tissue Culture Collection catalogs.

4.10.12 RECEPTOR/LIGAND ACTIVITY

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A polypeptide of the present invention may also demonstrate activity as receptor, receptor ligand or inhibitor or agonist of receptor/ligand interactions. A polynucleotide of the invention can encode a polypeptide exhibiting such characteristics. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen

recognition and development of cellular and humoral immune responses. Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley- Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1-7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

By way of example, the polypeptides of the invention may be used as a receptor for a ligand(s) thereby transmitting the biological activity of that ligand(s). Ligands may be identified through binding assays, affinity chromatography, dihybrid screening assays, BIAcore assays, gel overlay assays, or other methods known in the art.

Studies characterizing drugs or proteins as agonist or antagonist or partial agonists or a partial antagonist require the use of other proteins as competing ligands. The polypeptides of the present invention or ligand(s) thereof may be labeled by being coupled to radioisotopes, colorimetric molecules or a toxin molecules by conventional methods. ("Guide to Protein Purification" Murray P. Deutscher (ed) Methods in Enzymology Vol. 182 (1990) Academic Press, Inc. San Diego). Examples of radioisotopes include, but are not limited to, tritium and carbon-14. Examples of colorimetric molecules include, but are not limited to, fluorescent molecules such as fluorescamine, or rhodamine or other colorimetric molecules. Examples of toxins include, but are not limited, to ricin.

4.10.13 DRUG SCREENING

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This invention is particularly useful for screening chemical compounds by using the novel polypeptides or binding fragments thereof in any of a variety of drug screening techniques. The polypeptides or fragments employed in such a test may either be free in solution, affixed to a solid support, borne on a cell surface or located intracellularly. One method of drug screening utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the polypeptide or a fragment thereof. Drugs are screened against such

transformed cells in competitive binding assays. Such cells, either in viable or fixed form, can be used for standard binding assays. One may measure, for example, the formation of complexes between polypeptides of the invention or fragments and the agent being tested or examine the diminution in complex formation between the novel polypeptides and an appropriate cell line, which are well known in the art.

Sources for test compounds that may be screened for ability to bind to or modulate (i.e., increase or decrease) the activity of polypeptides of the invention include (1) inorganic and organic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of either random or mimetic peptides, oligonucleotides or organic molecules.

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Chemical libraries may be readily synthesized or purchased from a number of commercial sources, and may include structural analogs of known compounds or compounds that are identified as "hits" or "leads" via natural product screening.

The sources of natural product libraries are microorganisms (including bacteria and fungi), animals, plants or other vegetation, or marine organisms, and libraries of mixtures for screening may be created by: (1) fermentation and extraction of broths from soil, plant or marine microorganisms or (2) extraction of the organisms themselves. Natural product libraries include polyketides, non-ribosomal peptides, and (non-naturally occurring) variants thereof. For a review, see *Science 282*:63-68 (1998).

Combinatorial libraries are composed of large numbers of peptides, oligonucleotides or organic compounds and can be readily prepared by traditional automated synthesis methods, PCR, cloning or proprietary synthetic methods. Of particular interest are peptide and oligonucleotide combinatorial libraries. Still other libraries of interest include peptide, protein, peptidomimetic, multiparallel synthetic collection, recombinatorial, and polypeptide libraries. For a review of combinatorial chemistry and libraries created therefrom, see Myers, Curr. Opin. Biotechnol. 8:701-707 (1997). For reviews and examples of peptidomimetic libraries, see Al-Obeidi et al., Mol. Biotechnol, 9(3):205-23 (1998); Hruby et al., Curr Opin Chem Biol, 1(1):114-19 (1997); Dorner et al., Bioorg Med Chem, 4(5):709-15 (1996) (alkylated dipeptides).

Identification of modulators through use of the various libraries described herein permits modification of the candidate "hit" (or "lead") to optimize the capacity of the "hit" to bind a polypeptide of the invention. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

The binding molecules thus identified may be complexed with toxins, e.g., ricin or cholera, or with other compounds that are toxic to cells such as radioisotopes. The toxin-binding

molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for a polypeptide of the invention. Alternatively, the binding molecules may be complexed with imaging agents for targeting and imaging purposes.

4.10.14 ASSAY FOR RECEPTOR ACTIVITY

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The invention also provides methods to detect specific binding of a polypeptide e.g. a ligand or a receptor. The art provides numerous assays particularly useful for identifying previously unknown binding partners for receptor polypeptides of the invention. For example, expression cloning using mammalian or bacterial cells, or dihybrid screening assays can be used to identify polynucleotides encoding binding partners. As another example, affinity chromatography with the appropriate immobilized polypeptide of the invention can be used to isolate polypeptides that recognize and bind polypeptides of the invention. There are a number of different libraries used for the identification of compounds, and in particular small molecules. that modulate (i.e., increase or decrease) biological activity of a polypeptide of the invention. Ligands for receptor polypeptides of the invention can also be identified by adding exogenous ligands, or cocktails of ligands to two cells populations that are genetically identical except for the expression of the receptor of the invention: one cell population expresses the receptor of the invention whereas the other does not. The response of the two cell populations to the addition of ligands(s) are then compared. Alternatively, an expression library can be co-expressed with the polypeptide of the invention in cells and assayed for an autocrine response to identify potential ligand(s). As still another example, BIAcore assays, gel overlay assays, or other methods known in the art can be used to identify binding partner polypeptides, including, (1) organic and inorganic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of random peptides, oligonucleotides or organic molecules.

The role of downstream intracellular signaling molecules in the signaling cascade of the polypeptide of the invention can be determined. For example, a chimeric protein in which the cytoplasmic domain of the polypeptide of the invention is fused to the extracellular portion of a protein, whose ligand has been identified, is produced in a host cell. The cell is then incubated with the ligand specific for the extracellular portion of the chimeric protein, thereby activating the chimeric receptor. Known downstream proteins involved in intracellular signaling can then be assayed for expected modifications i.e. phosphorylation. Other methods known to those in the art can also be used to identify signaling molecules involved in receptor activity.

4.10.15 ANTI-INFLAMMATORY ACTIVITY

Compositions of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Compositions with such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation intimation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Compositions of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material. Compositions of this invention may be utilized to prevent or treat conditions such as, but not limited to, sepsis, acute pancreatitis, endotoxin shock, cytokine induced shock, rheumatoid arthritis, chronic inflammatory arthritis, pancreatic cell damage from diabetes mellitus type 1, graft versus host disease, inflammatory bowel disease, inflamation associated with pulmonary disease, other autoimmune disease or inflammatory disease, an antiproliferative agent such as for acute or chronic mylegenous leukemia or in the prevention of premature labor secondary to intrauterine infections.

4.10.16 LEUKEMIAS

Leukemias and related disorders may be treated or prevented by administration of a therapeutic that promotes or inhibits function of the polynucleotides and/or polypeptides of the invention. Such leukemias and related disorders include but are not limited to acute leukemia, acute lymphocytic leukemia, acute myelocytic leukemia, myeloblastic, promyelocytic, myelomonocytic, monocytic, erythroleukemia, chronic leukemia, chronic myelocytic (granulocytic) leukemia and chronic lymphocytic leukemia (for a review of such disorders, see Fishman et al., 1985, Medicine, 2d Ed., J.B. Lippincott Co., Philadelphia).

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4.10.17 NERVOUS SYSTEM DISORDERS

Nervous system disorders, involving cell types which can be tested for efficacy of intervention with compounds that modulate the activity of the polynucleotides and/or polypeptides of the invention, and which can be treated upon thus observing an indication of therapeutic utility, include but are not limited to nervous system injuries, and diseases or

disorders which result in either a disconnection of axons, a diminution or degeneration of neurons, or demyelination. Nervous system lesions which may be treated in a patient (including human and non-human mammalian patients) according to the invention include but are not limited to the following lesions of either the central (including spinal cord, brain) or peripheral nervous systems:

- (i) traumatic lesions, including lesions caused by physical injury or associated with surgery, for example, lesions which sever a portion of the nervous system, or compression injuries;
- (ii) ischemic lesions, in which a lack of oxygen in a portion of the nervous system
 results in neuronal injury or death, including cerebral infarction or ischemia, or spinal cord infarction or ischemia;

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- (iii) infectious lesions, in which a portion of the nervous system is destroyed or injured as a result of infection, for example, by an abscess or associated with infection by human immunodeficiency virus, herpes zoster, or herpes simplex virus or with Lyme disease, tuberculosis, syphilis;
- (iv) degenerative lesions, in which a portion of the nervous system is destroyed or injured as a result of a degenerative process including but not limited to degeneration associated with Parkinson's disease, Alzheimer's disease, Huntington's chorea, or amyotrophic lateral sclerosis;
- (v) lesions associated with nutritional diseases or disorders, in which a portion of the nervous system is destroyed or injured by a nutritional disorder or disorder of metabolism including but not limited to, vitamin B12 deficiency, folic acid deficiency, Wernicke disease, tobacco-alcohol amblyopia, Marchiafava-Bignami disease (primary degeneration of the corpus callosum), and alcoholic cerebellar degeneration;
- (vi) neurological lesions associated with systemic diseases including but not limited to diabetes (diabetic neuropathy, Bell's palsy), systemic lupus erythematosus, carcinoma, or sarcoidosis;
 - (vii) lesions caused by toxic substances including alcohol, lead, or particular neurotoxins; and
- 30 (viii) demyelinated lesions in which a portion of the nervous system is destroyed or injured by a demyelinating disease including but not limited to multiple sclerosis, human immunodeficiency virus-associated myelopathy, transverse myelopathy or various etiologies, progressive multifocal leukoencephalopathy, and central pontine myelinolysis.

Therapeutics which are useful according to the invention for treatment of a nervous system disorder may be selected by testing for biological activity in promoting the survival or

differentiation of neurons. For example, and not by way of limitation, therapeutics which elicit any of the following effects may be useful according to the invention:

(i) increased survival time of neurons in culture;

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- (ii) increased sprouting of neurons in culture or in vivo;
- (iii) increased production of a neuron-associated molecule in culture or *in vivo*, *e.g.*, choline acetyltransferase or acetylcholinesterase with respect to motor neurons; or
 - (iv) decreased symptoms of neuron dysfunction in vivo.

Such effects may be measured by any method known in the art. In preferred, non-limiting embodiments, increased survival of neurons may be measured by the method set forth in Arakawa et al. (1990, J. Neurosci. 10:3507-3515); increased sprouting of neurons may be detected by methods set forth in Pestronk et al. (1980, Exp. Neurol. 70:65-82) or Brown et al. (1981, Ann. Rev. Neurosci. 4:17-42); increased production of neuron-associated molecules may be measured by bioassay, enzymatic assay, antibody binding, Northern blot assay, etc., depending on the molecule to be measured; and motor neuron dysfunction may be measured by assessing the physical manifestation of motor neuron disorder, e.g., weakness, motor neuron conduction velocity, or functional disability.

In specific embodiments, motor neuron disorders that may be treated according to the invention include but are not limited to disorders such as infarction, infection, exposure to toxin, trauma, surgical damage, degenerative disease or malignancy that may affect motor neurons as well as other components of the nervous system, as well as disorders that selectively affect neurons such as amyotrophic lateral sclerosis, and including but not limited to progressive spinal muscular atrophy, progressive bulbar palsy, primary lateral sclerosis, infantile and juvenile muscular atrophy, progressive bulbar paralysis of childhood (Fazio-Londe syndrome), poliomyelitis and the post polio syndrome, and Hereditary Motorsensory Neuropathy (Charcot-Marie-Tooth Disease).

4.10.18 OTHER ACTIVITIES

A polypeptide of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or

elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, co-factors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

4.10.19 IDENTIFICATION OF POLYMORPHISMS

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The demonstration of polymorphisms makes possible the identification of such polymorphisms in human subjects and the pharmacogenetic use of this information for diagnosis and treatment. Such polymorphisms may be associated with, e.g., differential predisposition or susceptibility to various disease states (such as disorders involving inflammation or immune response) or a differential response to drug administration, and this genetic information can be used to tailor preventive or therapeutic treatment appropriately. For example, the existence of a polymorphism associated with a predisposition to inflammation or autoimmune disease makes possible the diagnosis of this condition in humans by identifying the presence of the polymorphism.

Polymorphisms can be identified in a variety of ways known in the art which all generally involve obtaining a sample from a patient, analyzing DNA from the sample, optionally involving isolation or amplification of the DNA, and identifying the presence of the polymorphism in the DNA. For example, PCR may be used to amplify an appropriate fragment of genomic DNA which may then be sequenced. Alternatively, the DNA may be subjected to allele-specific oligonucleotide hybridization (in which appropriate oligonucleotides are hybridized to the DNA under conditions permitting detection of a single base mismatch) or to a single nucleotide extension assay (in which an oligonucleotide that hybridizes immediately adjacent to the position of the polymorphism is extended with one or more labeled nucleotides). In addition, traditional restriction fragment length polymorphism analysis (using restriction enzymes that provide differential digestion of the genomic DNA depending on the presence or absence of the polymorphism) may be performed. Arrays with nucleotide sequences of the present invention can be used to detect polymorphisms. The array can comprise modified

nucleotide sequences of the present invention in order to detect the nucleotide sequences of the present invention. In the alternative, any one of the nucleotide sequences of the present invention can be placed on the array to detect changes from those sequences.

Alternatively a polymorphism resulting in a change in the amino acid sequence could also be detected by detecting a corresponding change in amino acid sequence of the protein, e.g., by an antibody specific to the variant sequence.

4.10.20 ARTHRITIS AND INFLAMMATION

The immunosuppressive effects of the compositions of the invention against rheumatoid arthritis is determined in an experimental animal model system. The experimental model system is adjuvant induced arthritis in rats, and the protocol is described by J. Holoshitz, et at., 1983, Science, 219:56, or by B. Waksman et al., 1963, Int. Arch. Allergy Appl. Immunol., 23:129. Induction of the disease can be caused by a single injection, generally intradermally, of a suspension of killed Mycobacterium tuberculosis in complete Freund's adjuvant (CFA). The route of injection can vary, but rats may be injected at the base of the tail with an adjuvant mixture. The polypeptide is administered in phosphate buffered solution (PBS) at a dose of about 1-5 mg/kg. The control consists of administering PBS only.

The procedure for testing the effects of the test compound would consist of intradermally injecting killed Mycobacterium tuberculosis in CFA followed by immediately administering the test compound and subsequent treatment every other day until day 24. At 14, 15, 18, 20, 22, and 24 days after injection of Mycobacterium CFA, an overall arthritis score may be obtained as described by J. Holoskitz above. An analysis of the data would reveal that the test compound would have a dramatic affect on the swelling of the joints as measured by a decrease of the arthritis score.

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4.11 THERAPEUTIC METHODS

The compositions (including polypeptide fragments, analogs, variants and antibodies or other binding partners or modulators including antisense polynucleotides) of the invention have numerous applications in a variety of therapeutic methods. Examples of therapeutic applications include, but are not limited to, those exemplified herein.

4.11.1 EXAMPLE

One embodiment of the invention is the administration of an effective amount of the polypeptides or other composition of the invention to individuals affected by a disease or disorder that can be modulated by regulating the peptides of the invention. While the mode of

administration is not particularly important, parenteral administration is preferred. An exemplary mode of administration is to deliver an intravenous bolus. The dosage of the polypeptides or other composition of the invention will normally be determined by the prescribing physician. It is to be expected that the dosage will vary according to the age, weight, condition and response of the individual patient. Typically, the amount of polypeptide administered per dose will be in the range of about 0.01µg/kg to 100 mg/kg of body weight, with the preferred dose being about 0.1µg/kg to 10 mg/kg of patient body weight. For parenteral administration, polypeptides of the invention will be formulated in an injectable form combined with a pharmaceutically acceptable parenteral vehicle. Such vehicles are well known in the art and examples include water, saline, Ringer's solution, dextrose solution, and solutions consisting of small amounts of the human serum albumin. The vehicle may contain minor amounts of additives that maintain the isotonicity and stability of the polypeptide or other active ingredient. The preparation of such solutions is within the skill of the art.

15 4.12 PHARMACEUTICAL FORMULATIONS AND ROUTES OF ADMINISTRATION

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A protein or other composition of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources and including antibodies and other binding partners of the polypeptides of the invention) may be administered 20 to a patient in need, by itself, or in pharmaceutical compositions where it is mixed with suitable carriers or excipient(s) at doses to treat or ameliorate a variety of disorders. Such a composition may optionally contain (in addition to protein or other active ingredient and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the 25 carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. In further compositions, proteins of the invention may be combined 30 with other agents beneficial to the treatment of the disease or disorder in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet-derived growth factor (PDGF), transforming growth factors (TGF-α and TGF-β), insulin-like growth factor (IGF), as well as cytokines described herein.

The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or other active ingredient or complement its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein or other active ingredient of the invention, or to minimize side effects. Conversely, protein or other active ingredient of the present invention may be included in formulations of the particular clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects of the clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent (such as IL-1Ra, IL-1 Hy1, IL-1 Hy2, anti-TNF, corticosteroids, immunosuppressive agents). A protein of the present invention may be active in multimers (e.g., heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

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As an alternative to being included in a pharmaceutical composition of the invention including a first protein, a second protein or a therapeutic agent may be concurrently administered with the first protein (e.g., at the same time, or at differing times provided that therapeutic concentrations of the combination of agents is achieved at the treatment site). Techniques for formulation and administration of the compounds of the instant application may be found in "Remington's Pharmaceutical Sciences," Mack Publishing Co., Easton, PA, latest edition. A therapeutically effective dose further refers to that amount of the compound sufficient to result in amelioration of symptoms, e.g., treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, administered alone, a therapeutically effective dose refers to that ingredient alone. When applied to a combination, a therapeutically effective dose refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein or other active ingredient of the present invention is administered to a mammal having a condition to be treated. Protein or other active ingredient of the present invention may be administered in accordance with the method of the invention either alone or in combination with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co- administered with one or more cytokines, lymphokines or other hematopoietic factors, protein or other active ingredient of the present invention may be administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic

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factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein or other active ingredient of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

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4.12.1 ROUTES OF ADMINISTRATION

Suitable routes of administration may, for example, include oral, rectal, transmucosal, or intestinal administration; parenteral delivery, including intramuscular, subcutaneous, intramedullary injections, as well as intrathecal, direct intraventricular, intravenous, intraperitoneal, intranasal, or intraocular injections. Administration of protein or other active ingredient of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

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Alternately, one may administer the compound in a local rather than systemic manner, for example, via injection of the compound directly into a arthritic joints or in fibrotic tissue, often in a depot or sustained release formulation. In order to prevent the scarring process frequently occurring as complication of glaucoma surgery, the compounds may be administered topically, for example, as eye drops. Furthermore, one may administer the drug in a targeted drug delivery system, for example, in a liposome coated with a specific antibody, targeting, for example, arthritic or fibrotic tissue. The liposomes will be targeted to and taken up selectively by the afflicted tissue.

The polypeptides of the invention are administered by any route that delivers an effective dosage to the desired site of action. The determination of a suitable route of administration and an effective dosage for a particular indication is within the level of skill in the art. Preferably for wound treatment, one administers the therapeutic compound directly to the site. Suitable dosage ranges for the polypeptides of the invention can be extrapolated from these dosages or from similar studies in appropriate animal models. Dosages can then be adjusted as necessary by the clinician to provide maximal therapeutic benefit.

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4.12.2 COMPOSITIONS/FORMULATIONS

Pharmaceutical compositions for use in accordance with the present invention thus may be formulated in a conventional manner using one or more physiologically acceptable carriers comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. These pharmaceutical compositions may be

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manufactured in a manner that is itself known, e.g., by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping or lyophilizing processes. Proper formulation is dependent upon the route of administration chosen. When a therapeutically effective amount of protein or other active ingredient of the present invention is administered orally, protein or other active ingredient of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein or other active ingredient of the present invention, and preferably from about 25 to 90% protein or 10 other active ingredient of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. 15 When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein or other active ingredient of the present invention, and preferably from about 1 to 50% protein or other active ingredient of the present invention.

When a therapeutically effective amount of protein or other active ingredient of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein or other active ingredient of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein or other active ingredient solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein or other active ingredient of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art. For injection, the agents of the invention may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks's solution, Ringer's solution, or physiological saline buffer. For transmucosal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

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For oral administration, the compounds can be formulated readily by combining the active compounds with pharmaceutically acceptable carriers well known in the art. Such carriers

enable the compounds of the invention to be formulated as tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspensions and the like, for oral ingestion by a patient to be treated. Pharmaceutical preparations for oral use can be obtained from a solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients are, in particular, fillers such as sugars, including lactose, sucrose, mannitol, or sorbitol; cellulose preparations such as, for example, maize starch, wheat starch, rice starch, potato starch, gelatin, gum tragacanth, methyl cellulose, hydroxypropylmethyl-cellulose, sodium carboxymethylcellulose, and/or polyvinylpyrrolidone (PVP). If desired, disintegrating agents may be added, such as the cross-linked polyvinyl pyrrolidone, agar, or alginic acid or a salt thereof such as sodium alginate. Dragee cores are provided with suitable coatings. For this purpose, concentrated sugar solutions may be used, which may optionally contain gum arabic, talc, polyvinyl pyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for identification or to characterize different combinations of active compound doses.

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Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a plasticizer, such as glycerol or sorbitol. The push-fit capsules can contain the active ingredients in admixture with filler such as lactose, binders such as starches, and/or lubricants such as talc or magnesium stearate and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene glycols. In addition, stabilizers may be added. All formulations for oral administration should be in dosages suitable for such administration. For buccal administration, the compositions may take the form of tablets or lozenges formulated in conventional manner.

For administration by inhalation, the compounds for use according to the present invention are conveniently delivered in the form of an aerosol spray presentation from pressurized packs or a nebuliser, with the use of a suitable propellant, e.g., dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane, carbon dioxide or other suitable gas. In the case of a pressurized aerosol the dosage unit may be determined by providing a valve to deliver a metered amount. Capsules and cartridges of, e.g., gelatin for use in an inhaler or insufflator may be formulated containing a powder mix of the compound and a suitable powder base such as lactose or starch. The compounds may be formulated for parenteral administration by injection, e.g., by bolus injection or continuous infusion. Formulations for injection may be presented in unit dosage form, e.g., in ampules or in multi-dose containers, with

an added preservative. The compositions may take such forms as suspensions, solutions or emulsions in oily or aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing and/or dispersing agents.

Pharmaceutical formulations for parenteral administration include aqueous solutions of the active compounds in water-soluble form. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Optionally, the suspension may also contain suitable stabilizers or agents which increase the solubility of the compounds to allow for the preparation of highly concentrated solutions. Alternatively, the active ingredient may be in powder form for constitution with a suitable vehicle, e.g., sterile pyrogen-free water, before use.

The compounds may also be formulated in rectal compositions such as suppositories or retention enemas, e.g., containing conventional suppository bases such as cocoa butter or other glycerides. In addition to the formulations described previously, the compounds may also be formulated as a depot preparation. Such long acting formulations may be administered by implantation (for example subcutaneously or intramuscularly) or by intramuscular injection. Thus, for example, the compounds may be formulated with suitable polymeric or hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives, for example, as a sparingly soluble salt.

A pharmaceutical carrier for the hydrophobic compounds of the invention is a co-solvent system comprising benzyl alcohol, a nonpolar surfactant, a water-miscible organic polymer, and an aqueous phase. The co-solvent system may be the VPD co-solvent system. VPD is a solution of 3% w/v benzyl alcohol, 8% w/v of the nonpolar surfactant polysorbate 80, and 65% w/v polyethylene glycol 300, made up to volume in absolute ethanol. The VPD co-solvent system (VPD:5W) consists of VPD diluted 1:1 with a 5% dextrose in water solution. This co-solvent system dissolves hydrophobic compounds well, and itself produces low toxicity upon systemic administration. Naturally, the proportions of a co-solvent system may be varied considerably without destroying its solubility and toxicity characteristics. Furthermore, the identity of the co-solvent components may be varied: for example, other low-toxicity nonpolar surfactants may be used instead of polysorbate 80; the fraction size of polyethylene glycol may be varied; other biocompatible polymers may replace polyethylene glycol, e.g. polyvinyl pyrrolidone; and other sugars or polysaccharides may substitute for dextrose. Alternatively, other delivery systems for hydrophobic pharmaceutical compounds may be employed. Liposomes and emulsions are well

known examples of delivery vehicles or carriers for hydrophobic drugs. Certain organic solvents such as dimethylsulfoxide also may be employed, although usually at the cost of greater toxicity. Additionally, the compounds may be delivered using a sustained-release system, such as semipermeable matrices of solid hydrophobic polymers containing the therapeutic agent. Various types of sustained-release materials have been established and are well known by those skilled in the art. Sustained-release capsules may, depending on their chemical nature, release the compounds for a few weeks up to over 100 days. Depending on the chemical nature and the biological stability of the therapeutic reagent, additional strategies for protein or other active

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ingredient stabilization may be employed.

The pharmaceutical compositions also may comprise suitable solid or gel phase carriers or excipients. Examples of such carriers or excipients include but are not limited to calcium carbonate, calcium phosphate, various sugars, starches, cellulose derivatives, gelatin, and polymers such as polyethylene glycols. Many of the active ingredients of the invention may be provided as salts with pharmaceutically compatible counter ions. Such pharmaceutically acceptable base addition salts are those salts which retain the biological effectiveness and properties of the free acids and which are obtained by reaction with inorganic or organic bases such as sodium hydroxide, magnesium hydroxide, ammonia, trialkylamine, dialkylamine, monoalkylamine, dibasic amino acids, sodium acetate, potassium benzoate, triethanol amine and the like.

The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) or other active ingredient(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable

lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides, sulfatides, lysolecithins, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent Nos. 4,235,871; 4,501,728; 4,837,028; and 4,737,323, all of which are incorporated herein by reference.

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The amount of protein or other active ingredient of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein or other active ingredient of the present invention with which to treat each individual patient. Initially, the attending physician will administer low doses of protein or other active ingredient of the present invention and observe the patient's response. Larger doses of protein or other active ingredient of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01 µg to about 100 mg (preferably about 0.1 µg to about 10 mg, more preferably about 0.1 µg to about 1 mg) of protein or other active ingredient of the present invention per kg body weight. For compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic. composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein or other active ingredient of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing or other active ingredient-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices for the compositions

may be biodegradable and chemically defined calcium sulfate, tricalcium phosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxyapatite, bioglass, aluminates, or other ceramics. Matrices may be comprised of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalcium phosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability. Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

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15 A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate, 20 poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt %, preferably 1-10 wt % based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the 25 protein the opportunity to assist the osteogenic activity of the progenitor cells. In further compositions, proteins or other active ingredients of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF-α and TGF-β), and 30 insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to humans, are desired patients for such treatment with proteins or other active ingredients of the present invention. The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue regeneration will be determined by the attending physician considering various factors which

modify the action of the proteins, e.g., amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (e.g., bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either in vivo or ex vivo into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA). Cells may also be cultured ex vivo in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced in vivo for therapeutic purposes.

4.12.3 EFFECTIVE DOSAGE

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Pharmaceutical compositions suitable for use in the present invention include compositions wherein the active ingredients are contained in an effective amount to achieve its intended purpose. More specifically, a therapeutically effective amount means an amount effective to prevent development of or to alleviate the existing symptoms of the subject being treated. Determination of the effective amount is well within the capability of those skilled in the art, especially in light of the detailed disclosure provided herein. For any compound used in the method of the invention, the therapeutically effective dose can be estimated initially from appropriate in vitro assays. For example, a dose can be formulated in animal models to achieve a circulating concentration range that can be used to more accurately determine useful doses in humans. For example, a dose can be formulated in animal models to achieve a circulating concentration range that includes the IC₅₀ as determined in cell culture (*i.e.*, the concentration of the test compound which achieves a half-maximal inhibition of the protein's biological activity). Such information can be used to more accurately determine useful doses in humans.

A therapeutically effective dose refers to that amount of the compound that results in amelioration of symptoms or a prolongation of survival in a patient. Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, e.g., for determining the LD₅₀ (the dose lethal to 50% of the

population) and the ED₅₀ (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio between LD₅₀ and ED₅₀. Compounds which exhibit high therapeutic indices are preferred. The data obtained from these cell culture assays and animal studies can be used in formulating a range of dosage for use in human. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED₅₀ with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. The exact formulation, route of administration and dosage can be chosen by the individual physician in view of the patient's condition. See, e.g., Fingl et al., 1975, in "The Pharmacological Basis of Therapeutics", Ch. 1 p.1. Dosage amount and interval may be adjusted individually to provide plasma levels of the active moiety which are sufficient to maintain the desired effects, or minimal effective concentration (MEC). The MEC will vary for each compound but can be estimated from in vitro data. Dosages necessary to achieve the MEC will depend on individual characteristics and route of administration. However, HPLC assays or bioassays can be used to determine plasma concentrations.

Dosage intervals can also be determined using MEC value. Compounds should be administered using a regimen which maintains plasma levels above the MEC for 10-90% of the time, preferably between 30-90% and most preferably between 50-90%. In cases of local administration or selective uptake, the effective local concentration of the drug may not be related to plasma concentration.

An exemplary dosage regimen for polypeptides or other compositions of the invention will be in the range of about 0.01 μ g/kg to 100 mg/kg of body weight daily, with the preferred dose being about 0.1 μ g/kg to 25 mg/kg of patient body weight daily, varying in adults and children. Dosing may be once daily, or equivalent doses may be delivered at longer or shorter intervals.

The amount of composition administered will, of course, be dependent on the subject being treated, on the subject's age and weight, the severity of the affliction, the manner of administration and the judgment of the prescribing physician.

30 4.12.4 PACKAGING

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The compositions may, if desired, be presented in a pack or dispenser device which may contain one or more unit dosage forms containing the active ingredient. The pack may, for example, comprise metal or plastic foil, such as a blister pack. The pack or dispenser device may be accompanied by instructions for administration. Compositions comprising a compound of the

invention formulated in a compatible pharmaceutical carrier may also be prepared, placed in an appropriate container, and labeled for treatment of an indicated condition.

4.13 ANTIBODIES

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Also included in the invention are antibodies to proteins, or fragments of proteins of the invention. The term "antibody" as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin (Ig) molecules, i.e., molecules that contain an antigen binding site that specifically binds (immunoreacts with) an antigen. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, F_{ab} , F_{ab} and $F_{(ab)^2}$ fragments, and an F_{ab} expression library. In general, an antibody molecule obtained from humans relates to any of the classes IgG, IgM, IgA, IgE and IgD, which differ from one another by the nature of the heavy chain present in the molecule. Certain classes have subclasses as well, such as IgG_1 , IgG_2 , and others. Furthermore, in humans, the light chain may be a kappa chain or a lambda chain. Reference herein to antibodies includes a reference to all such classes, subclasses and types of human antibody species.

An isolated related protein of the invention may be intended to serve as an antigen, or a portion or fragment thereof, and additionally can be used as an immunogen to generate antibodies that immunospecifically bind the antigen, using standard techniques for polyclonal and monoclonal antibody preparation. The full-length protein can be used or, alternatively, the invention provides antigenic peptide fragments of the antigen for use as immunogens. An antigenic peptide fragment comprises at least 6 amino acid residues of the amino acid sequence of the full length protein, such as an amino acid sequence shown in SEQ ID NO: 1787, and encompasses an epitope thereof such that an antibody raised against the peptide forms a specific immune complex with the full length protein or with any fragment that contains the epitope. Preferably, the antigenic peptide comprises at least 10 amino acid residues, or at least 15 amino acid residues, or at least 20 amino acid residues, or at least 30 amino acid residues. Preferred epitopes encompassed by the antigenic peptide are regions of the protein that are located on its surface; commonly these are hydrophilic regions.

In certain embodiments of the invention, at least one epitope encompassed by the antigenic peptide is a region of -related protein that is located on the surface of the protein, e.g., a hydrophilic region. A hydrophobicity analysis of the human related protein sequence will indicate which regions of a related protein are particularly hydrophilic and, therefore, are likely to encode surface residues useful for targeting antibody production. As a means for targeting antibody production, hydropathy plots showing regions of hydrophilicity and hydrophobicity may be generated by any method well known in the art, including, for example, the Kyte

Doolittle or the Hopp Woods methods, either with or without Fourier transformation. See, e.g., Hopp and Woods, 1981, Proc. Nat. Acad. Sci. USA 78: 3824-3828; Kyte and Doolittle 1982, J. Mol. Biol. 157: 105-142, each of which is incorporated herein by reference in its entirety. Antibodies that are specific for one or more domains within an antigenic protein, or derivatives, fragments, analogs or homologs thereof, are also provided herein.

A protein of the invention, or a derivative, fragment, analog, homolog or ortholog thereof, may be utilized as an immunogen in the generation of antibodies that immunospecifically bind these protein components.

Various procedures known within the art may be used for the production of polyclonal or monoclonal antibodies directed against a protein of the invention, or against derivatives, fragments, analogs homologs or orthologs thereof (see, for example, Antibodies: A Laboratory Manual, Harlow E, and Lane D, 1988, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, incorporated herein by reference). Some of these antibodies are discussed below.

5.13.1 Polyclonal Antibodies

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For the production of polyclonal antibodies, various suitable host animals (e.g., rabbit, goat, mouse or other mammal) may be immunized by one or more injections with the native protein, a synthetic variant thereof, or a derivative of the foregoing. An appropriate immunogenic preparation can contain, for example, the naturally occurring immunogenic protein, a chemically synthesized polypeptide representing the immunogenic protein, or a recombinantly expressed immunogenic protein. Furthermore, the protein may be conjugated to a second protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response include, but are not limited to, Freund's (complete and incomplete), mineral gels (e.g., aluminum hydroxide), surface active substances (e.g., lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.), adjuvants usable in humans such as Bacille Calmette-Guerin and Corynebacterium parvum, or similar immunostimulatory agents. Additional examples of adjuvants which can be employed include MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate).

The polyclonal antibody molecules directed against the immunogenic protein can be isolated from the mammal (e.g., from the blood) and further purified by well known techniques, such as affinity chromatography using protein A or protein G, which provide primarily the IgG fraction of immune serum. Subsequently, or alternatively, the specific antigen which is the

target of the immunoglobulin sought, or an epitope thereof, may be immobilized on a column to purify the immune specific antibody by immunoaffinity chromatography. Purification of immunoglobulins is discussed, for example, by D. Wilkinson (The Scientist, published by The Scientist, Inc., Philadelphia PA, Vol. 14, No. 8 (April 17, 2000), pp. 25-28).

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5.13.2 Monoclonal Antibodies

The term "monoclonal antibody" (MAb) or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one molecular species of antibody molecule consisting of a unique light chain gene product and a unique heavy chain gene product. In particular, the complementarity determining regions (CDRs) of the monoclonal antibody are identical in all the molecules of the population. MAbs thus contain an antigen binding site capable of immunoreacting with a particular epitope of the antigen characterized by a unique binding affinity for it.

Monoclonal antibodies can be prepared using hybridoma methods, such as those described by Kohler and Milstein, Nature, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes can be immunized in vitro. The immunizing agent will typically include the protein antigen, a fragment thereof or a fusion protein thereof. Generally, either peripheral blood lymphocytes are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding, Monoclonal Antibodies: Principles and Practice, Academic Press, (1986) pp. 59-103). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells can be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego,

California and the American Type Culture Collection, Manassas, Virginia. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies (Kozbor, <u>J. Immunol., 133</u>:3001 (1984); Brodeur et al., <u>Monoclonal Antibody Production Techniques and Applications</u>, Marcel Dekker, Inc., New York, (1987) pp. 51-63).

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The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against the antigen. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an in vitro binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, Anal. Biochem., 107:220 (1980). Preferably, antibodies having a high degree of specificity and a high binding affinity for the target antigen are isolated.

After the desired hybridoma cells are identified, the clones can be subcloned by limiting dilution procedures and grown by standard methods. Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium.

Alternatively, the hybridoma cells can be grown in vivo as ascites in a mammal.

The monoclonal antibodies secreted by the subclones can be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

The monoclonal antibodies can also be made by recombinant DNA methods, such as those described in U.S. Patent No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA can be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. The DNA also can be modified, for example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences (U.S. Patent No. 4,816,567; Morrison, Nature 368, 812-13 (1994)) or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin

polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

5 5.13.2 Humanized Antibodies

The antibodies directed against the protein antigens of the invention can further comprise humanized antibodies or human antibodies. These antibodies are suitable for administration to humans without engendering an immune response by the human against the administered immunoglobulin. Humanized forms of antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')2 or other antigen-10 binding subsequences of antibodies) that are principally comprised of the sequence of a human immunoglobulin, and contain minimal sequence derived from a non-human immunoglobulin. Humanization can be performed following the method of Winter and co-workers (Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-327 (1988); Verhoeyen et al., 15 Science, 239:1534-1536 (1988)), by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. (See also U.S. Patent No. 5,225,539.) In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies can also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the 20 humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones et al., 1986; Riechmann et al., 1988; and Presta, Curr. Op. Struct. Biol., 25 2:593-596 (1992)).

5.13.3 Human Antibodies

Fully human antibodies relate to antibody molecules in which essentially the entire

sequences of both the light chain and the heavy chain, including the CDRs, arise from human
genes. Such antibodies are termed "human antibodies", or "fully human antibodies" herein.

Human monoclonal antibodies can be prepared by the trioma technique; the human B-cell
hybridoma technique (see Kozbor, et al., 1983 Immunol Today 4: 72) and the EBV hybridoma
technique to produce human monoclonal antibodies (see Cole, et al., 1985 In: MONOCLONAL

ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Human monoclonal

antibodies may be utilized in the practice of the present invention and may be produced by using human hybridomas (see Cote, et al., 1983. Proc Natl Acad Sci USA 80: 2026-2030) or by transforming human B-cells with Epstein Barr Virus in vitro (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96).

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In addition, human antibodies can also be produced using additional techniques, including phage display libraries (Hoogenboom and Winter, J. Mol. Biol., 227:381 (1991); Marks et al., J. Mol. Biol., 222:581 (1991)). Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in Marks et al. (Bio/Technology 10, 779-783 (1992)); Lonberg et al. (Nature 368 856-859 (1994)); Morrison (Nature 368, 812-13 (1994)); Fishwild et al. (Nature Biotechnology 14, 845-51 (1996)); Neuberger (Nature Biotechnology 14, 826 (1996)); and Lonberg and Huszar (Intern. Rev. Immunol. 13 65-93 (1995)).

Human antibodies may additionally be produced using transgenic nonhuman animals which are modified so as to produce fully human antibodies rather than the animal's endogenous antibodies in response to challenge by an antigen. (See PCT publication WO94/02602). The endogenous genes encoding the heavy and light immunoglobulin chains in the nonhuman host have been incapacitated, and active loci encoding human heavy and light chain immunoglobulins are inserted into the host's genome. The human genes are incorporated, for example, using yeast artificial chromosomes containing the requisite human DNA segments. An animal which provides all the desired modifications is then obtained as progeny by crossbreeding intermediate transgenic animals containing fewer than the full complement of the modifications. The preferred embodiment of such a nonhuman animal is a mouse, and is termed the Xenomouse 1M as disclosed in PCT publications WO 96/33735 and WO 96/34096. This animal produces B cells which secrete fully human immunoglobulins. The antibodies can be obtained directly from the animal after immunization with an immunogen of interest, as, for example, a preparation of a polyclonal antibody, or alternatively from immortalized B cells derived from the animal, such as hybridomas producing monoclonal antibodies. Additionally, the genes encoding the immunoglobulins with human variable regions can be recovered and expressed to obtain the antibodies directly, or can be further modified to obtain analogs of antibodies such as, for example, single chain Fv molecules.

An example of a method of producing a nonhuman host, exemplified as a mouse, lacking expression of an endogenous immunoglobulin heavy chain is disclosed in U.S. Patent No. 5,939,598. It can be obtained by a method including deleting the J segment genes from at least one endogenous heavy chain locus in an embryonic stem cell to prevent rearrangement of the locus and to prevent formation of a transcript of a rearranged immunoglobulin heavy chain locus, the deletion being effected by a targeting vector containing a gene encoding a selectable marker; and producing from the embryonic stem cell a transgenic mouse whose somatic and germ cells contain the gene encoding the selectable marker.

A method for producing an antibody of interest, such as a human antibody, is disclosed in U.S. Patent No. 5,916,771. It includes introducing an expression vector that contains a nucleotide sequence encoding a heavy chain into one mammalian host cell in culture, introducing an expression vector containing a nucleotide sequence encoding a light chain into another mammalian host cell, and fusing the two cells to form a hybrid cell. The hybrid cell expresses an antibody containing the heavy chain and the light chain.

In a further improvement on this procedure, a method for identifying a clinically relevant epitope on an immunogen, and a correlative method for selecting an antibody that binds immunospecifically to the relevant epitope with high affinity, are disclosed in PCT publication WO 99/53049.

5.13.4 Fab Fragments and Single Chain Antibodies

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According to the invention, techniques can be adapted for the production of single-chain antibodies specific to an antigenic protein of the invention (see e.g., U.S. Patent No. 4,946,778). In addition, methods can be adapted for the construction of F_{ab} expression libraries (see e.g., Huse, et al., 1989 Science 246: 1275-1281) to allow rapid and effective identification of monoclonal F_{ab} fragments with the desired specificity for a protein or derivatives, fragments, analogs or homologs thereof. Antibody fragments that contain the idiotypes to a protein antigen may be produced by techniques known in the art including, but not limited to: (i) an $F_{(ab)/2}$ fragment produced by pepsin digestion of an antibody molecule; (ii) an F_{ab} fragment generated by reducing the disulfide bridges of an $F_{(ab)/2}$ fragment; (iii) an F_{ab} fragment generated by the treatment of the antibody molecule with papain and a reducing agent and (iv) F_v fragments.

5.13.5 Bispecific Antibodies

Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the

binding specificities is for an antigenic protein of the invention. The second binding target is any other antigen, and advantageously is a cell-surface protein or receptor or receptor subunit.

Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities (Milstein and Cuello, Nature, 305:537-539 (1983)). Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the correct bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunecker et al., 1991 EMBO J., 10:3655-3659.

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Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism. For further details of generating bispecific antibodies see, for example, Suresh et al., Methods in Enzymology, 121:210 (1986).

According to another approach described in WO 96/27011, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers which are recovered from recombinant cell culture. The preferred interface comprises at least a part of the CH3 region of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (e.g. tyrosine or tryptophan). Compensatory "cavities" of identical or similar size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (e.g. alanine or threonine). This provides a mechanism for increasing the yield of the heterodimer over other unwanted end-products such as homodimers.

Bispecific antibodies can be prepared as full length antibodies or antibody fragments (e.g. F(ab')₂ bispecific antibodies). Techniques for generating bispecific antibodies from antibody fragments have been described in the literature. For example, bispecific antibodies can be prepared using chemical linkage. Brennan et al., Science 229:81 (1985) describe a procedure wherein intact antibodies are proteolytically cleaved to generate F(ab')₂ fragments. These fragments are reduced in the presence of the dithiol complexing agent sodium arsenite to

stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the Fab'-TNB derivatives is then reconverted to the Fab'-thiol by reduction with mercaptoethylamine and is mixed with an equimolar amount of the other Fab'-TNB derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

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Additionally, Fab' fragments can be directly recovered from E. coli and chemically coupled to form bispecific antibodies. Shalaby et al., J. Exp. Med. 175:217-225 (1992) describe the production of a fully humanized bispecific antibody F(ab')₂ molecule. Each Fab' fragment was separately secreted from E. coli and subjected to directed chemical coupling in vitro to form the bispecific antibody. The bispecific antibody thus formed was able to bind to cells overexpressing the ErbB2 receptor and normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

Various techniques for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers. Kostelny et al., J. Immunol. 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the Fab' portions of two different antibodies by gene fusion. The antibody homodimers were reduced at the hinge region to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by Hollinger et al., Proc. Natl. Acad. Sci. USA 90:6444-6448 (1993) has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain (V_H) connected to a light-chain variable domain (V_L) by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the V_H and V_L domains of one fragment are forced to pair with the complementary V_L and V_H domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (sFv) dimers has also been reported. See, Gruber et al., J. Immunol. 152:5368 (1994).

Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. Tutt et al., <u>J. Immunol.</u> 147:60 (1991). Exemplary bispecific antibodies can bind to two different epitopes, at least one of which originates in the protein antigen of the invention. Alternatively, an anti-antigenic arm of an immunoglobulin molecule can be combined with an arm which binds to a triggering molecule on a leukocyte such as a T-cell receptor molecule (e.g. CD2, CD3, CD28, or B7), or Fc receptors for IgG (FcyR), such as FcyRI (CD64), FcyRII (CD32) and FcyRIII (CD16) so as to focus cellular

defense mechanisms to the cell expressing the particular antigen. Bispecific antibodies can also be used to direct cytotoxic agents to cells which express a particular antigen. These antibodies possess an antigen-binding arm and an arm which binds a cytotoxic agent or a radionuclide chelator, such as EOTUBE, DPTA, DOTA, or TETA. Another bispecific antibody of interest binds the protein antigen described herein and further binds tissue factor (TF).

5.13.6 Heteroconjugate Antibodies

Heteroconjugate antibodies are also within the scope of the present invention.

Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells (U.S. Patent No. 4,676,980), and for treatment of HIV infection (WO 91/00360; WO 92/200373; EP 03089). It is contemplated that the antibodies can be prepared in vitro using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins can be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in U.S. Patent No. 4,676,980.

5.13.7 Effector Function Engineering

It can be desirable to modify the antibody of the invention with respect to effector function, so as to enhance, e.g., the effectiveness of the antibody in treating cancer. For example, cysteine residue(s) can be introduced into the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated can have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). See Caron et al., J. Exp Med., 176: 1191-1195 (1992) and Shopes, J. Immunol., 148: 2918-2922 (1992). Homodimeric antibodies with enhanced antitumor activity can also be prepared using heterobifunctional cross-linkers as described in Wolff et al. Cancer Research, 53: 2560-2565 (1993). Alternatively, an antibody can be engineered that has dual Fc regions and can thereby have enhanced complement lysis and ADCC capabilities. See Stevenson et al., Anti-Cancer Drug Design, 3: 219-230 (1989).

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5.13.8 Immunoconjugates

The invention also pertains to immunoconjugates comprising an antibody conjugated to a cytotoxic agent such as a chemotherapeutic agent, toxin (e.g., an enzymatically active toxin of bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (i.e., a radioconjugate).

Chemotherapeutic agents useful in the generation of such immunoconjugates have been described above. Enzymatically active toxins and fragments thereof that can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from Pseudomonas aeruginosa), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, Aleurites fordii proteins, dianthin proteins, Phytolaca americana proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, crotin, sapaonaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes. A variety of radionuclides are available for the production of radioconjugated antibodies. Examples include ²¹²Bi, ¹³¹I, ¹³¹In, ⁹⁰Y, and ¹⁸⁶Re.

Conjugates of the antibody and cytotoxic agent are made using a variety of bifunctional protein-coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutareldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta et al., Science, 238: 1098 (1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. See WO94/11026.

In another embodiment, the antibody can be conjugated to a "receptor" (such streptavidin) for utilization in tumor pretargeting wherein the antibody-receptor conjugate is administered to the patient, followed by removal of unbound conjugate from the circulation using a clearing agent and then administration of a "ligand" (e.g., avidin) that is in turn conjugated to a cytotoxic agent.

4.14 COMPUTER READABLE SEQUENCES

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In one application of this embodiment, a nucleotide sequence of the present invention can be recorded on computer readable media. As used herein, "computer readable media" refers to any medium which can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. A skilled artisan can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising computer readable medium having recorded thereon

a nucleotide sequence of the present invention. As used herein, "recorded" refers to a process for storing information on computer readable medium. A skilled artisan can readily adopt any of the presently known methods for recording information on computer readable medium to generate manufactures comprising the nucleotide sequence information of the present invention.

A variety of data storage structures are available to a skilled artisan for creating a computer readable medium having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on computer readable medium. The sequence information can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and Microsoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like. A skilled artisan can readily adapt any number of data processor structuring formats (e.g. text file or database) in order to obtain computer readable medium having recorded thereon the nucleotide sequence information of the present invention.

By providing any of the nucleotide sequences SEQ ID NO:1-1786 and 3573-5358 or a representative fragment thereof; or a nucleotide sequence at least 95% identical to any of the nucleotide sequences of SEQ ID NO:1-1786 and 3573-5358 in computer readable form, a skilled artisan can routinely access the sequence information for a variety of purposes. Computer software is publicly available which allows a skilled artisan to access sequence information provided in a computer readable medium. The examples which follow demonstrate how software which implements the BLAST (Altschul et al., J. Mol. Biol. 215:403-410 (1990)) and BLAZE (Brutlag et al., Comp. Chem. 17:203-207 (1993)) search algorithms on a Sybase system is used to identify open reading frames (ORFs) within a nucleic acid sequence. Such ORFs may be protein encoding fragments and may be useful in producing commercially important proteins such as enzymes used in fermentation reactions and in the production of commercially useful metabolites.

As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based systems are suitable for use in the present invention. As stated above, the computer-based systems of the present invention comprise a data storage means having stored therein a nucleotide sequence of the present invention and the necessary hardware means and

software means for supporting and implementing a search means. As used herein, "data storage means" refers to memory which can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded thereon the nucleotide sequence information of the present invention.

As used herein, "search means" refers to one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of a known sequence which match a particular target sequence or target motif. A variety of known algorithms are disclosed publicly and a variety of commercially available software for conducting search means are and can be used in the computer-based systems of the present invention. Examples of such software includes, but is not limited to, Smith-Waterman, MacPattern (EMBL), BLASTN and BLASTA (NPOLYPEPTIDEIA). A skilled artisan can readily recognize that any one of the available algorithms or implementing software packages for conducting homology searches can be adapted for use in the present computer-based systems. As used herein, a "target sequence" can be any nucleic acid or amino acid sequence of six or more nucleotides or two or more amino acids. A skilled artisan can readily recognize that the longer a target sequence is, the less likely a target sequence will be present as a random occurrence in the database. The most preferred sequence length of a target sequence is from about 10 to 300 amino acids, more preferably from about 30 to 100 nucleotide residues. However, it is well recognized that searches for commercially important fragments, such as sequence fragments involved in gene expression and protein processing, may be of shorter length.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration which is formed upon the folding of the target motif. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzyme active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, promoter sequences, hairpin structures and inducible expression elements (protein binding sequences).

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4.15 TRIPLE HELIX FORMATION

In addition, the fragments of the present invention, as broadly described, can be used to control gene expression through triple helix formation or antisense DNA or RNA, both of which methods are based on the binding of a polynucleotide sequence to DNA or RNA.

35 Polynucleotides suitable for use in these methods are preferably 20 to 40 bases in length and are

designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 15241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Olmno, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide.

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4.16 DIAGNOSTIC ASSAYS AND KITS

The present invention further provides methods to identify the presence or expression of one of the ORFs of the present invention, or homolog thereof, in a test sample, using a nucleic acid probe or antibodies of the present invention, optionally conjugated or otherwise associated with a suitable label.

In general, methods for detecting a polynucleotide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polynucleotide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polynucleotide of the invention is detected in the sample. Such methods can also comprise contacting a sample under stringent hybridization conditions with nucleic acid primers that anneal to a polynucleotide of the invention under such conditions, and amplifying annealed polynucleotides, so that if a polynucleotide is amplified, a polynucleotide of the invention is detected in the sample.

In general, methods for detecting a polypeptide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polypeptide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polypeptide of the invention is detected in the sample.

In detail, such methods comprise incubating a test sample with one or more of the antibodies or one or more of the nucleic acid probes of the present invention and assaying for binding of the nucleic acid probes or antibodies to components within the test sample.

Conditions for incubating a nucleic acid probe or antibody with a test sample vary. Incubation conditions depend on the format employed in the assay, the detection methods employed, and the type and nature of the nucleic acid probe or antibody used in the assay. One skilled in the art will recognize that any one of the commonly available hybridization, amplification or immunological assay formats can readily be adapted to employ the nucleic acid

probes or antibodies of the present invention. Examples of such assays can be found in Chard, T., An Introduction to Radioimmunoassay and Related Techniques, Elsevier Science Publishers, Amsterdam, The Netherlands (1986); Bullock, G.R. et al., Techniques in Immunocytochemistry, Academic Press, Orlando, FL Vol. 1 (1982), Vol. 2 (1983), Vol. 3 (1985); Tijssen, P., Practice and Theory of immunoassays: Laboratory Techniques in Biochemistry and Molecular Biology, Elsevier Science Publishers, Amsterdam, The Netherlands (1985). The test samples of the present invention include cells, protein or membrane extracts of cells, or biological fluids such as sputum, blood, serum, plasma, or urine. The test sample used in the above-described method will vary based on the assay format, nature of the detection method and the tissues, cells or extracts used as the sample to be assayed. Methods for preparing protein extracts or membrane extracts of cells are well known in the art and can be readily be adapted in order to obtain a sample which is compatible with the system utilized.

In another embodiment of the present invention, kits are provided which contain the necessary reagents to carry out the assays of the present invention. Specifically, the invention provides a compartment kit to receive, in close confinement, one or more containers which comprises: (a) a first container comprising one of the probes or antibodies of the present invention; and (b) one or more other containers comprising one or more of the following: wash reagents, reagents capable of detecting presence of a bound probe or antibody.

In detail, a compartment kit includes any kit in which reagents are contained in separate containers. Such containers include small glass containers, plastic containers or strips of plastic or paper. Such containers allows one to efficiently transfer reagents from one compartment to another compartment such that the samples and reagents are not cross-contaminated, and the agents or solutions of each container can be added in a quantitative fashion from one compartment to another. Such containers will include a container which will accept the test sample, a container which contains the antibodies used in the assay, containers which contain wash reagents (such as phosphate buffered saline, Tris-buffers, etc.), and containers which contain the reagents used to detect the bound antibody or probe. Types of detection reagents include labeled nucleic acid probes, labeled secondary antibodies, or in the alternative, if the primary antibody is labeled, the enzymatic, or antibody binding reagents which are capable of reacting with the labeled antibody. One skilled in the art will readily recognize that the disclosed probes and antibodies of the present invention can be readily incorporated into one of the established kit formats which are well known in the art.

4.17 MEDICAL IMAGING

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The novel polypeptides and binding partners of the invention are useful in medical imaging of sites expressing the molecules of the invention (e.g., where the polypeptide of the invention is involved in the immune response, for imaging sites of inflammation or infection). See, e.g., Kunkel et al., U.S. Pat. NO. 5,413,778. Such methods involve chemical attachment of a labeling or imaging agent, administration of the labeled polypeptide to a subject in a pharmaceutically acceptable carrier, and imaging the labeled polypeptide *in vivo* at the target site.

4.18 SCREENING ASSAYS

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Using the isolated proteins and polynucleotides of the invention, the present invention further provides methods of obtaining and identifying agents which bind to a polypeptide encoded by an ORF corresponding to any of the nucleotide sequences set forth in SEQ ID NO:1-1786 and 3573-5358, or bind to a specific domain of the polypeptide encoded by the nucleic acid. In detail, said method comprises the steps of:

- (a) contacting an agent with an isolated protein encoded by an ORF of the present invention, or nucleic acid of the invention; and
 - (b) determining whether the agent binds to said protein or said nucleic acid.

In general, therefore, such methods for identifying compounds that bind to a polynucleotide of the invention can comprise contacting a compound with a polynucleotide of the invention for a time sufficient to form a polynucleotide/compound complex, and detecting the complex, so that if a polynucleotide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Likewise, in general, therefore, such methods for identifying compounds that bind to a polypeptide of the invention can comprise contacting a compound with a polypeptide of the invention for a time sufficient to form a polypeptide/compound complex, and detecting the complex, so that if a polypeptide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Methods for identifying compounds that bind to a polypeptide of the invention can also comprise contacting a compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a receptor gene sequence in the cell, and detecting the complex by detecting reporter gene sequence expression, so that if a polypeptide/compound complex is detected, a compound that binds a polypeptide of the invention is identified.

Compounds identified via such methods can include compounds which modulate the activity of a polypeptide of the invention (that is, increase or decrease its activity, relative to

activity observed in the absence of the compound). Alternatively, compounds identified via such methods can include compounds which modulate the expression of a polynucleotide of the invention (that is, increase or decrease expression relative to expression levels observed in the absence of the compound). Compounds, such as compounds identified via the methods of the invention, can be tested using standard assays well known to those of skill in the art for their ability to modulate activity/expression.

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The agents screened in the above assay can be, but are not limited to, peptides, carbohydrates, vitamin derivatives, or other pharmaceutical agents. The agents can be selected and screened at random or rationally selected or designed using protein modeling techniques.

For random screening, agents such as peptides, carbohydrates, pharmaceutical agents and the like are selected at random and are assayed for their ability to bind to the protein encoded by the ORF of the present invention. Alternatively, agents may be rationally selected or designed. As used herein, an agent is said to be "rationally selected or designed" when the agent is chosen based on the configuration of the particular protein. For example, one skilled in the art can readily adapt currently available procedures to generate peptides, pharmaceutical agents and the like, capable of binding to a specific peptide sequence, in order to generate rationally designed antipeptide peptides, for example see Hurby et al., Application of Synthetic Peptides: Antisense Peptides," In Synthetic Peptides, A User's Guide, W.H. Freeman, NY (1992), pp. 289-307, and Kaspczak et al., Biochemistry 28:9230-8 (1989), or pharmaceutical agents, or the like.

In addition to the foregoing, one class of agents of the present invention, as broadly described, can be used to control gene expression through binding to one of the ORFs or EMFs of the present invention. As described above, such agents can be randomly screened or rationally designed/selected. Targeting the ORF or EMF allows a skilled artisan to design sequence specific or element specific agents, modulating the expression of either a single ORF or multiple ORFs which rely on the same EMF for expression control. One class of DNA binding agents are agents which contain base residues which hybridize or form a triple helix formation by binding to DNA or RNA. Such agents can be based on the classic phosphodiester, ribonucleic acid backbone, or can be a variety of sulfhydryl or polymeric derivatives which have base attachment capacity.

Agents suitable for use in these methods preferably contain 20 to 40 bases and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Okano, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription

from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide and other DNA binding agents.

Agents which bind to a protein encoded by one of the ORFs of the present invention can be used as a diagnostic agent. Agents which bind to a protein encoded by one of the ORFs of the present invention can be formulated using known techniques to generate a pharmaceutical composition.

10 4.19 USE OF NUCLEIC ACIDS AS PROBES

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Another aspect of the subject invention is to provide for polypeptide-specific nucleic acid hybridization probes capable of hybridizing with naturally occurring nucleotide sequences. The hybridization probes of the subject invention may be derived from any of the nucleotide sequences SEQ ID NO:1-1786 and 3573-5358. Because the corresponding gene is only expressed in a limited number of tissues, a hybridization probe derived from of any of the nucleotide sequences SEQ ID NO:1-1786 and 3573-5358 can be used as an indicator of the presence of RNA of cell type of such a tissue in a sample.

Any suitable hybridization technique can be employed, such as, for example, in situ hybridization. PCR as described in US Patents Nos. 4,683,195 and 4,965,188 provides additional uses for oligonucleotides based upon the nucleotide sequences. Such probes used in PCR may be of recombinant origin, may be chemically synthesized, or a mixture of both. The probe will comprise a discrete nucleotide sequence for the detection of identical sequences or a degenerate pool of possible sequences for identification of closely related genomic sequences.

Other means for producing specific hybridization probes for nucleic acids include the cloning of nucleic acid sequences into vectors for the production of mRNA probes. Such vectors are known in the art and are commercially available and may be used to synthesize RNA probes in vitro by means of the addition of the appropriate RNA polymerase as T7 or SP6 RNA polymerase and the appropriate radioactively labeled nucleotides. The nucleotide sequences may be used to construct hybridization probes for mapping their respective genomic sequences. The nucleotide sequence provided herein may be mapped to a chromosome or specific regions of a chromosome using well known genetic and/or chromosomal mapping techniques. These techniques include in situ hybridization, linkage analysis against known chromosomal markers, hybridization screening with libraries or flow-sorted chromosomal preparations specific to known chromosomes, and the like. The technique of fluorescent in situ hybridization of

chromosome spreads has been described, among other places, in Verma et al (1988) Human Chromosomes: A Manual of Basic Techniques, Pergamon Press, New York NY.

Fluorescent in situ hybridization of chromosomal preparations and other physical chromosome mapping techniques may be correlated with additional genetic map data. Examples of genetic map data can be found in the 1994 Genome Issue of Science (265:1981f). Correlation between the location of a nucleic acid on a physical chromosomal map and a specific disease (or predisposition to a specific disease) may help delimit the region of DNA associated with that genetic disease. The nucleotide sequences of the subject invention may be used to detect differences in gene sequences between normal, carrier or affected individuals.

4.20 PREPARATION OF SUPPORT BOUND OLIGONUCLEOTIDES

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Oligonucleotides, i.e., small nucleic acid segments, may be readily prepared by, for example, directly synthesizing the oligonucleotide by chemical means, as is commonly practiced using an automated oligonucleotide synthesizer.

Support bound oligonucleotides may be prepared by any of the methods known to those of skill in the art using any suitable support such as glass, polystyrene or Teflon. One strategy is to precisely spot oligonucleotides synthesized by standard synthesizers. Immobilization can be achieved using passive adsorption (Inouye & Hondo, (1990) J. Clin. Microbiol. 28(6) 1469-72); using UV light (Nagata et al., 1985; Dahlen et al., 1987; Morrissey & Collins, (1989) Mol. Cell Probes 3(2) 189-207) or by covalent binding of base modified DNA (Keller et al., 1988; 1989); all references being specifically incorporated herein.

Another strategy that may be employed is the use of the strong biotin-streptavidin interaction as a linker. For example, Broude et al. (1994) Proc. Natl. Acad. Sci. USA 91(8) 3072-6, describe the use of biotinylated probes, although these are duplex probes, that are immobilized on streptavidin-coated magnetic beads. Streptavidin-coated beads may be purchased from Dynal, Oslo. Of course, this same linking chemistry is applicable to coating any surface with streptavidin. Biotinylated probes may be purchased from various sources, such as, e.g., Operon Technologies (Alameda, CA).

Nunc Laboratories (Naperville, IL) is also selling suitable material that could be used. Nunc Laboratories have developed a method by which DNA can be covalently bound to the microwell surface termed Covalink NH. CovaLink NH is a polystyrene surface grafted with secondary amino groups (>NH) that serve as bridge-heads for further covalent coupling. CovaLink Modules may be purchased from Nunc Laboratories. DNA molecules may be bound to CovaLink exclusively at the 5'-end by a phosphoramidate bond, allowing immobilization of more than 1 pmol of DNA (Rasmussen et al., (1991) Anal. Biochem. 198(1) 138-42).

The use of CovaLink NH strips for covalent binding of DNA molecules at the 5'-end has been described (Rasmussen et al., (1991). In this technology, a phosphoramidate bond is employed (Chu et al., (1983) Nucleic Acids Res. 11(8) 6513-29). This is beneficial as immobilization using only a single covalent bond is preferred. The phosphoramidate bond joins the DNA to the CovaLink NH secondary amino groups that are positioned at the end of spacer arms covalently grafted onto the polystyrene surface through a 2 nm long spacer arm. To link an oligonucleotide to CovaLink NH via an phosphoramidate bond, the oligonucleotide terminus must have a 5'-end phosphate group. It is, perhaps, even possible for biotin to be covalently bound to CovaLink and then streptavidin used to bind the probes.

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More specifically, the linkage method includes dissolving DNA in water (7.5 ng/ul) and denaturing for 10 min. at 95°C and cooling on ice for 10 min. Ice-cold 0.1 M 1-methylimidazole, pH 7.0 (1-MeIm₇), is then added to a final concentration of 10 mM 1-MeIm₇. A ss DNA solution is then dispensed into CovaLink NH strips (75 ul/well) standing on ice.

Carbodiimide 0.2 M 1-ethyl-3-(3-dimethylaminopropyl)-carbodiimide (EDC), dissolved in 10 mM 1-MeIm₇, is made fresh and 25 ul added per well. The strips are incubated for 5 hours at 50°C. After incubation the strips are washed using, e.g., Nunc-Immuno Wash; first the wells are washed 3 times, then they are soaked with washing solution for 5 min., and finally they are washed 3 times (where in the washing solution is 0.4 N NaOH, 0.25% SDS heated to 50°C).

It is contemplated that a further suitable method for use with the present invention is that described in PCT Patent Application WO 90/03382 (Southern & Maskos), incorporated herein by reference. This method of preparing an oligonucleotide bound to a support involves attaching a nucleoside 3'-reagent through the phosphate group by a covalent phosphodiester link to aliphatic hydroxyl groups carried by the support. The oligonucleotide is then synthesized on the supported nucleoside and protecting groups removed from the synthetic oligonucleotide chain under standard conditions that do not cleave the oligonucleotide from the support. Suitable reagents include nucleoside phosphoramidite and nucleoside hydrogen phosphorate.

An on-chip strategy for the preparation of DNA probe for the preparation of DNA probe arrays may be employed. For example, addressable laser-activated photodeprotection may be employed in the chemical synthesis of oligonucleotides directly on a glass surface, as described by Fodor *et al.* (1991) Science 251(4995) 767-73, incorporated herein by reference. Probes may also be immobilized on nylon supports as described by Van Ness *et al.* (1991) Nucleic Acids Res. 19(12) 3345-50; or linked to Teflon using the method of Duncan & Cavalier (1988) Anal. Biochem. 169(1) 104-8; all references being specifically incorporated herein.

To link an oligonucleotide to a nylon support, as described by Van Ness *et al.* (1991), requires activation of the nylon surface via alkylation and selective activation of the 5'-amine of oligonucleotides with cyanuric chloride.

One particular way to prepare support bound oligonucleotides is to utilize the light-generated synthesis described by Pease *et al.*, (1994) PNAS USA 91(11) 5022-6, incorporated herein by reference). These authors used current photolithographic techniques to generate arrays of immobilized oligonucleotide probes (DNA chips). These methods, in which light is used to direct the synthesis of oligonucleotide probes in high-density, miniaturized arrays, utilize photolabile 5'-protected *N*-acyl-deoxynucleoside phosphoramidites, surface linker chemistry and versatile combinatorial synthesis strategies. A matrix of 256 spatially defined oligonucleotide probes may be generated in this manner.

4.21 PREPARATION OF NUCLEIC ACID FRAGMENTS

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The nucleic acids may be obtained from any appropriate source, such as cDNAs, genomic DNA, chromosomal DNA, microdissected chromosome bands, cosmid or YAC inserts, and RNA, including mRNA without any amplification steps. For example, Sambrook *et al.* (1989) describes three protocols for the isolation of high molecular weight DNA from mammalian cells (p. 9.14-9.23).

DNA fragments may be prepared as clones in M13, plasmid or lambda vectors and/or prepared directly from genomic DNA or cDNA by PCR or other amplification methods. Samples may be prepared or dispensed in multiwell plates. About 100-1000 ng of DNA samples may be prepared in 2-500 ml of final volume.

The nucleic acids would then be fragmented by any of the methods known to those of skill in the art including, for example, using restriction enzymes as described at 9.24-9.28 of Sambrook et al. (1989), shearing by ultrasound and NaOH treatment.

Low pressure shearing is also appropriate, as described by Schriefer et al. (1990) Nucleic Acids Res. 18(24) 7455-6, incorporated herein by reference). In this method, DNA samples are passed through a small French pressure cell at a variety of low to intermediate pressures. A lever device allows controlled application of low to intermediate pressures to the cell. The results of these studies indicate that low-pressure shearing is a useful alternative to sonic and enzymatic DNA fragmentation methods.

One particularly suitable way for fragmenting DNA is contemplated to be that using the two base recognition endonuclease, CviII, described by Fitzgerald et al. (1992) Nucleic Acids Res. 20(14) 3753-62. These authors described an approach for the rapid fragmentation and fractionation

of DNA into particular sizes that they contemplated to be suitable for shotgun cloning and sequencing.

The restriction endonuclease CviJI normally cleaves the recognition sequence PuGCPy between the G and C to leave blunt ends. Atypical reaction conditions, which alter the specificity of this enzyme (CviJI**), yield a quasi-random distribution of DNA fragments form the small molecule pUC19 (2688 base pairs). Fitzgerald et al. (1992) quantitatively evaluated the randomness of this fragmentation strategy, using a CviJI** digest of pUC19 that was size fractionated by a rapid gel filtration method and directly ligated, without end repair, to a lac Z minus M13 cloning vector. Sequence analysis of 76 clones showed that CviJI** restricts pyGCPy and PuGCPu, in addition to PuGCPy sites, and that new sequence data is accumulated at a rate consistent with random fragmentation.

As reported in the literature, advantages of this approach compared to sonication and agarose gel fractionation include: smaller amounts of DNA are required (0.2-0.5 ug instead of 2-5 ug); and fewer steps are involved (no preligation, end repair, chemical extraction, or agarose gel electrophoresis and elution are needed

Irrespective of the manner in which the nucleic acid fragments are obtained or prepared, it is important to denature the DNA to give single stranded pieces available for hybridization. This is achieved by incubating the DNA solution for 2-5 minutes at 80-90°C. The solution is then cooled quickly to 2°C to prevent renaturation of the DNA fragments before they are contacted with the chip. Phosphate groups must also be removed from genomic DNA by methods known in the art.

4.22 PREPARATION OF DNA ARRAYS

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Arrays may be prepared by spotting DNA samples on a support such as a nylon membrane. Spotting may be performed by using arrays of metal pins (the positions of which correspond to an array of wells in a microtiter plate) to repeated by transfer of about 20 nl of a DNA solution to a nylon membrane. By offset printing, a density of dots higher than the density of the wells is achieved. One to 25 dots may be accommodated in 1 mm², depending on the type of label used. By avoiding spotting in some preselected number of rows and columns, separate subsets (subarrays) may be formed. Samples in one subarray may be the same genomic segment of DNA (or the same gene) from different individuals, or may be different, overlapped genomic clones. Each of the subarrays may represent replica spotting of the same samples. In one example, a selected gene segment may be amplified from 64 patients. For each patient, the amplified gene segment may be in one 96-well plate (all 96 wells containing the same sample). A plate for each of the 64 patients is prepared. By using a 96-pin device, all samples may be spotted on one 8 x 12 cm membrane.

Subarrays may contain 64 samples, one from each patient. Where the 96 subarrays are identical, the dot span may be 1 mm² and there may be a 1 mm space between subarrays.

Another approach is to use membranes or plates (available from NUNC, Naperville, Illinois) which may be partitioned by physical spacers e.g. a plastic grid molded over the membrane, the grid being similar to the sort of membrane applied to the bottom of multiwell plates, or hydrophobic strips. A fixed physical spacer is not preferred for imaging by exposure to flat phosphor-storage screens or x-ray films.

The present invention is illustrated in the following examples. Upon consideration of the present disclosure, one of skill in the art will appreciate that many other embodiments and variations may be made in the scope of the present invention. Accordingly, it is intended that the broader aspects of the present invention not be limited to the disclosure of the following examples. The present invention is not to be limited in scope by the exemplified embodiments which are intended as illustrations of single aspects of the invention, and compositions and methods which are functionally equivalent are within the scope of the invention. Indeed, numerous modifications and variations in the practice of the invention are expected to occur to those skilled in the art upon consideration of the present preferred embodiments. Consequently, the only limitations which should be placed upon the scope of the invention are those which appear in the appended claims.

All references cited within the body of the instant specification are hereby incorporated by reference in their entirety.

20 5.0 EXAMPLES

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5.1.1 EXAMPLE 1

Novel Nucleic Acid Sequences Obtained From Various Libraries

A plurality of novel nucleic acids were obtained from cDNA libraries prepared from various human tissues and in some cases isolated from a genomic library derived from human chromosome using standard PCR, SBH sequence signature analysis and Sanger sequencing techniques. The inserts of the library were amplified with PCR using primers specific for the vector sequences which flank the inserts. Clones from cDNA libraries were spotted on nylon membrane filters and screened with oligonucleotide probes (e.g., 7-mers) to obtain signature sequences. The clones were clustered into groups of similar or identical sequences. Representative clones were selected for sequencing.

In some cases, the 5' sequence of the amplified inserts was then deduced using a typical Sanger sequencing protocol. PCR products were purified and subjected to fluorescent dye terminator cycle sequencing. Single pass gel sequencing was done using a 377 Applied Biosystems (ABI) sequencer to obtain the novel nucleic acid sequences. In some cases RACE (Random Amplification of cDNA Ends) was performed to further extend the sequence in the 5' direction.

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5.1.2 EXAMPLE 2

Assemblage of Novel Nucleic Acids

The contigs or nucleic acids of the present invention, designated as SEQ ID NO: 3573-5358 were assembled using an EST sequence as a seed. Then a recursive algorithm was used to extend the seed EST into an extended assemblage, by pulling additional sequences from different databases (i.e., Hyseq's database containing EST sequences, dbEST version 114, gb pri 114, and UniGene version 101) that belong to this assemblage. The algorithm terminated when there was no additional sequences from the above databases that would extend the assemblage. Inclusion of component sequences into the assemblage was based on a BLASTN hit to the extending assemblage with BLAST score greater than 300 and percent identity greater than 95%.

A polypeptide was predicted to be encoded by each of SEQ ID NO:3573-5358 as set forth below. The polypeptides was predicted using a software program called FASTY (available from http://fasta.bioch.virginia.edu) which selects a polypeptides based on a comparison of translated novel polynucleotide to known polynucleotides (W.R. Pearson, Methods in Enzymology, 183:63-98 (1990), herein incorporated by reference. The predicted polypeptides are shown in Table 7.

5.2.2 EXAMPLE 3

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Novel Nucleic Acids

Using PHRAP (Univ. of Washington) or CAP4 (Paracel), a full length gene cDNA sequence and its corresponding protein sequence were generated from the assemblage. Any frame shifts and incorrect stop codons were corrected by hand editing. During editing, the sequence was checked using FASTY and/or BLAST against Genebank. Other computer programs which may have been used in the editing process were phredPhrap and Consed (University of Washington) and ed-ready, ed-ext and gc-zip-2 (Hyseq, Inc.). The full-length nucleotide, including splice variants resulting from these procedures are shown in the Sequence Listing as SEQ ID NOS:1-327.

Table 1 shows the various tissue sources of SEQ ID NO: 1-327.

The nearest neighbor results for SEQ ID NO: 1-327 were obtained by a FASTA version 3 search against Genpept release 117, using FASTXY algorithm. FASTXY is an improved version of FASTA alignment which allows in-codon frame shifts. The nearest neighbor result showed the closest homologue for SEQ ID NO: 1-327 from Genpept. The translated amino acid sequences for which the nucleic acid sequence encodes are shown in the Sequence Listing. The nearest neighbor results for SEQ ID NO: 1-327 are shown in Table 2 below.

Using eMatrix software package (Stanford University, Stanford, CA) (Wu et al., J. Comp. Biol., Vol. 6 pp. 219-235 (1999) herein incorporated by reference), all the sequences were examined to determine whether they had identifiable signature regions. Table 3 shows the

signature region found in the indicated polypeptide sequences, the description of the signature, the eMatrix p-value(s) and the position(s) of the signature within the polypeptide sequence.

Using the pFam software program (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1) pp. 320-322 (1998) herein incorporated by reference) all the polypeptide sequences were examined for domains with homology to certain peptide domains. Table 4 shows the name of the domain found, the description, the p-value and the pFam score for the identified domain within the sequence.

The nucleotide sequence within the sequences that codes for signal peptide sequences and their cleavage sites can be determine from using Neural Network SignalP V1.1 program (from Center for Biological Sequence Analysis, The Technical University of Denmark). The process for identifying prokaryotic and eukaryotic signal peptides and their cleavage sites are also disclosed by Henrik Nielson, Jacob Engelbrecht, Soren Brunak, and Gunnar von Heijne in the publication "Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites" Protein Engineering, Vol. 10, no. 1, pp. 1-6 (1997), incorporated herein by reference. A maximum S score and a mean S score, as described in the Nielson et as reference, was obtained for the polypeptide sequences. Table 5 shows the position of the signal peptide in each of the polypeptides and the maximum score and mean score associated with that signal peptide.

5.3.2 EXAMPLE 4

Novel Nucleic Acids

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Using PHRAP (Univ. of Washington) or CAP4 (Paracel), a full length gene cDNA sequence and its corresponding protein sequence were generated from the assemblage. Any frame shifts and incorrect stop codons were corrected by hand editing. During editing, the sequence was checked using FASTY and/or BLAST against Genbank (i.e., dbEST version 117, gb pri 117, UniGene version 117, Genpept release 117). Other computer programs which may have been used in the editing process were phredPhrap and Consed (University of Washington) and ed-ready, edext and gc-zip-2 (Hyseq, Inc.). The full-length nucleotide, including splice variants resulting from these procedures are shown in the Sequence Listing as SEQ ID NOS: 328-1413.

Table 1 shows the various tissue sources of SEQ ID NO: 328-1413.

The nearest neighbor results for SEQ ID NO: 328-1413 were obtained by a BLASTP version 2.0al 19MP-WashU search against Genpept release 118, using BLAST algorithm. The nearest neighbor result showed the closest homologue for SEQ ID NO: 328-1413 from Genpept. The translated amino acid sequences for which the nucleic acid sequence encodes are shown in

the Sequence Listing. The nearest neighbor results for SEQ ID NO: 328-1413 are shown in Table 2 below.

Using eMatrix software package (Stanford University, Stanford, CA) (Wu et al., J. Comp. Biol., Vol. 6 pp. 219-235 (1999) herein incorporated by reference), all the sequences were examined to determine whether they had identifiable signature regions. Table 3 shows the signature region found in the indicated polypeptide sequences, the description of the signature, the eMatrix p-value(s) and the position(s) of the signature within the polypeptide sequence.

Using the pFam software program (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1) pp. 320-322 (1998) herein incorporated by reference) all the polypeptide sequences were

10 examined for domains with homology to certain peptide domains. Table 4 shows the name of the domain found, the description, the p-value and the pFam score for the identified domain within the sequence.

The nucleotide sequence within the sequences that codes for signal peptide sequences and their cleavage sites can be determine from using Neural Network SignalP V1.1 program (from Center for Biological Sequence Analysis, The Technical University of Denmark). The process for identifying prokaryotic and eukaryotic signal peptides and their cleavage sites are also disclosed by Henrik Nielson, Jacob Engelbrecht, Soren Brunak, and Gunnar von Heijne in the publication "Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites" Protein Engineering, Vol. 10, no. 1, pp. 1-6 (1997), incorporated herein by reference. A maximum S score and a mean S score, as described in the Nielson et as reference, was obtained for the polypeptide sequences. Table 5 shows the position of the signal peptide in each of the polypeptides and the maximum score and mean score associated with that signal peptide.

25 **5.3.2 EXAMPLE 5**

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Novel Nucleic Acids

Using PHRAP (Univ. of Washington) or CAP4 (Paracel), a full length gene cDNA sequence and its corresponding protein sequence were generated from the assemblage. Any frame shifts and incorrect stop codons were corrected by hand editing. During editing, the sequence was checked using FASTY and/or BLAST against Genbank (i.e., dbEST version 117, gb pri 117, UniGene version 117, Genpept release 117). Other computer programs which may have been used in the editing process were phredPhrap and Consed (University of Washington) and ed-ready, edext and gc-zip-2 (Hyseq, Inc.). The full-length nucleotide sequences, including splice variants resulting from these procedures are shown in the Sequence Listing as SEQ ID NOS: 1414-1652.

Table 1 shows the various tissue sources of SEQ ID NO: 1414-1652.

The nearest neighbor results for SEQ ID NO: 1414-1652 were obtained by a BLASTP version 2.0al 19MP-WashU search against Genpept release 118, using BLAST algorithm. The nearest neighbor result showed the closest homologue for SEQ ID NO: 1414-1652 from Genpept. The translated amino acid sequences for which the nucleic acid sequence encodes are shown in the Sequence Listing. The nearest neighbor results for SEQ ID NO: 1414-1652 are shown in Table 2 below.

Using eMatrix software package (Stanford University, Stanford, CA) (Wu et al., J. Comp. Biol., Vol. 6 pp. 219-235 (1999) herein incorporated by reference), all the sequences were examined to determine whether they had identifiable signature regions. Table 3 shows the signature region found in the indicated polypeptide sequences, the description of the signature, the eMatrix p-value(s) and the position(s) of the signature within the polypeptide sequence.

Using the pFam software program (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1) pp. 320-322 (1998) herein incorporated by reference) all the polypeptide sequences were examined for domains with homology to certain peptide domains. Table 4 shows the name of the domain found, the description, the p-value and the pFam score for the identified domain within the sequence.

The nucleotide sequence within the sequences that codes for signal peptide sequences and their cleavage sites can be determine from using Neural Network SignalP V1.1 program (from Center for Biological Sequence Analysis, The Technical University of Denmark). The process for identifying prokaryotic and eukaryotic signal peptides and their cleavage sites are also disclosed by Henrik Nielson, Jacob Engelbrecht, Soren Brunak, and Gunnar von Heijne in the publication "Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites" Protein Engineering, Vol. 10, no. 1, pp. 1-6 (1997), incorporated herein by reference. A maximum S score and a mean S score, as described in the Nielson et as reference, was obtained for the polypeptide sequences. Table 5 shows the position of the signal peptide in each of the polypeptides and the maximum score and mean score associated with that signal peptide.

5.4.2 EXAMPLE 6

30 <u>Novel Nucleic Acids</u>

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Using PHRAP (Univ. of Washington) or CAP4 (Paracel), a full length gene cDNA sequence and its corresponding protein sequence were generated from the assemblage. Any frame shifts and incorrect stop codons were corrected by hand editing. During editing, the sequence was checked using FASTY and/or BLAST against Genbank (i.e., dbEST version 118, gb pri 118,

UniGene version 118, Genpept release 118). Other computer programs which may have been used in the editing process were phredPhrap and Consed (University of Washington) and ed-ready, edext and gc-zip-2 (Hyseq, Inc.). The full-length nucleotide sequences, including splice variants resulting from these procedures are shown in the Sequence Listing as SEQ ID NOS: 1653-1745.

Table 1 shows the various tissue sources of SEQ ID NO: 1653-1745.

The homology for SEQ ID NO: 1653-1745 were obtained by a BLASTP version 2.0al 19MP-WashU search against Genpept release 118, using BLAST algorithm. The results showed homologues for SEQ ID NO: 1653-1745 from Genpept. The translated amino acid sequences for which the nucleic acid sequence encodes are shown in the Sequence Listing. The homologues with identifiable functions for SEQ ID NO: 1653-1745 are shown in Table 2 below.

Using eMatrix software package (Stanford University, Stanford, CA) (Wu et al., J. Comp. Biol., Vol. 6 pp. 219-235 (1999) herein incorporated by reference), all the sequences were examined to determine whether they had identifiable signature regions. Table 3 shows the signature region found in the indicated polypeptide sequences, the description of the signature, the eMatrix p-value(s) and the position(s) of the signature within the polypeptide sequence.

Using the pFam software program (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1) pp. 320-322 (1998) herein incorporated by reference) all the polypeptide sequences were examined for domains with homology to certain peptide domains. Table 4 shows the name of the domain found, the description, the p-value and the pFam score for the identified domain within the sequence.

The nucleotide sequence within the sequences that codes for signal peptide sequences and their cleavage sites can be determine from using Neural Network SignalP V1.1 program (from Center for Biological Sequence Analysis, The Technical University of Denmark). The process for identifying prokaryotic and eukaryotic signal peptides and their cleavage sites are also disclosed by Henrik Nielson, Jacob Engelbrecht, Soren Brunak, and Gunnar von Heijne in the publication "Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites" Protein Engineering, Vol. 10, no. 1, pp. 1-6 (1997), incorporated herein by reference. A maximum S score and a mean S score, as described in the Nielson et as reference, was obtained for the polypeptide sequences. Table 5 shows the position of the signal peptide in each of the polypeptides and the maximum score and mean score associated with that signal peptide.

5.5.2 EXAMPLE 7

Novel Nucleic Acids

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Using PHRAP (Univ. of Washington) or CAP4 (Paracel), a full length gene cDNA sequence and its corresponding protein sequence were generated from the assemblage. Any frame shifts and incorrect stop codons were corrected by hand editing. During editing, the sequence was checked using FASTY and/or BLAST against Genbank (i.e., dbEST version 119, gb pri 119, UniGene version 119, Genpept release 119). Other computer programs which may have been used

in the editing process were phredPhrap and Consed (University of Washington) and ed-ready, edext and gc-zip-2 (Hyseq, Inc.). The full-length nucleotide, including splice variants resulting from these procedures are shown in the Sequence Listing as SEQ ID NOS: 1746-1768.

Table 1 shows the various tissue sources of SEQ ID NO: 1746-1768.

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The homology for SEQ ID NO: 1746-1768 were obtained by a BLASTP version 2.0al 19MP-WashU search against Genpept release 119, using BLAST algorithm. The results showed homologues for SEQ ID NO: 1746-1768 from Genpept. The translated amino acid sequences for which the nucleic acid sequence encodes are shown in the Sequence Listing. The homologues with identifiable functions for SEQ ID NO: 1746-1768 are shown in Table 2 below.

Using eMatrix software package (Stanford University, Stanford, CA) (Wu et al., J. Comp. Biol., Vol. 6 pp. 219-235 (1999) herein incorporated by reference), all the sequences were examined to determine whether they had identifiable signature regions. Table 3 shows the signature region found in the indicated polypeptide sequences, the description of the signature, the eMatrix p-value(s) and the position(s) of the signature within the polypeptide sequence.

Using the PFam software program (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1) pp. 320-322 (1998) herein incorporated by reference) all the polypeptide sequences were examined for domains with homology to certain peptide domains. Table 4 shows the name of the domain found, the description, the p-value and the PFam score for the identified domain within the sequence.

The nucleotide sequence within the sequences that codes for signal peptide sequences and their cleavage sites can be determine from using Neural Network SignalP V1.1 program (from Center for Biological Sequence Analysis, The Technical University of Denmark). The process for identifying prokaryotic and eukaryotic signal peptides and their cleavage sites are also disclosed by Henrik Nielson, Jacob Engelbrecht, Soren Brunak, and Gunnar von Heijne in the publication "Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites" Protein Engineering, Vol. 10, no. 1, pp. 1-6 (1997), incorporated herein by reference. A maximum S score and a mean S score, as described in the Nielson et as reference, was obtained for the polypeptide sequences. Table 5 shows the position of the signal peptide in each of the polypeptides and the maximum score and mean score associated with that signal peptide.

5.6.2 EXAMPLE 8

Novel Nucleic Acids

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Using PHRAP (Univ. of Washington) or CAP4 (Paracel), a full length gene cDNA sequence and its corresponding protein sequence were generated from the assemblage. Any frame shifts and incorrect stop codons were corrected by hand editing. During editing, the sequence was checked using FASTY and/or BLAST against Genbank (i.e., dbEST version 120, gb pri 120, UniGene version 120, Genpept release 120). Other computer programs which may have been used in the editing process were phredPhrap and Consed (University of Washington) and ed-ready, edext and gc-zip-2 (Hyseq, Inc.). The translated amino acid sequences for which the nucleic acid sequence encodes are shown in the Sequence Listing. The full-length nucleotide, including splice variants resulting from these procedures are shown in the Sequence Listing as SEQ ID NOS: 1769-1786.

Table 1 shows the various tissue sources of SEQ ID NO: 1769-1786.

The homology for SEQ ID NO: 1769-1786 were obtained by a BLASTP version 2.0al 19MP-WashU search against Genpept release 120 and the amino acid version of Geneseq released on October 26, 2000, using BLAST algorithm. The results showed homologues for SEQ ID NO: 1769-1786 from Genpept. The homologues with identifiable functions for SEQ ID NO: 1769-1786 are shown in Table 2 below.

Using eMatrix software package (Stanford University, Stanford, CA) (Wu et al., J. Comp. Biol., Vol. 6 pp. 219-235 (1999) herein incorporated by reference), all the sequences were examined to determine whether they had identifiable signature regions. Table 3 shows the signature region found in the indicated polypeptide sequences, the description of the signature, the eMatrix p-value(s) and the position(s) of the signature within the polypeptide sequence.

Using the pFam software program (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1) pp. 320-322 (1998) herein incorporated by reference) all the polypeptide sequences were examined for domains with homology to certain peptide domains. Table 4 shows the name of the domain found, the description, the p-value and the pFam score for the identified domain within the sequence.

The nucleotide sequence within the sequences that codes for signal peptide sequences and their cleavage sites can be determine from using Neural Network SignalP V1.1 program (from Center for Biological Sequence Analysis, The Technical University of Denmark). The process for identifying prokaryotic and eukaryotic signal peptides and their cleavage sites are also disclosed by Henrik Nielson, Jacob Engelbrecht, Soren Brunak, and Gunnar von Heijne in the publication "Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites" Protein Engineering, Vol. 10, no. 1, pp. 1-6 (1997), incorporated herein by

reference. A maximum S score and a mean S score, as described in the Nielson et as reference, was obtained for the polypeptide sequences. Table 5 shows the position of the signal peptide in each of the polypeptides and the maximum score and mean score associated with that signal peptide.

Table 6 is a correlation table of all of the sequences and the SEQ ID NOS.

TABLE 1

TABLE			
Tissue Origin	RNA Source	Hyseq Library Name	. SEQ ID NOS:
adult brain	GIBCO	AB3001	9 19-21 50-51 65-66 72 78 80 82
	1	120001	85 87 107-108 113 116 123 138
1	j		140 150-152 159 169 177 192-193
	ļ		202 203 212 214 225 226 226 227
1	1		202-203 212-214 225-226 235-236
- }	ļ		251 258 268-269 272 280-281 295
1	1 .		298 301 321 326 331-332 334 356-
i	Į.		357 362 369 379 382-383 416 423
1	1	·	443 459-460 473 475 477 488 496
[500 503 519 526 547 574 582 587
j	}		608-609 613 618 633-634 645-646
1			652 657-658 660 669-671 678 687
	1		695 697 710 715 724 731 775-777
ļ			796 804 811 857-859 862 869 899-
	j i		900 912 919 922 924-929 933 936
	i		962 979 988-989 996 1001 1004-
			1008 1018 1039 1047 1059 1064
	(1000 1010 1039 104/ 1059 1064
1]		1067 1070 1078 1082 1107 1113
1			1116-1117 1131 1134-1137 1140
1	}		1149 1151 1157 1180 1206 1229
1			1234 1241 1243 1258 1272-1273
	į		1279 1288-1290 1294 1307-1308
1	j		1312 1320 1323 1330 1356 1360-
			1361 1368 1373-1375 1379 1391
	1		1400 1417 1446 1468 1482 1493-
1			1494 1501-1503 1506-1507 1512
			1517 1522-1524 1530-1533 1537
1	1		1549 1565 1578 1598 1606 1608
1			1623 1625 1627 1639 1643 1648-
1 1			1649 1653 1664 1667 1671 1696
1 1			1734 1741 1743-1744 1760-1761
	i		1771
adult brain	GIBCO	ABD003	3 12-14 18-19 25 30-31 34-36 43-
)			45 E0 E2 EC ED CO CE CC CO CO
	1		45 50-51 56 58 60 65-66 68-69 80
·	1		82 85 87 92 104 107-108 112-113
j j			115-116 123-124 131-132 135-137
1			139 142 146 148-149 152 154 157
1 1			159 163 165 167 169 172 180 192-
j j	1	. 1	193 196-197 199 203 208 210 212-
1 1	1		214 223 233 235-237 247 257 259
1 1	1		261 268-269 272 276 280-281 284-
Į į	1		288 291-292 295 297 300-301 304
1 1	j		307 317 320-321 323 327 329-331
1	1		333-334 345-349 356-357 379-381
	[393 401 408 414 419 424 426-428
[1	1	430 433-436 438-439 443 445 449
}	ľ	ļ	453-454 459-461 468 471-473 476-
	[ĺ	478 483 491 494 496 500 503 507-
	,	. 1	508 516 519-520 525-527 534 536-
j	1		540 542-543 545 553 555 560 569-
	1	{	570 574-576 586-588 593 595 597
	1	ī	574 500-500 595 595 597
i .		j	601 606-609 616-620 C22 C22 C22
j.	1	ĺ	601 606-609 615-620 622-623 625
			628-633 635-636 643 645-649 653
			628-633 635-636 643 645-649 653 655-656 660-665 668-670 676 681
			628-633 635-636 643 645-649 653 655-656 660-665 668-670 676 681 687 701 710 715 717 724-728 735
			628-633 635-636 643 645-649 653 655-656 660-665 668-670 676 681 687 701 710 715 717 724-728 735 743 745-746 750 753 759 765-766
			628-633 635-636 643 645-649 653 655-656 660-665 668-670 676 681 687 701 710 715 717 724-728 735 743 745-746 750 753 759 765-766 773 775-778 786 789 796 799-800
		1	628-633 635-636 643 645-649 653 655-656 660-665 668-670 676 681 687 701 710 715 717 724-728 735 743 745-746 750 753 759 765-766 773 775-778 786 789 796 799-800 802-803 810-811 815 817 820-821
		1	628-633 635-636 643 645-649 653 655-656 660-665 668-670 676 681 687 701 710 715 717 724-728 735 743 745-746 750 753 759 765-766 773 775-778 786 789 796 799-800 802-803 810-811 815 817 820-821 832 834-836 840 845-847 851 858-
			628-633 635-636 643 645-649 653 655-656 660-665 668-670 676 681 687 701 710 715 717 724-728 735 743 745-746 750 753 759 765-766 773 775-778 786 789 796 799-800 802-803 810-811 815 817 820-821 832 834-836 840 845-847 851 858-861 864 869 874 878 883 897 901-
			628-633 635-636 643 645-649 653 655-656 660-665 668-670 676 681 687 701 710 715 717 724-728 735 743 745-746 750 753 759 765-766 773 775-778 786 789 796 799-800 802-803 810-811 815 817 820-821 832 834-836 840 845-847 851 858-861 864 869 874 878 883 897 901-902 904-905 908 911-914 916 921-
			628-633 635-636 643 645-649 653 655-656 660-665 668-670 676 681 687 701 710 715 717 724-728 735 743 745-746 750 753 759 765-766 773 775-778 786 789 796 799-800 802-803 810-811 815 817 820-821 832 834-836 840 845-847 851 858-861 864 869 874 878 883 897 901-902 904-905 908 911-914 916 921-
			628-633 635-636 643 645-649 653 655-656 660-665 668-670 676 681 687 701 710 715 717 724-728 735 743 745-746 750 753 759 765-766 773 775-778 786 789 796 799-800 802-803 810-811 815 817 820-821 832 834-836 840 845-847 851 858-861 864 869 874 878 883 897 901-902 904-905 908 911-914 916 921-922 924-927 929 932-934 936-939
			628-633 635-636 643 645-649 653 655-656 660-665 668-670 676 681 687 701 710 715 717 724-728 735 743 745-746 750 753 759 765-766 773 775-778 786 789 796 799-800 802-803 810-811 815 817 820-821 832 834-836 840 845-847 851 858-861 864 869 874 878 883 897 901-902 904-905 908 911-914 916 921-922 924-927 929 932-934 936-939 941-942 945 955-958 963 966-969
			628-633 635-636 643 645-649 653 655-656 660-665 668-670 676 681 687 701 710 715 717 724-728 735 743 745-746 750 753 759 765-766 773 775-778 786 789 796 799-800 802-803 810-811 815 817 820-821 832 834-836 840 845-847 851 858-861 864 869 874 878 883 897 901-902 904-905 908 911-914 916 921-922 924-927 929 932-934 936-939 941-942 945 955-958 963 966-969 977 979-980 985-986 990 992-993
			628-633 635-636 643 645-649 653 655-656 660-665 668-670 676 681 687 701 710 715 717 724-728 735 743 745-746 750 753 759 765-766 773 775-778 786 789 796 799-800 802-803 810-811 815 817 820-821 832 834-836 840 845-847 851 858-861 864 869 874 878 883 897 901-902 904-905 908 911-914 916 921-922 924-927 929 932-934 936-939 941-942 945 955-958 963 966-969 977 979-980 985-986 990 992-993 997-1001 1005-1007 1012 1017-
			628-633 635-636 643 645-649 653 655-656 660-665 668-670 676 681 687 701 710 715 717 724-728 735 743 745-746 750 753 759 765-766 773 775-778 786 789 796 799-800 802-803 810-811 815 817 820-821 832 834-836 840 845-847 851 858-861 864 869 874 878 883 897 901-902 904-905 908 911-914 916 921-922 924-927 929 932-934 936-939 941-942 945 955-958 963 966-969 977 979-980 985-986 990 992-993 997-1001 1005-1007 1012 1017-1020 1023-1024 1029-1031 1034
			628-633 635-636 643 645-649 653 655-656 660-665 668-670 676 681 687 701 710 715 717 724-728 735 743 745-746 750 753 759 765-766 773 775-778 786 789 796 799-800 802-803 810-811 815 817 820-821 832 834-836 840 845-847 851 858-861 864 869 874 878 883 897 901-902 904-905 908 911-914 916 921-922 924-927 929 932-934 936-939 941-942 945 955-958 963 966-969 977 979-980 985-986 990 992-993 997-1001 1005-1007 1012 1017-

Tissue Origin	DNA Source	Viena	
	RNA Source	Hyseq Library Name	SEQ ID NOS:
	1		1097 1103 1107 1109 1112 1116~
	1		1117 1119 1121 1124 1127 1130
	ł		1134 1144-1145 1149 1151 1157- 1158 1167 1170 1178 1184 1188
	1		1190 1193-1194 1200 1202 1215-
			1217 1220 1226-1227 1229 1231
}		ļ	1241 1243 1247 1252 1258 1263
!	1		1267 1269 1279 1281 1284 1286-
			1289 1293-1294 1306-1307 1312
ļ	1		1316-1320 1326 1333 1338 1341 1344 1348 1351 1355-1357 1368
}			1374 1377 1380 1386 1389-1390
,			1394 1400 1409 1414 1422-1423
			1425-1427 1437 1443 1446 1454
			1456 1458-1459 1468 1470-1472
			1478 1482-1483 1487-1488 1493
[1497 1499 1506 1508-1511 1517
		ı	1522-1524 1530-1533 1545-1546
ļ			1548-1550 1552 1557-1559·1563 1565 1567 1569 1571 1586 1588
[1591 1593 1595 1598-1601 1608
			1611 1620-1621 1624-1626 1628
	}		1630-1632 1636 1640-1641 1644-
	(l		1645 1647 1649 1653-1655 1657
			1664 1667 1669 1673 1678-1681
	į		1686 1690 1694-1696 1701 1709 1711 1719 1722-1723 1726-1727
	į į		1731-1733 1738 1740 1743-1744
			1747 1749 1753 1757-1758 1760-
			1761 1765 1771 1785
adult brain	Clontech	ABR001	9 29 68-69 113 115 146 152 206
			223 245 277 307 320 324 330-331
	}		344 348 352 362 379 384 393 404
:	1		408 414 441-442 454 469 481 490 506 517 586 597 631 641 659 691
	}		715 799 803 833 865 871 875 880
	[882 908 920 937 1000 1005-1006
	1		1027 1036 1041 1043 1075 1107
•			1112 1121 1127 1136-1137 1144-
	1		1147 1231 1238-1239 1280 1293
			1320 1345 1355 1361 1383-1384 1400 1417 1448 1456 1476 1507
			1570 1572 1609-1610 1614 1620
	ľ		1626 1645 1653 1754 1759 1770
44015			1786
adult brain	Clontech	ABR006	5-8 15-16 168 212-213 271 278
•	1		280-281 291-292 300-301 310 314
	ľ	[321 326 336-338 341 352 357 359-
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į	ł	ł	960 963 971 975 977 981 990 992- 993 1007 1016 1029-1030 1034-
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1	į	[1409 1423-1424 1430 1435-1437
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	}	J	1496-1497 1501 1505 1509-1513
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	1	1	1549 1563 1565 1567 1569 1571
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		1	1717 1724 1730 1737-1738 1752
		j	1767 1779
Genomic DNA	Research	BAC001	686 1352 1412
from BAC 63I18	Genetics		
	(CITE BAC	Į.	
	Library)		
Genomic DNA	Research	BAC002	1411-1412
from BAC 39316	Genetics	1	1
	(CITB BAC	}	· ·
	Library)	<u></u>	<u> </u>

Tissue Origin	RNA Source	Hyseq	SEQ ID NOS:
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Genomic DNA	Research	BAC003	1352
from BAC 39316	Genetics (CITB BAC		
1	Library)		
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}	_		80 93 100 120-121 169 201 237
			251-252 272 278 311 348 363 382
			413 415 424 430 443 483 502 542-
1			543 562 564 607 616-617 626 635
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	;		1185 1189 1199 1270 1369 1481
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			1669 1671 1690 1719 1727 1731- 1732 1739 1741 1760-1761 1779
bone marrow	Clontech	BM:D001	3-8 11 13 18 29-31 33 35-36 40
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			235-237 242-244 255 258 260 263-
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			333 339 343 352 357-358 370-371 382 384-385 387 389 394 408 410
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			569-577 581 583-586 588 593 601
			603-604 608-609 613-619 621-622
			632-633 636-637 642 649-650 656-
, j			660 666 670 672 674-675 679 683
			701 708 716 718-720 731 735-736 740-742 744-745 752 761 765 772-
			773 775-778 780 785-786 789-791
			796 798 802 810-812 823-824 826
}	j	ļ	830 832-833 837-838 843-844 848-
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	1	[914 922-924 927 930-931 937 939-
1	ľ	ľ	941 952-953 955-958 963 969 973
ŀ	Ì	}	976 981 985 987 990 992 995 1000
j	j	j	1002 1005-1007 1013 1016 1025
Į.			1028-1031 1033 1035 1037 1039 1042 1044 1047 1050 1053-1054
Ì	į		1059 1061 1063 1066 1070-1071
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		- }	1145 1163 1172 1178 1197 1199-
{	(1200 1202 1216-1217 1224 1227-
ł	}	ł	1228 1240 1246 1254 1261 1266 1270 1278 1281 1295 1287 1290-
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		ſ	1346 1349 1353 1356 1361 1367
	ľ		1369 1372-1374 1379-1380 1394
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Tissue Origin	RNA Source	Hyseq	SEQ ID NOS:
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•	1	•	1626-1628 1630-1632 1634 1636
	ļ	ļ	1638-1639 1641 1646-1647 1651
		İ	1653-1655 1661-1662 1676-1681
ĺ	1		1684 1686 1690 1702 1707 1711
}			1713-1714 1717 1720 1722-1723
<u> </u>			1727 1737-1738 1740 1758 1767 1772 1781-1782 1785-1786
bone marrow	Clontech	BMD002	11 15-16 19 30-31 35-36 68-69 75
		2,2002	83-84 93 99 103 108-109 118 137
}			139 169-170 174 177 180 190 193
			212-213 219 222 225-226 232 237
ł	1		255 259 264 273-274 284 286 290-
}	İ		292 295 301 303-304 307 312-313
			316 324 326 330 334-335 348 352-
			353 357 360 370-373 384 386-387 397 403-404 414-416 421 425-427
]		429-430 433-436 440 444 451 454
	,		465-466 472 475 478 491 493 516
i	[520 523 525 531 545 548 552 566
į	1		569-570 581 583 590-591 597-598
}	· ·		601 616-617 621 641 650 652 656
[1		659 671 674-675 679 684 710 718-
1	1		719 728 734 737-738 742 761 765 774-778 790 811 814 818 830 834-
)	j		836 854-855 859 866 869 871 878-
ļ			879 884 889 892 904 922-923 932
İ	1		990 992 998 1001 1004 1016 1036
}	}		1042 1048 1051 1054-1055 1058
ļ			1088-1089 1106 1112-1114 1155
1	1		1157 1192 1200 1223 1227-1228
}	}		1236-1237 1260-1261 1282-1283 1285 1287 1295 1314 1317-1321
ļ			1324-1327 1330 1333 1341 1343
[[,	1347 1350 1353 1355-1357 1367
Ì			1369-1370 1373 1377 1379 1381
			1383-1384 1394 1397 1400 1406
			1413 1417 1425-1427 1438 1442
		•	1446 1459-1460 1470 1493 1505
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1			1631 1634 1646 1649 1653 1656
	[1658 1669-1670 1683-1684 1687-
}			1688 1690-1693 1696 1699 1702
			1704 1707-1709 1711 1720 1722-
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		·	1738-1740 1743-1746 1752 1755
]		1760-1761 1767 1777 1781-1782 1786
bone marrow	Clontech	BMD004	73-74 503 922 1036 1711
bone marrow	Clontech	EMD007	95-96 866 1320 1475
adult colon	Invitrogen	CLN001	17 56-58 103 110 117 144 150 171
	[179 185 188-189 201 204-206 210
	i	1	218-221 225-226 231 237 251 277
	[288 310 312 320 333 359 386 388
]	İ	394 408 420 455 481 485 503 510-
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·	l l		786 788 826-827 848-850 854-855
]	}	858 866 872 898 918 921-923 953
		ļ	976 983 993 1005-1006 1017 1020
	ļ Ì	1	1025 1027 1054-1055 1063 1068-
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Tissue Origin	RNA Source	Hyseq	SEQ ID NOS:
		Library Name	
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}			1688 1701 1713-1714 1724 1740
Mixture of 16			1765
tissues -	Various	CTL016	401 1490 1686
mRNAs	Vendors		ì
Mixture of 16	Various	CTL021	
tissues -	Vendors	CIPOSI	312 7B2 1132-1133 1403 1712 1715
mRNAs'	Venuora		
adult cervix	BioChain	OUW OF THE	
duit cervix	BIOCHAIN	CVX001	1 4-8 11 13 18-21 25-26 30-31 33
			37-39 43 46-47 58 61 64-66 71
			73-74 82 85 94 100 103-104 113
	ļ		118 122 126 130 134 140 147 153-
	i		156 163 170 179 181 186 192 195-
	[196 198 201-202 218-219 222 229-
j	j		231 257 266 276-277 285-286 288
}	I		298 301-302 304 307 312-314 324
1	1		326 329-330 332 335 342 352 358
			362 371-372 376 379 381-382 384
			388 398 400 410 414 416 419-420
			426-427 430-431 433-436 439 446
	j		448 461-462 464 471-477 479 482- 483 491 493 496 503 506 510-513
'			516-517 526 530 535 542-544 546-
1	1	i	547 557 561 572-573 575-577 581-
	. [582 585-586 588-589 593-594 600
ļ			602 604-605 607-609 612 615-619
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Ţ			708-709 711 713 720-721 727 729
		ļ	731-732 737 745-747 753-754 760
,			765 771 774-777 780 790 793 796
	ł		798 800 803 805 818 826 828 831-
	ļ		832 834-836 843 847-848 851-855
]			857-860 864-866 869 871 876 878-
	1		880 882 887 890-891 897 899-902
[905-908 912-913 916 918-919 922
İ	1		927 932 934-938 944 948 955-956
	1	1	958 963-964 967 969-970 972 976
	1	!	978-979 983 985 990 992 1000
Į	ŀ	ĺ	1005-1007 1016-1017 1024 1027
1	1	ł	1033 1036 1038 1045 1047 1053-
•	j	j	1056 1066-1067 1071 1073 1075
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Į	ł	ì	1134 1139 1146-1149 1163 1167
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1	}		1349 1353-1354 1360 1372-1374
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^{*}The 16 tissue-mRNAs and their vendor source, are as follows: 1) Normal adult brain mRNA (Invitrogen), 2) normal adult kidney mRNA (Invitrogen), 3) normal adult liver mRNA (Invitrogen), 4) normal fetal brain mRNA (Invitrogen), 5) normal fetal kidney mRNA (Invitrogen), 6) normal fetal liver mRNA (Invitrogen), 7) normal fetal skin mRNA (Invitrogen), 8) human adrenal gland mRNA (Clontech), 9) human bone marrow mRNA (Clontech), 10) human leukemia lymphablastic mRNA (Clontech), 11) human thymus mRNA (Clontech), 12) human lymph node mRNA (Clontech), 13) human spinal cord mRNA (Clontech), 14) human thyroid mRNA (Clontech), 15) human esophagus mRNA (BioChain), 16) human conceptional umbilical cord mRNA (BioChain).

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Tissue Origin	T DATA Carras	1132	
	RNA Source	Hyseq Library Name	SEQ ID NOS:
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		}	1503 1506 1512 1522 1527-1528 1531 1533 1541 1547 1569 1571
		ļ	1585 1589 1597-1598 1600 1608-
	ľ	}	1609 1614-1616 1620 1623-1624
	•	ļ	1626-1628 1630 1638 1641 1643
	1		1649 1653 1656 1662 1667 1669
	1		1674-1675 1683 1685-1688 1699
			1702 1709-1710 1715 1717 1722
	[1724 1729 1731-1732 1735-1739
	ŀ		1741 1743-1744 1748-1749 1755 1760-1762 1767 1773 1778 1785-
]	ŀ		1786
diaphragm	BioChain	DIA002	137 282 289 730 780 986 1409
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endothelial	Strategene	EDT001	3 5-10 13 15-21 24-26 29 34 37-
cells			39 42 44-45 50-51 53-55 57-58
]			60-61 65-66 68-69 73-74 77-78 80
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			161-163 166-172 176-179 187 190
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			267-269 272 276-277 279-281 284-
			285 288 290 295-296 301-302 310-
			311 313 316 321 325 329 331-333
	'	ĺ	335 340 342 351-355 360 371 375 380-382 384 387 390 392 397 400
	J	ļ	407-408 410 412 414 416 425-427
	Ì		431 434-436 439 444-445 449 454
1			463-464 472-475 477-479 486 488-
]	ļ	490 497-498 500-504 510-513 516-
1	İ		519 522 524 526-528 532-534 536-
İ	ļ		540 542-546 548 561-563 566-567
		•	572-576 579 581 585-586 589 593
	ł		595 597 599 603 607-612 615-617 620 622 626 630 632-634 638-641
. <u> </u>	ļ		644 647 656-660 662-664 670 673
		į	678 680-682 692-697 707 709-710
i	ł	l	712-713 719 730 732 734 736 738
j	*		743-746 751 759 768 771 773 775~
ŀ		1	778. 783 786-789 793 800 803 805-
ł		ł	807 810-811 814 816-818 821-822
	j	1	824 826 828-829 832 834-638 842~ 845 848-850 854-860 862 864 869
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į	[1216-1217 1219 1221 1225 1229 1232-1235 1238-1241 1243-1244
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			TOOL TOOL TOOL

			CEO YD MOE.
Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
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			1400 1406 1408 1414 1417 1419
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}) .		1631 1634 1636 1638 1641 1643-
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			1771-1773 1776 1779 1783-1786
<u> </u>	Genomic DNA	EPM001	286 686 1297 1303-1304 1352
Genomic clones		EPMOOL	1411-1412 1754
from the short	from		1411-1412 1/34
arm of	Genetic		
chromosome 8	Research	ES0002	131-132 261 289 380 503 860 892
esophagus	BioChain	E50002	1000 1007 1397
		EDROGI	62-63 89 112 126 194 322 336-338
fetal brain	Clontech	FBR001	379 391 411 481 546 563 607 679
1	l		710 867 1012 1031 1055 1251 1262
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	1		1732 1746 1765
	67	FBR004	68-69 90-91 139 212-213 301 331
fetal brain	Clontech	PBRUU4	362 374 403 436 611 645-646 659
Ì			668 670 691 785 805 845 1163
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J	ļ	ŀ	1387 1410 1416 1430 1496 1536
ļ	ŀ	Į.	1547 1593
	61	7777006	5-9 25 43 60 62-63 65-66 70 72
fetal brain	Clontech	FBR006	80 87 92 101 103 108 114 136 139
1		J ·	149 152-153 157 168 171-172 175
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}	}	}	689 691-694 696-697 699 701 706
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1	1		806-807 810 817-818 826 839 843
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1350-1351 1357 1367 1369 1379	
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	i	1	400 405 408-410 412 414-416 421-
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muscle spinal cord	Clontech	SPC001	
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TO MINISTER	SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	· · · · · · · · · · · · · · · · · · ·
1		NUMBER		DDGCATT 110A		IDENTITY
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Ye6656 Homo Membrane-bound protein 2389 99 99 99 99 99 99 99	1	141/36	1	Human PRO1114 protein	1398	100
API13116 Momo aspiens PRO943.	2	Y66656		Membrane-bound protein	2389	90
A NP017806 Mus muscullus Zn-15 transcription factor G551 77				PRO943.	250.5	1 3 3
AP017806 Mus musculus Zn-15 transcription factor 5551 77	3	AF113136	Homo sapiens		3043	100
SO2761 Momo sapiens Tibromectir precursor 10535 98	4	1 2000		kinase-M; IRAK-M		
8 X02761		- J		Zn-15 transcription factor		1
8 X02761 Homo sapiens fibronectic precursor 12564 59 9 AJ011679 Homo sapiens Rah6 6TPase activating 5251 59 10 W88501 Homo sapiens Rah6 6TPase activating 5251 59 11 AP117754 Homo sapiens thyroid hormone receptor 11336 58 12 297630 Homo sapiens Catyloid hormone receptor 11336 58 12 297630 Homo sapiens Catyloid hormone receptor 11336 58 12 297630 Homo sapiens Catyloid hormone receptor 11336 58 13 Y58620 Homo sapiens Catyloid hormone receptor 11336 58 14 AF213457 Homo AF213461 Homo sapiens Rak6x11ke Akkyrin 3, node of Ranvier (ankyrin				fibronectic precursor		1
20			Homo sapiens	fibronectin precursor	1	
New No. New	9	AJ011679		Rab6 GTPase activating		1
HP10415-ancoded protein. Section		1	}	protein, GAPCenA	1 3232	
AP117754 Homo sapiens Lhyroid hormone receptor 11336 98	10	W88501	Homo sapiens	Human stomach carcinoma clone	2381	100
12 297630 Homo sapiens 63466811, 4 (novel protein complex 1896 100	-;	3511555	<u></u>		<u> </u>	
12 297630 Homo sapiens Component TRAP240 297630 Homo sapiens Component TRAP240 297630 Homo sapiens Component TRAP240 298 297630 Homo sapiens Protein regulating gene expression PRG-13. 298 29	11	AF117754	Homo sapiens	,	11336	98
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Similar to ANK3 (ankyrin 3, node of Ranvier (ankyrin 6))	12	297630	Homo sapiens	dJ466N1 4 (nove) protein	1006	1,00
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14	13	Y58620	Homo sapiens		1894	98
Sapiens	14-	78212457	11000			
16	-3	AF21395/	1	criggering receptor expressed	1238	100
AF201303 Homo sapiens Mirr oribeta-binding protein 3130 98	16	AF233453		PACK-like protein DBVCBB3	2224	-
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19		1		RIP60	3230) 30
19				dynactin 1 p150 isoform	6377	100
AB032903	19	U00059			174	26
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Reductase isolog	21	AB032903	Homo ganiene	reductase isolog	1405	
22 AF140507 Homo sapiens Ca2+/calmodulin-dependent protein kinase kinase beta 3083 99 23 AF140507 Homo sapiens Ca2+/calmodulin-dependent protein kinase kinase beta 2300 99 24 AJ289131 Homo sapiens Chondroitin 4-0-sulfotransferase 2211 99 25 U33460 Homo sapiens DNA-directed RNA polymerase I, largest subunit 8777 98 26 Y44488 Homo sapiens ACRF30R2 variant protein. 1387 100 27 U43701 Homo sapiens ribosomal protein L23a 767 97 28 U02032 Homo sapiens ribosomal protein L23a 767 97 29 Y41324 Homo sapiens Human ubiquitin conjugation encoded by gene 17 clone hnFIY7. 1083 99 30 W71749 Homo sapiens Human ubiquitin conjugation system protein 2. 82 31 W71749 Homo sapiens long-chain 2-hydroxy acid loxidase HAOX2 1811 100 33 229481 Homo sapiens sold hydroxyanthranilic acid dioxygenase 1507 99 34 AB001451		1	I TOMO BUDZENIA		1485	1 99
Protein kinase kinase beta 2300 99	22	AF140507	Homo sapiens	Ca2+/calmodulin-dependent	3083	99
Protein kinase kinase beta Protein kinase kinase beta Protein kinase kinase beta Protein kinase kinase beta Protein kinase kinase beta Protein kinase kinase beta Protein kinase kinase beta Protein kinase kinase beta Protein kinase kinase kinase beta Protein kinase kinase beta Protein kinase kinase kinase beta Protein kinase kinase kinase beta Protein kinase kinase kinase beta Protein kinase kinase kinase beta Protein kinase kinase kinase beta Protein kinase kinase kinase beta Protein kinase kinase kinase beta Protein kinase kinase kinase beta Protein kinase kinase kinase beta Protein kinase kinase kinase beta Protein kinase kinase kinase beta Protein kinase kinase kinase beta Protein kinase kinase kinase beta Protein kinase kinase beta Protein kinase kinase beta Protein kinase kinase beta Protein kinase kinase beta Protein kinase kinase beta Protein kinase kinase beta Protein kinase kinase beta Protein kinase kinase kinase beta Protein kinase kinase kinase beta Protein kinase kinase kinase beta Protein kinase kinase kinase beta Protein kinase kinase kinase beta Protein kinase kinase kinase beta Protein kinase kinase kinase beta Protein kinase kinase kinase beta Protein kinase kinase kinase beta Protein kinase kinase kinase kinase kinase kinase kinase beta Protein kinase k				protein kinase kinase beta		
AJ289131	23	AF140507	Homo sapiens	Ca2+/calmodulin-dependent	2300	99
Sulfotransferase	24	A 7205171				[
DNA-directed RNA polymerase 8777 98	44	MU209131	nomo sapiens		2211	99
Sapiens I, largest subunit 1387 100	25	U33460	Homo		0277	
26 Y44488 Homo sapiens ACRP30R2 variant protein. 1387 100 27 U43701 Homo sapiens ribosomal protein L23a 791 100 28 U02032 Homo sapiens ribosomal protein L23a 767 97 29 Y41324 Homo sapiens Human secreted protein 1083 99 30 W71749 Homo sapiens Human ubiquitin conjugation system protein 2. 715 90 31 W71749 Homo sapiens Human ubiquitin conjugation system protein 2. 631 82 32 AF231917 Homo sapiens long-chain 2-hydroxy acid oxidase HAOVA 1811 100 33 Z29481 Homo sapiens 3-hydroxyanthranilic acid dioxygenase 1507 99 34 AB001451 Homo sapiens precursor polypeptide (AA -34 1667 99 36 Y00644 Homo sapiens precursor polypeptide (AA -34 1104 98 37 Y78795 Homo sapiens Human antizuai-2 (AZ-2) amino acid sequence. 78				I. largest subunit	8///	98
27 U43701 Homo sapiens ribosomal protein L23a 791 100 28 U02032 Homo sapiens ribosomal protein L23a 767 97 29 Y41324 Homo sapiens Human secreted protein 1083 99 30 W71749 Homo sapiens Human ubiquitin conjugation system protein 2. 715 90 31 W71749 Homo sapiens Human ubiquitin conjugation system protein 2. 631 82 32 AF231917 Homo sapiens long-chain 2-hydroxy acid oxidase HAOVA 1811 100 33 Z29481 Homo sapiens 3-hydroxyanthranilic acid dioxygenase 1507 99 34 AB001451 Homo sapiens Sck 2869 100 35 Y00644 Homo sapiens precursor polypeptide (AA -34 to 287) 1667 99 36 Y78795 Homo sapiens Human antizuai-2 (AZ-2) amino acid sequence. 78 38 Y78795 Homo sapiens Human antizuai-2 (AZ-2) amino acid sequence. 4726 99	'	Y44488	Homo sapiens		1387	100
28			Homo sapiens	ribosomal protein L23a		
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HNFIY17. Homo sapiens Human ubiquitin conjugation 715 90 90 915 90 915	29	Y41324	Homo sapiens		1083	99
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W71749			Momo sapiens	system protein 2	715	90
Bystem protein 2.	31	W71749	Homo sapiens	Human ubiquitin conjugation	631	82
Oxidase HAOX2			-		002	V2
Oxidase HAOX2	32	AF231917	Homo sapiens	long-chain 2-hydroxy acid	1811	100
dioxygenase 1507 334 AB001451 Homo sapiens Sck 2869 100	<u>, </u>					
34 AB001451 Homo sapiens Sck 2869 100 35 Y00644 Homo sapiens precursor polypeptide (AA -34 1667 99 99 36 Y00644 Homo sapiens precursor polypeptide (AA -34 1104 98 100 10	3.3	229481	Homo sapiens		1507	99
100 100	34	AB001457	Uomo monda			
to 287) 36 Y00644 Homo sapiens precursor polypeptide (AA -34 1104 98 to 287) 37 Y78795 Homo sapiens Human antizuai-2 (AZ-2) amino 3586 78 acid sequence. 38 Y78795 Homo sapiens Human antizuai-2 (AZ-2) amino 4726 99						
36 Y00644 Homo sapiens precursor polypeptide (AA -34 1104 98 to 287) 37 Y78795 Homo sapiens Human antizuai-2 (AZ-2) amino acid sequence. 3586 78 acid sequence. 38 Y78795 Homo sapiens Human antizuai-2 (AZ-2) amino 4726 99	-		TOWN PAPTEUS		1667	99
to 287) Y78795 Homo sapiens Human antizuai-2 (AZ-2) amino 3586 78 acid sequence. Y78795 Homo sapiens Human antizuai-2 (AZ-2) amino 4726 99	36	Y00644	Homo sapiens		1104	
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38 Y78795 Homo saplens Human antizuai-2 (AZ-2) amino 4726 99	37	¥78795	Homo sapiens		3586	78
1 diament ancistating (AZ-2) amino 4/26 99	1			acid sequence.	}	- }
acid sequence.	"	178795	Homo saplens		4726	99
		. — — _ .l.	<u> </u>	acia sequence.		

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
39	¥78795	Homo sapiens	Human antizuai-2 (AZ-2) amino acid sequence.	3556	77
40	U93121	Homo sapiens	M-phase phosphoprotein-1	3747	100
41	¥42750	Homo sapiens	Human calcium binding protein 1 (CaBP-1).	795	100
42	AP282626	Homo sapiens	latexin	1189	100
43	G02150	Homo sapiens	Human secreted protein, SEQ ID NO: 6231.	384	94
44	U19617	Mus musculus	Elf-1	2724	88
45	U19617	Mus musculus	Elf-1	2062	86
46	AF100758	Homo sapiens	osteoinductive factor OIF	1538	100
47	Y87591	Homo saplens	Human SPROUTY-1 protein, SEQ ID NO:24.	1737	99
	X04145	Homo sapiens	T3 gamma precursor (aa -22 to 160)	942	99
51	X63547	Homo sapiens	oncogene	5845	99
52	M94043	Rattus	rab-related GTP-binding	1089	96
53	L31783	norvegicus Mus musculus	protein uridine kinase	 	L
54	X83973	Homo sapiens	transcription factor	917	71 98
55	AF224741	Homo sapiens	chloride channel protein 7	4128	98
56	W74805	Homo sapiens	Human secreted protein	1491	100
			encoded by gene 77 clone HOEAS24.		100
57	Z50907	Homo sapiens	Human TBC-1 cDNA from second transcript.	4824	100
58	D79994	Homo sapiens	similar to ankyrin of Chromatium vinosum.	6089	99
59	D79994	Homo sapiens	similar to ankyrin of Chromatium vinosum.	4014	91
60	Y59738	Homo sapiens	Human normal ovarian tissue derived protein 15.	601	100
61	AB031069	Homo sapiens	protein containing CXXC domain 1	1390	100
62	Y66660	Homo sapiens	Membrane-bound protein PR0783.	2492	99
63	Y66660	Homo sapiens	Membrane-bound protein PRO783.	1709	99
64	S70011	Rattus sp.	tricarboxylate carrier	895	55
65	AF139518	Rattus norvegicus	A-kinase anchor protein	178	24
66	W29666	Homo sapiens	Homo sapiens DH1308_1 clone secreted protein.	157	30
67	AJ245738	Homo sapiens	claudin-15	1206	100
68	AF099138	Rattus norvegicus	GLUT4 vesicle protein	4183	87
69	AF099138	Rattus norvegicus	GLUT4 vesicle protein	4906	86
70	282059	Caenorhabdit is elegans	Similarity to Drosophila ring canal protein comes from this gene	1285	44
71	AF224278	Homo sapiens	PMEPAl protein	1282	100
72	AF126426	Homo sapiens	neurotrimin	1809	100
73	Y41652	Homo sapiens	Human MEK2 protein sequence.	2065	99
74	Y41652	Homo sapiens	Human MEK2 protein sequence.	1207	100
75	AF188622	Mus musculus	selectively expressed in embryonic epithelia protein-1	1485	74
76	AE000406	Escherichia coli	putative DNA topoisomerase	950	100
,	X99302	Homo sapiens	Pop1	655	100
77					
77 78	AL136538	Schizosaccha romyces pombe	similarity to S. cerevisiae ktil2 protein	210	31

SEQ	ACCESSION	SPECIES	DECCOT DETON		
ID No:	NUMBER		DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
80	AL096768	Homo sapiens		2033	100
			(phosphatidylserine decarboxylase (PSSC, EC 4.1.1.65))		
81	AL096768	Homo sapiens	,	1220	96
			(phosphatidylserine decarboxylase (PSSC, EC 4.1.1.65))		
82	X57351	Homo sapiens	1-8D	677	98
83	AC005594	Homo sapiens) · · · · · · · · · · · · · · · · · · ·	2700	98
84	X73113	Homo sapiens		5959	99
85	AF097330	Homo sapiens	CLIC4	1305	99
87	AB018423 AF272151	Mus musculus	1 comery concerning brocern	1360	78
88	AF196329	Homo sapiens		3084	99
89	AB016879	sapiens	triggering receptor expressed on monocytes 1	1	100
		Arabidopsis thaliana	contains similarity to pre- mRNA splicing factor-gene_id:MRB17.2	634	36
90	AJ133721	Mus musculus	homeodomain protein	654	57
91	AJ242864 A61971	Mus musculus	phtf protein	619	61
92	X99365	unidentified		11676	99
94	Y87231	Homo sapiens	Human PRO1250 (UNQ633) amino acid sequence SEQ ID NO:86.	3890	100
	16/231	Homo sapiens	Human signal peptide containing protein HSPP-8 SEQ ID NO:8.	1031	100
95	AF227741	Rattus norvegicus	protein kinase WNKI	2428	95
96	AF227741	Rattus norvegicus	protein kinase WNK1	1961	94
97	Y92513	Homo sapiens	Human OXRE-10.	1626	100
98	AL021366	Homo sapiens	cICK0721Q.3 (Kinesin related protein)	3423	100
99 100	AC005783	Homo sapiens	R33083_1	1974	99
100	Y95293 AL118501	Homo sapiens	Human GEF containing NEK-like kinase substrate sGNK.	4092	99
		Homo sapiens	dJ1191N16.1 (A novel protein (translation of the cDNA DKFZp566A0946, Em:AL050069))	1509	100
102	AJ006267	Homo sapiens	ClpX-like protein	3233	100
103	AF100753	Homo sapiens	ancient ubiquitous 46 kDa protein AUP1	2042	96
105	AB015982 AF151074	Homo sapiens	serine/threonine kinase	4718	100
106	M35522	Canis	HSPC240	831	64
107	R99800	familiaris Homo sapiens	GTP-binding protein (rab7)	354	50
		. .	NTII-1 nerve protein, facilitates regeneration of nerve cells.	2337	93
108	AF125533	Homo sapiens	NADH-cytochrome b5 reductase isoform	1290	93
109	AC005614	Homo sapiens	F23269_2	3369	99
110	AF064729	Homo sapiens	RAN binding protein 16	3285	100
111	X52425	Homo sapiens	interleukin 4 receptor	4496	100
113	Y41686	Homo sapiens	Human PRO274 protein sequence.	2285	100
114	W15506	Homo sapiens	Mitogen activating protein kinase ERK1.	1991	100
115	Y71071	Homo sapiens	Human membrane transport protein, MTRP-16.	1190	99
		Homo sapiens	dJ398G3.1 (ortholog of rat CPG2)	3497	99
116		Mus musculus	evectin-2	1124	90
	W30891	Homo	Human cytostatin III protein.	715	99

SEO	ACCESSION	SPECIES	DESCRIPTION	T GHYMY	
ID	NUMBER	SPECIES	DESCRIPTION	SMITH-	\$ TD TO TO TO TO TO TO TO TO TO TO TO TO TO
NO:	Nondak			WATERMAN	IDENTITY
		sapiens	 	SCORE	
118	AF116618	Homo sapiens	PRO1038	1469	100
119	Y08915	Homo sapiens	alpha 4 protein	1748	100
12C	AF098070	Drosophila	Lis1 homolog	192	39
		melanogaster	and homorog	192	39
121	AF052432	Homo sapiens	katanin p80 subunit	181	37
122	¥70743	Homo sapiens	PSEQ-1 protein encoded by	2637	98
			NSEQ gene associated with	2037	70
ĺ	1		matrix remodelling.	1	1
123	AF083246	Homo sapiens	HSPC028	2132	100
124	Y27096	Homo sapiens	Human viral receptor protein	833	99
		1	(ACVRP).	555	1 3 3
125	M63109	Leishmania	glycoprotein 96-92	172	27
	1	major	1	[- '
126	U75467	Drosophila	Atu	935	36
L	}	melanogaster	}	1	[]
127	Z68220	Caenorhabdit	Similarity to Human ADP/ATP	438	43
		is elegans	carrier protein		1.0
128	AF095927	Rattus	protein phosphatase 2C	1927	94
		norvegicus		i	ł
129	W92958	Homo sapiens	Human zsig44 protein.	463	100
130	AF115391	Lactobacillu	ribokinase RbsK	508	37
	<u> </u>	s sakei			Ĭ
131	X93498	Homo sapiens	21-Glutamic Acid-Rich Protein	1250	100
132	X93498	Homo sapiens	21-Glutamic Acid-Rich Protein	916	87
133	W52811	Homo sapiens	Human DBI/ACBP -like protein	705	97
134	70141		(DBIH).	1	
134	Y84444	Homo sapiens	Amino acid sequence of a	3230	100
	1	\	human RNA-associated		
135	M69181	<u> </u>	protein.	ļ	ļ
136	W74882	Homo sapiens	non-muscle myosin B	189	20
720	W/4882	Homo sapiens	Human secreted protein	480	100
		ļ	encoded by gene 154 clone		
137	W78200	Homo sapiens	1	<u> </u>	
	1170200	nono saprens	Human secreted protein encoded by gene 75 clone	855	99
	}		HHGAU81.		j
138	AL033520	Homo sapiens	dJ349A12.1 (similar to	424	
		-iomo bupiens	KIAA0701 protein)	424	39
139	AF020261	Santalum	proline rich protein	119	30
	1	album	Francis radii processi	1 -13	30
140	X70394	Homo sapiens	zinc finger protein	1634	100
14).	Y06439	Homo sapiens	Human protease HUPM-8.	936	100
142	268493	Caenorhabdit	predicted using Genefinder	365	42
		is elegans	F	383	42
143	AB018107	Arabidopsis	ADP-ribosylation factor-like	596	65
		thaliana	protein] - -
144	AF161483	Homo sapiens	HSPC134	580	51
145	Y84902	Homo sapiens	A.human proliferation and	480	100
			apoptosis related protein.		
146	AB004906	Ipomoea	transposase	146	20
		purpurea			'
147	AC007357	Arabidopsis	F3F19.18	647	31
		thaliana			
148	W75155	Homo sapiens	Human secreted protein	1494	98
i			encoded by gene 41 clone		
145	5.00		HNTME13.	ļ i	
149	AF056490	Homo sapiens	cAMP-specific	3710	99
			phosphodiesterase 8A		
150	Y58171	Homo	Human hydrolase homologue	785	99
		sapiens	нн-7.		į
151	U10397	Saccharomyce	Yhr148wp	515	53
1 = 3	V-73.4-73	s cerevisiae			
152	X73478	Homo sapiens	phosphotyrosyl phosphatase	1719	99
153	AL049697	-	activator		{
	١ دود ډوس	Homo sapiens	dJ382I10.5.1 (novel protein	2034	99

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	γ
ID	NUMBER	or Lettes	DESCRIPTION	WATERMAN	IDENTITY
NO:		ţ	1	SCORE	1DENTITI
		†	similar to arginyl-tRNA)		
154	AF169802	Homo sapiens	cytochrome b5 reductase b5R.2	1455	199
155	X94703	Homo sapiens	rab28	1126	99
156	Y25716	Homo sapiens	Human secreted protein	1471	100
			encoded from gene 6.		
158	W77404	Homo sapiens	Secreted salivary polypeptide	937	100
159	Y17248	Homo sapiens	zsig32. Human protein kinase	 	
139	11/240	Homo saprens	inhibitor-2 (PKI-2).	383	100
160	J04970	Homo sapiens	carboxypeptidase M precursor	2395	100
161	W54040	Homo sapiens	Human interferon-inducible	484	98
		I I Dapie	protein, HIFI.	101	"
162	AL022724	Homo sapiens	dJ413H6.1.1 (hamster	1357	100
		•	Androgen-dependent Expressed		1
	Ì		Protein LIKE PUTATIVE	1	Ì
			protein) (isoform 1)	1	
163	AF125535	Homo sapiens	pp21 homolog	193	45
164	G03632	Homo sapiens	Human secreted protein, SEQ	463	97
		<u> </u>	ID NO: 7713.	1	
165	AJ250839	Homo sapiens	serine/threonine protein	1442	71
166	L09649	 	kinase	 	L
±66	109649	Zymomonas mobilis	zm2	173	37
167	¥73337	Homo sapiens	HTRM clone 1944530 protein	1	
10,	1/333/	nomo saptens	sequence.	1204	100
168	W88645	Homo sapiens	Secreted protein encoded by	1084	100
		nomo saprema	gene 112 clone HUKFC71.	1084	100
169	AF214731	Homo sapiens	ATP-dependent RNA helicase	4402	100
170	AE000871	Methanobacte	conserved protein	166	27
	l.	rium		1	1 "
	1	thermoautotr		(
		ophicum		1	1
171	¥27684	Homo sapiens	Human secreted protein	821	100
			encoded by gene No. 118.	1	}
172 173	AF226044	Homo sapiens	HSNFRK	2904	130
174	AJ245946 D43949	Homo sapiens		779	100
175	Y07923	Homo sapiens	This gene is novel.	3202	100
176	W90338	Homo sapiens	GTP-binding protein Human DP1 homologue protein.	1205	100
	H30336	sapiens	Adman ber nomorogue proteir.	966	100
177	¥41675	Homo sapiens	Human channel-related	1122	100
		nome Dapiens	molecule HCRM-3.	1122	100
178	Y41674	Homo sapiens	Human channel-related	936	99
		•	molecule HCRM-2.		
179	AF220492	Homo sapiens	krueppel-like zinc finger	4100	99
			protein HZF2] .	
180	X03084	Homo sapiens	Clq B-chain precursor	1240	100
181	U57344	Mus musculus	Meis3	1813	89
183	U57344	Mus musculus	Meis3	1743	86
184	U57344	Mus musculus	Meis3	1070	86
185	AF033120	Homo sapiens	p53 regulated PA26-T2 nuclear	1389	58
186	AF200357	Mus musculus	protein		
187	W75058		pantothenate kinase 1 beta	1605	82
~~′	# / JV36	Homo sapiens	Human secreted protein encoded by gene 2 clone	1188	99
1		[HLDBG33.		ŀ
188	AJ292529	Homo sapiens	suppressor of sterile four 1	2424	100
190	X54134	Homo sapiens	protein-tyrosine phosphatase	3705	100
191	Y22203	Homo sapiens	Human calcium-binding	1083	99
1	ļ		phosphoprotein, CBPP-1,		,,
ţ			protein sequence.	į į	í
192	W63692	Homo	Human secreted protein 12.	1975	100
		sapiens	•		}
193	W87772	Homo sapiens	Human serum glucocorticoid-	2605	99
		bapacino		2003	,
	""	none suprems	regulated kinase (H-SGK2) polypeptide.	2003]

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	
ID No:	NUMBER		DESCRIPTION	WATERMAN SCORE	IDENTITY
194	AF084259	Mus musculus	bromodomain-containing protein BP75	693	54
195	Y00752	Rattus norvegicus	serine dehydratase (AA 1 - 327)	994	61
196	W95349	Homo sapiens	Human foetal brain secreted protein fh170 7.	2596	100
197	AB028859	Homo sapiens	hDj9	1890	100
198	W95633	Homo sapiens	gene clone hm236 1.	1614	100
199	Y44277	Homo sapiens	Human nucleic acid methylase- 2.	2096	99
200	AB030039	Homo sapiens	hPACPL1	2258	100
201	X54162	Homo sapiens	64 Kd autoantigen	2918	99
202	G02061	Homo sapiens	Human secreted protein, SEQ ID NO: 6142.	558	99
203	X13885	Nicotiana tabacum	extensin (AA 1-620)	185	33
204	J04204	Bos taurus	32 kd accessory protein	1837	100
205	J04204	Bos taurus	32 kd accessory protein	1101	100
207	Y87283	Homo sapiens	Human signal peptide containing protein HSPP-60 SEQ ID NO:60.	1318	100
208	¥02860	Homo sapiens	Fragment of human secreted protein encoded by gene 65.	936	98
209	AL121889	Homo sapiens	dJ1076E17.1 (KIAA0823 protein (continues in AL023803))	694	54
210	AF226732	Homo sapiens	NPD007	1345	76
211	X66295	Mus musculus		970	73
212	Z29328	Homo sapiens	Ubiquitin-conjugating enzyme UbcH2	966	100
213	Z29328	Homo sapiens	Ubiquitin-conjugating enzyme UbcH2	542	98
214	AJ002030	Homo sapiens	progresterone binding protein	1163	100
215	X70649	Homo sapiens	member of DEAD box protein family	3933	100
216	AF250558	Homo sapiens	claudin-2	1169	99
217	AL021453	Homo sapiens	dJ821D11.1 (PUTATIVE protein)	259	100
218	Y08565	Homo sapiens	UDP-GalNAc:polypeptide N- acetylgalactosaminyltransfera se	3331	99
219	Y94452	Homo sapiens	Human inflammation associated protein	2067	100
220	AL035521	Arabidopsis thaliana	putative protein	315	42
221	AL031786	Schizosaccha romyces pombe	putative proline-trna synthetase	811	41
222	AL109736	Schizosaccha romyces pombe	WD repeat protein	626	40
223	X52493	Glycine max	DNA-directed RNA polymerase	136	23
224	AL035659	Homo sapiens	dJ979N1.1 (dJ979N1.1)	5199	98
225	AB032401	Mus musculus	mmDj4	1761	92
226	AB032401	Mus musculus	mnDj4	1988	92
227	X83502	Saccharomyce s cerevisiae	J1007	112	26
228	X83502	Saccharomyce s cerevisiae	J1007	79	25
229	AF143723	Homo sapiens	heat shock protein HSP60	2557	99
230	Y66677	Homo sapiens	Membrane-bound protein PRO828.	982	100
231	AB027466	Homo sapiens	spondin 2	1756	99
232	W95634	Homo sapiens	Homo sapiens secreted protein.	1391	100
233	W00365	Homo sapiens	Human cyclin Bl.	2218	99
234	Y53762	Homo sapiens	A GTP-binding polypeptide	1017	100

SEO	ACCESSION	SPECIES	DESCRIPTION		
ID	NUMBER	DEECTES	DESCRIPTION	SMITH-	*
NO:	1,01,22,0			WATERMAN	IDENTITY
			designated RAQ.	SCORE	<u> </u>
235	250749	Homo sapiens			
236	Z50749	Homo sapiens	yeast sds22 nomolog	1800	100
237	AB026491			1754	98
238	AJ270205	Homo sapiens	_L	2137	100
230	AU2/0205	caudatum	putative	114	37
j		caudatum	phosphatidylinositol-4-		Ì
239 .	AB030189	Mus musculus	phosphate 5-kinase		<u> </u>
237	MD030183	Mus musculus	contains transmembrane (TM)	710	93
240	W56538	Homo sapiens	region and ATP binding region		1
240	M26226	Homo sapiens	Human hedgehog interacting	3785	99
241	W56538	Homo sapiens	protein (HIP).		}
241	M20270	nomo sapiens	Human hedgehog interacting	3436	99
242	AF155107	 	protein (HIP).	_	1 .
243		Homo sapiens	NY-REN-37 antigen	996	99
243	AF155107	Homo sapiens		1005	100
244	AL031320	Homo sapiens	dJ20N2.1 (novel protein	763	99
	ļ		similar to yeast and		
1	t	1	bacterial cytosine	į	Ì
245			deaminase)		
245	U37026	Rattus	sodium channel beta 2 subunit	162	30
		norvegicus	<u></u>		
246	AL078599	Homo sapiens	dJ991C6.1 (novel protein	2391	98
	i		similar to C. elegans	ĺ	
		<u>L</u>	F55A12.9 (Tr:P91086))		1
247	U32274	Saccharomyce	Ydr386wp; CAI: 0.12	191	37
		s cerevisiae		1.	- '
248	Y41719	Homo	Human PRO864 protein	1879	100
	<u> </u>	sapiens	sequence.		
249	AB029434	Homo sapiens	ghrelin precursor	611	100
250	X97831	Rattus	carnitine/acylcarnitine	246	38
	<u> </u>	norvegicus	carrier protein		1
251	WB0993	Homo	Human RIP-interacting factor	1724	100
		sapiens	RIF.		1
252	Y94873	Homo	Human protein clone HP02632.	1876	100
	<u></u>	sapiens		1	
253	W59878	Homo sapiens	Amino acid sequence of the	765	100
			CDNA clone AIF-2 (HEBGM49).		-00
254	AL354533	Leishmania	possible adenylate kinase	265	34
		major	•		-
255	AF233322	Mus musculus	zinc transporter like 2	1916	95
256	Y78113	Homo sapiens	Human cytokine signal	2247	99
	ł	_	regulator CKSR-1 SEQ ID		-
			NO:1.		
257	AL035539	Arabidopsis	putative amino acid transport	390	27
	İ	thaliana	protein	320	~ /
258	W74787	Homo sapiens	Human secreted protein	1171	100
	(_	encoded by gene 58 clone		100
	ŀ		HHFHN61.		
259	AL035689	Homo sapiens	dJ187J11.1 (novel protein	974	100
		-	similar to protein kinase C	3,7	100
	ł	1	inhibitors)		
260	AE000909	Methanobacte	serine/threonine protein	363	30
	}	rium	kinase related protein	363	30
	1	thermoautotr	process.		!
		ophicum	I		:
261	AL050131	Homo sapiens	hypothetical protein	636	
262	AF019661	Mus musculus	zeta proteasome chain; PSMA5	626	100
263	AL035593	Homo sapiens	dJ310J6.1 (novel-protein)	1214	100
264	AL022318	Homo sapiens	bK150C2.3 (PUTATIVE novel	821	100
			protein similar to APOBEC1)	1072	100
265	AP205940	Homo sapiens	endomucin		
266	AL023583	Homo sapiens		1289	100
267	AL034548		dJ500L14.1 (novel protein)	789	100
		our eabteus	dJ1103G7.3 (novel protein	1888	99
	ļ	j	kinase domains containing	}	}
			protein similar to phosphoprotein C8FW)	ļ	į.

SEQ	ACCESSION	SPECIES	Busch		
ID	NUMBER	OI BCIES	DESCRIPTION	SMITH-	
NO:				WATERMAN	IDENTITY
268	AF161470	Homo sapiens	HSPC121	1884	98
269	AF161470	Homo sapiens	HSPC121	1232	96
270	X90763	Homo	HHa5 hair keratin type I	2190	1 96
L		sapiens	intermediate filament	2130) 39
271	AF207600	Homo sapiens	ethanolamine kinase	1952	100
272	M32334	Homo sapiens	intercellular adhesion	1436	100
L		<u>.</u>	molecule 2	1-100	100
273	AF161483	Homo sapiens		663	61
274	Y53052	Homo sapiens		587	100
	1	1	df202_3 protein sequence SEQ		1 200
			ID NO:110.	İ	1
276	Y77576	Homo sapiens	Human cytoskeletal protein	762	100
1	1		(HCYT) (clone 2195418).		
277	AF077042	Homo sapiens		1269	100
070-			homolog		
278	Y94907	Homo sapiens		1619	98
1]		cal06_19x protein sequence	1	1
279			SEQ ID NO:20.		1
219	Y68788	Homo sapiens	Amino acid sequence of a	2801	-99
1	1	ł	human phosphorylation	1]
280	005134		effector PHSP-20.		ļ
280	275134	Canis	rod transducin	1816	100
281	275134	familiaris			1
261	275134	Canis	rod transducin	1718	96
282	27340000	familiaris		1	1
283	AF249873	Homo sapiens	muscle-specific protein	1395	100
284	AL050007	Homo sapiens	hypothetical protein	405	98
285	AF201931	Homo sapiens	DC1	1859	99
285	AF156102	Homo sapiens	ELL complex EAP30 subunit	1318	99
200	Y35897	Homo sapiens	Extended human secreted	1250	99
		1	protein sequence, SEQ ID NO.	1	ł
287	U88964	ļ.,	146.		
288	AL050143	Homo sapiens	HEM45	923	100
289	AJ011098	Homo sapiens	hypothetical protein	598	100
290	Y66724	Homo sapiens	telethonin	574	100
1 250	100/24	Homo sapiens	Membrane-bound protein	2321	100
291	AF034801	Homo sapiens	PRO836.	L	
292	AF034801		liprin-alpha4	2565	98
293	AL049851	Homo sapiens Homo sapiens	liprin-alpha4	2590	100
""	VD042027	HOMO Bapiens	dJ889J22B.1 (novel protein	1738	100
294	Y73348	Homo sapiens	(isoform 1))		
	1.0010	nomo saprens	HTRM clone 839651 protein sequence.	1245	99
295	L11672	Homo sapiens	zinc finger protein	[i	
296	AL035423	Homo sapiens	dJ2013.1 (brain mitochondrial	1694	44
-		Savrens	carrier protein-1 (BMCP1))	1024	79
297	AF198532	Homo sapiens	lymphoid enhancer binding	L	
		onbigits	factor-1	2173	100
298	AF161417	Homo sapiens	HSPC299		
299	AF159141	Homo sapiens	breast cancer metastasis-	1147	85
1	l		suppressor 1	1236	99
300	U26397	Rattus	inositol polyphosphate 4-	160	
	ł	norvegicus	phosphatase	180	30
301	AF036145	Homo sapiens	meningioma-expressed antigen	7450	
		*	5	3458	100
		Homo sapiens	GlcNac-1-P transferase	2067	99
303			butyrophilin-like protein		
			BUTR-1	~ ' -	50
304	AJ222644	Arabidopsis	asparaginyl-tRNA synthetase	659	<u> </u>
	1	thaliana		650	50
305	AF054180	Ното	hematopoietic cell derived	351	79
		sapiens	zinc finger protein	221	13
			APOBEC-1 stimulating protein	3056	
308			Human GPRW receptor		100
		sapiens	polypeptide.	-/41	100
309	AJ131891		DNA polymerase mu	2598	100

SEQ	ACCESSION	SPECIES	DESCRIPTION	T CHARGE	
ID	NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN	IDENTITY
NO:	None			SCORE	IDENTITY
310	AF293335	Homo sapiens	p30 DBC	1248	92
311	AF176525	Mus musculus	F-box protein FBL12	1501	93
312	X57802	Homo sapiens	immunoglobulin lambda light	959 .	81
1	1	1	chain		
313	236715	Homo sapiens	Net	2048	98
314	AF161532	Homo sapiens	HSPC047	727	100
315	AF208068	Homo sapiens	kelch-like protein KLHL3a	3046	100
316	Y66666	Homo	Membrane-bound protein	1166	100
		sapiens	PRO1013.		<u> </u>
317	Y29666	Homo sapiens	Human Ras protein RAPR-1.	1253	98
318	AJ387747	Homo sapiens	sialin	2614	99
319	AF161362	Homo sapiens	HSPC099	224	40
320	¥68773	Homo sapiens	Amino acid sequence of a	2243	99
1			human phosphorylation effector PHSP-5.	1	
321	AJ238379	Homo sapiens	putative TH1 protein		
322	AB040812	Homo sapiens	protein kinase PAK5	3013 3792	100
323	Y95013	Homo sapiens	Human secreted protein	913	100
	1 -33025	l nome supreme	vc48_1, SEQ ID NO:66.	1 313	100
324	Y13381	Homo sapiens	Amino acid sequence of	1976	100
[,	protein PRO271.		1 200
325	Y94944	Homo sapiens	Human secreted protein clone	2305	98
]	bf157 16 protein sequence		
			SEQ ID NO:94.		İ
326	Y76884	Homo sapiens	Retinoblastoma binding	6728	99
			protein-7sequence.)
327	AF198532	Homo sapiens	lymphoid enhancer binding	2173	100
328	278013		factor-1		
346	2/8013	Caenorhabdit is elegans	Similarity to Drosophila	569	33
		is elegans	Cadherin-related tumor suppressor		
329	AF212921	Mus musculus	MMTV receptor variant 1	484	94
330	275330	Homo	nuclear protein SA-1	6492	99
1		sapiens]	and the production of the prod	0432	""
}		>R65207		l	
1		R65207 02-		1	
İ	Í	MAR-1995 27-	.		
ļ		AUG-1993	·	J	
ĺ.		Human stromalin-1.			,
!		[Homo			
		sapiens	,		
331	AL008583	Homo sapiens	dJ327J16.3 (supported by	2133	99
			GENSCAN, FGENES and GENEWISE)	2133	'
332	Y36104	Homo sapiens	Extended human secreted	310	41
		_	protein sequence, SEQ ID NO.		
			489.		j i
333	AJ271669	Homo sapiens	putative sialoglycoprotease	1747	100
334	AF156598		p53-regulated DDA3	997	64
335	М99058	Eimeria	em100 gene is homologous the	154	26
336	Y85564	maxima	Eimeria tenella gene et100		
330	102304	Homo sapiens	Human homologue of UNC-53	3386	97
337	Y85564	Homo sapiens	(Hs-UNC-53/1) sequence. Human homologue of UNC-53	2602	
	1	nomo saprens	(Hs-UNC-53/1) sequence.	2602	94
338	Y85564	Homo sapiens	Human homologue of UNC-53	3147	98
	-		(Hs-UNC-53/1) sequence.	374.	'"
339	266561	Caenorhabdit	Similarity to Human rab13	716	34
		is elegans	protein (PIR Acc. No.		
	{	-	A49647).		
340	AB021643	Homo	gonadotropin inducible	2761	99
		sapiens	transcription repressor-3	·	· .
341	G01946	Homo sapiens	Human secreted protein, SEQ	465	98
			TD 110 C000	, .	
345	100000		ID NO: 6027.		<u> </u>
342 343	AF020591 L29154	Homo sapiens	zinc finger protein immunoglobulin heavy chain	1091 439 ·	48

SEO	ACCESSION	SPECIES	DECONTRACT		
ID	NUMBER	SPECIES	DESCRIPTION	SMITH-	*
NO:				WATERMAN SCORE	IDENTITY
			VDJ region	- SCORE	
344	U10281	Sus scrofa	gastric mucin	279	24
345	AK000404	Homo sapiens		1177	99
346	L22557	Rattus norvegicus	calmodulin-binding protein	1949	84
347	L22557	Rattus norvegicus	calmodulin-binding protein	2363	91
348	AL049481	Arabidopsis thaliana	AIG1-like protein	316	30
350	AJ251516	Mus musculus	cysteine and histidine-rich protein	1460	99
351	AK024477	Homo sapiens	FLJ00070 protein	1773	100
352	U50133	Homo sapiens	ankyrin	502	33
353	AK000625	Homo sapiens	unnamed protein product	721	100
354	AF161420	Homo sapiens	HSPC302	2623	97
353	AJ010014	Homo sapiens	M96A protein	1269	47
356	AF151029	Homo sapiens	HSPC195	941	91
357	AL022327	Homo sapiens	dJ355C18.1 (KIAA0027)	1911	100
358	W78128	Homo sapiens	Human secreted protein	1117	100
			encoded by gene 3 clone HOSBI96.		
359	X03414	Drosophila melanogaster	Kr polypeptide	316	45
360	AF151079	Homo sapiens		643	100
361	Y53886	Homo sapiens	A suppressor of cytokine	530	41
			signalling protein designated HSCOP-6.		
362	AF254741	Drosophila melanogaster	Centaurin Gamma 1A	681	46
363	AF213465	Homo sapiens	dual oxidase	2016	100
364	AF181562	·Homo sapiens	prosaas	1319	100
365	AF181562	Homo sapiens	proSAAS	1024	99
366 367	U73200	Mus musculus	pll6Rip	884	82
	AF263744	Homo sapiens	erbb2-interacting protein ERBIN	4973	99
368 369	U37501	Mus musculus	laminin alpha 5 chain	5867	72
	AF043695	Caenorhabdit is elegans	similar to the protein phosphates 2c family	549	36
370	¥73440	Homo sapiens	Human secreted protein clone yj23_1 protein sequence SEQ ID NO:102.	1484	99
371 372	AF272833	Homo sapiens	misato	2869	97
373	AF198454	Homo sapiens	epithelial protein lost in neoplasm beta	3927	100
	Y73345	Homo sapiens	HTRM clone 438283 protein sequence.	273	65 C8
374	AF169017	Homo sapiens	formiminotransferase cyclodeaminase	2717	98
375	A95106	unidentified	RED ALPHA	1202	99
376	W74828	Homo sapiens	Human secreted protein encoded by gene 100 clone HLQAB52.	1012	99
377	Y32131	Homo sapiens	Human LYST-2 protein.	3556	99
378	M14912	Homo sapiens	pol	132	86
379	AF090934	Homo sapiens	PR00518	382	100
380	X66363	Homo sapiens	serine/threonine protein kinase	2499	100
381	Y41699	Homo sapiens	Human PRO703 protein sequence.	2362	100
382	AF174498	Homo sapiens	GR AF-1 specific protein phosphatase	7008	98
383	U64608	Caenorhabdit is elegans	coded for by C. elegans cDNA yk173c12.5	246	36
384	U50133	Homo sapiens	ankyrin	502	33
385	AJ238520	Homo sapiens	putative transcription	4123	97
			factor-like nuclear regulator	<u> </u>	

Sec	SEQ	ACCESSION	SPECIES			
1887 AP208845 Homo sapiens MH-001 Lambda light 1375 59	ID NO:	NUMBER	SPECIES	DESCRIPTION	WATERMAN	IDENTITY
390 X57821			Homo sapiens	BM-003		99
191 195564 Nomo sapiene Nome	389	X57821	Homo sapiens			1
193	390	AF182404	Homo sapiens	,	1670	99
393 AF178432 Homo sapiens SH3 protein 3700 100	391	Y85564	Homo sapiens		3386	97
394 AF229928 Drosophila melanogaster m		_	Homo sapiens	SH3 protein	3700	100
Metalogaster Mus M	394	AF229928	Drosophila	cytoplasmic protein 89BC	1616	
396 Y69197 Homo splens	305	7510170				
Numan Detaily agreeted 16.6 98		_ !				.1. =
398 ALJ390137 Homo sapiens hypothetical protein 263 51			-	human betaIV-spectrin protein.	1626	98
AF217525 Nome aspiens Down syndrome cell adhesion 5337 60	L_ 1			zinc finger protein neuro-d4	749	60
ALO22599 Schlzosaccha molecule Schlzosaccha molecule MD repeat protein M47 27	1			hypothetical protein	263	51
ACO04859		AF217525	Homo sapiens		5337	60
AC004859	400	AL022599	romyces	WD repeat protein	447	27
AB010266 Mus musculus tenascin-X 10246 62	401	AC004859		dehydrogenase ; similar to	4176	78
AL133288 Homo sapiens GJ671D7.1 (similar to D.melanogaster CG5986 protein) D.melanogaster CG5986 S88		AB010266	Mus musculus		10246	62
404	403	AL133288	Homo sapiens	D.melanogaster CG5986		
A05	404	Z68753			888	48
is elegans	405	Z78013		Similarity to Drosophila	550	
API55106 Homo sapiens NY-REN-36 antigen 1168 100				Cadherin-related tumor	363	33
108				domain 2	1196	97
15.8 39 15.8 39 15.8 15.8 39 15.8 15.8 39 15.8 15.8 30 15.8 15.				NY-REN-36 antigen	1168	100
AF249744 Homo sapiens RhoGEF 2733 100] .		1538	99
### ### ### ### ### ### ### ### ### ##					184	30
### ### ##############################		1			2733	100
ALO31658 Homo sapiens dJ310013.7 (novel protein similar to H. roretzi HRPET-3) 414 X57398 Homo sapiens pm5 protein 3-methylcrotonyl-CoA carboxylase biotin-containing subunit 416 U43503 Saccharomyce Lphip 115 42 417 AL160493 Leishmania possible t26f17.21 239 35 major 418 Y08100 Homo sapiens Human PRO331 protein. 330 29 419 U15131 Homo sapiens Human PRO331 protein. 330 29 420 AP117946 Homo sapiens Link guanine nucleotide 2363 100 exchange factor II melanogaster 422 AF302150 Homo sapiens phypothetical protein 433 94 421 AF302150 Homo sapiens hypothetical protein 433 94 422 AF302150 Homo sapiens hypothetical protein 433 94 423 AL137530 Homo sapiens Mypothetical protein 433 94 424 X63753 Homo sapiens Markk like protein kinase 1693 100 425 AB027249 Homo sapiens tumor endothelial marker 7 1084 55					2072	94
Similar to H. roretzi HRPET-33 Similar to H. roretzi HRPET-33 Similar to H. roretzi HRPET-33 Similar to H. roretzi HRPET-33 Similar to H. roretzi HRPET-33 Similar to H. roretzi HRPET-33 Similar to H. roretzi HRPET-33 Similar to H. roretzi HRPET-33 Similar to H. roretzi HRPET-34 Similar to H. roretzi HRPET-35 Similar to H. roretzi HRPET-35 Similar to H. roretzi HRPET-35 Similar to H. roretzi HRPET-36 Similar to H. roretzi HRPET-36 Similar to H. roretzi HRPET-37		1			4880	100
AB029826 Homo sapiens 3-methylcrotonyl-CoA 2961 99 416 U43503 Saccharomyce Lphip 115 42 417 AL160493 Leishmania possible t26f17.21 239 35 418 Y08100 Homo sapiens Human PR0331 protein. 330 29 419 U15131 Homo sapiens p126 2228 54 420 AF117946 Homo sapiens Link guanine nucleotide 2363 100 421 AF190635 Drosophila ankyrin 2 755 30 422 AF302150 Homo sapiens phosphoinositol 3-phosphate- 1962 100 423 AL137530 Homo sapiens hypothetical protein 433 94 424 X63753 Homo sapiens MAPKK like protein kinase 1693 100 426 AF279144 Homo sapiens tumor endothelial marker 7 1084 55		ALO31658		similar to H. roretzi HRPET-	776	98
AB029826					6131	99
416 U43503 Saccharomyce s cerevisiae Lphip 115 42 417 AL160493 Leishmania possible t26f17.21 239 35 418 Y08100 Homo sapiens Human PRO331 protein. 330 29 419 U15131 Homo sapiens p126 2228 54 420 AP117946 Homo sapiens Link guanine nucleotide exchange factor II 2363 100 421 AF190635 Drosophila ankyrin 2 755 30 422 AF302150 Homo phosphoinositol 3-phosphate-sapiens binding protein-2 1962 100 423 AL137530 Homo sapiens hypothetical protein 433 94 424 X63753 Homo sapiens son-a 7269 100 425 AB027249 Homo sapiens MAPKK like protein kinase 1693 100 426 AF279144 Homo sapiens tumor endothelial marker 7 1084 55	415	AB029826	Homo sapiens	carboxylase biotin-containing	2961 .	
417 AL160493 Leishmania major possible t26f17.21 239 35 418 Y08100 Homo sapiens Human PRO331 protein. 330 29 419 U15131 Homo sapiens p126 2228 54 420 AF117946 Homo sapiens Link guanine nucleotide exchange factor II 2363 100 421 AF190635 Drosophila melanogaster ankyrin 2 755 30 422 AF302150 Homo sapiens binding protein-2 1962 100 423 AL137530 Homo sapiens hypothetical protein 433 94 424 X63753 Homo sapiens son-a 7269 100 425 AB027249 Homo sapiens MAPKK like protein kinase 1693 100 426 AF279144 Homo sapiens tumor endothelial marker 7 1084 55	416	U43503			115	42
418 Y08100 Homo saplens Human PRO331 protein. 330 29 419 U15131 Homo sapiens p126 2228 54 420 AF117946 Homo sapiens Link guanine nucleotide exchange factor II 2363 100 421 AF190635 Drosophila ankyrin 2 755 30 422 AF302150 Homo sapiens binding protein-2 1962 100 423 AL137530 Homo sapiens hypothetical protein 433 94 424 X63753 Homo sapiens son-a 7269 100 425 AB027249 Homo sapiens MAPKK like protein kinase 1693 100 426 AF279144 Homo sapiens tumor endothelial marker 7 1084 55	417	AL160493	Leishmania	possible t26f17.21	239	35
19	418	Y08100		Human DDO331 protoin	1220	
AF117946 Homo sapiens Link guanine nucleotide 2363 100					1	
AF190635 Drosophila ankyrin 2 755 30						
Melanogaster				exchange factor II		
Sapiens Sapi			melanogaster		755	30
423 AL137530 Homo sapiens hypothetical protein 433 94 424 X63753 Homo sapiens son-a 7269 100 425 AB027249 Homo sapiens MAPKK like protein kinase 1693 100 426 AF279144 Homo sapiens tumor endothelial marker 7 1084 55			sapiens	phosphoinositol 3-phosphate- binding protein-2	1962	100
424 X63753 Homo sapiens son-a 7269 100 425 AB027249 Homo sapiens MAPKK like protein kinase 1693 100 426 AF279144 Homo sapiens tumor endothelial marker 7 1084 55			Homo sapiens		433	94
425 AB027249 Homo sapiens MAPKK like protein kinase 1693 100 426 AF279144 Homo sapiens tumor endothelial marker 7 1084 55			Homo sapiens			
to the supreme country endocuterial marker / 1084 55					1693	
	320	NE2/9144	Homo sapiens		1084	55

TABLE 2

SEQ ID NO: 427 428 429 430 431 432 433	ACCESSION NUMBER AF279144 AE003683 Y07829 AF096897 U41387 AF023674 AF146760 AB006697	Homo sapiens Drosophila melanogaster Homo sapiens Drosophila melanogaster Homo sapiens Homo sapiens Homo sapiens Arabidopsis thaliana	precursor CG8312 gene product RING finger protein pushover Gu protein nephrocystin septin 2-like cell division control protein cleft lip and palate	SMITH- WATERMAN SCORE 1259 149 2201 4442 4021 3783 2284	1DENTITY 56 29 99 47 99 100
427 428 429 430 431 432 433	AE003683 Y07829 AF096897 U41387 AF023674 AF146760 AB006697	Drosophila melanogaster Homo sapiens Drosophila melanogaster Homo sapiens Homo sapiens Homo sapiens Arabidopsis thaliana	precursor CG8312 gene product RING finger protein pushover Gu protein nephrocystin septin 2-like cell division control protein cleft lip and palate	SCORE 1259 149 2201 4442 4021 3783	56 29 99 47 99
428 429 430 431 432 433	AE003683 Y07829 AF096897 U41387 AF023674 AF146760 AB006697	Drosophila melanogaster Homo sapiens Drosophila melanogaster Homo sapiens Homo sapiens Homo sapiens Arabidopsis thaliana	precursor CG8312 gene product RING finger protein pushover Gu protein nephrocystin septin 2-like cell division control protein cleft lip and palate	1259 149 2201 4442 4021 3783	99 47 99 100
429 430 431 432 433	Y07829 AF096897 U41387 AF023674 AF146760 AB006697	melanogaster Homo sapiens Drosophila melanogaster Homo sapiens Homo sapiens Homo sapiens Arabidopsis thaliana	CG8312 gene product RING finger protein pushover Gu protein nephrocystin septin 2-like cell division control protein cleft lip and palate	2201 4442 4021 3783	99 47 99 100
431 432 433	AF096897 U41387 AF023674 AF146760 AB006697	Homo sapiens Drosophila melanogaster Homo sapiens Homo sapiens Homo sapiens Arabidopsis thaliana	RING finger protein pushover Gu protein nephrocystin septin 2-like cell division control protein cleft lip and palate	4442 4021 3783	99 100
431 432 433	U41387 AF023674 AF146760 AB006697	Drosophila melanogaster Homo sapiens Homo sapiens Homo sapiens Arabidopsis thaliana	pushover Gu protein nephrocystin septin 2-like cell division control protein cleft lip and palate	4442 4021 3783	99 100
432	AF023674 AF146760 AB006697 Y94247	Homo sapiens Homo sapiens Homo sapiens Arabidopsis thaliana	Gu protein nephrocystin septin 2-like cell division control protein cleft lip and palate	4021 3783	99
432	AF023674 AF146760 AB006697 Y94247	Homo sapiens Homo sapiens Arabidopsis thaliana	nephrocystin septin 2-like cell division control protein cleft lip and palate	3783	100
433	AF146760 AB006697 Y94247	Homo sapiens Arabidopsis thaliana	septin 2-like cell division control protein cleft lip and palate	3783	100
	AB006697	sapiens Arabidopsis thaliana	control protein		
434	Y94247	thaliana	cleft lip and palate		100
ŀ			associated transmembrane protein-like	886	42
437	37046545	Homo sapiens	Human calcium binding protein hCBP.	1704	100
438	AB040672	Homo sapiens	UDP-GalNAc: polypeptide N- acetylgalactosaminyltransfera se	1075	63
439	AF105228	Bos taurus	tuftelin	285	33
440	R06463	Homo sapiens	Derived protein of clone ICA13 (ATCC 40553).	3073	99
441	X14971	Mus musculus	alpha-adaptin (A) (AA 1-977)	4897	
442	X53773	Rattus norvegicus	alpha-c large chain (AA 1- 938)	3979	98 81
443	Y66689	Homo sapiens	Membrane-bound protein	3299	99
444	AC067754	Arabidopsis	PRO1136. unknown protein; 20348-23707	114	33
445	AF229032	thaliana Mus musculus			
446	AF056035	Rattus	piL s-nexilin	2077	93
447	AF132484	norvegicus		2662	85
448	W89024	Mus musculus Homo sapiens	unknown	478	51
449			Polypeptide fragment encoded by gene 156.	528	45
450	AF161445 Z68753	Homo sapiens	HSPC327	1606	100
		Caenorhabdit is elegans	2C518.3b	951	49
451	W39160	Homo sapiens	Human partial complement factor H protein fragment 3.	155	32
452	W85727	Homo sapiens	Novel protein (Clone BM46 10).	2799	99
453	Y53629	Homo sapiens	A bone marrow secreted protein designated BMS115.	2810	100
454	D87438	Homo sapiens	Similar to a C.elegans protein in cosmid C14H10	4069	100
455	AF240468	Homo sapiens	nicastrin	3687	100
456	Z15005	Homo sapiens	CENP-E	13305	99
457	M59216	Homo sapiens	gamma-aminobutyric acid receptor beta-1 subunit	2477	100
458	Y73467	Homo sapiens	Human secreted protein clone yd61_1 protein sequence SEQ ID NO:156.	966	100
459	W67824	Homo sapiens	Human secreted protein encoded by gene 18 clone HSLFM29.	535	100
460	AF163151	Homo sapiens	dentin sialophosphoprotein precursor	279	19
461	D87446	Homo sapiens	Similar to a C.elegans protein encoded in cosmid C27F2 (U40419)	9196	99
	G04044	Homo sapiens	Human secreted protein, SEQ ID NO: 8125.	486	93
	AC002398	Homo sapiens	F25965_1	1018	100
	AF064856 AF223408	Rattus sp.	7acomp protein	1845	84
*03	ME223408	Homo sapiens	B99	3686	99

TABLE 2

SEQ	ACCESSION	SPECIES	DESCRIPTION	- CHAMMA	
ID	NUMBER	0.2022	DESCRIPTION	SMITH- WATERMAN	TDUMETON
NO:	1	1	İ	SCORE	IDENTITY
466	AF223408	Homo sapiens	1899	2878	
467	AF104415	Mus musculus		6336	87
468	U53450	Rattus	Jun dimerization protein 1	196	91
	,	norvegicus	JDP-1	196	49
469	AL031297	Homo sapiens	1 -	3564	
470	AF257077	Homo sapiens	eukaryotic translation	1274	99
l			initiation factor EIF2B	12/4	95
			subunit 3		
471	L28125	Podospora	beta transducin-like protein	284	38
i		anserina	The production of the production	204	38
472	Y84903	Homo sapiens	A human proliferation and	2337	100
ĺ		•	apoptosis related protein.	2337	100
473	AF144237	Homo sapiens	LOMP protein	252	44
474	Y71213	Homo sapiens		838	100
1	Į.	Ī	related polypeptide IMX39.		
475	Y95006	Homo sapiens	Human secreted protein	3411	100
ı	}	1	vel3 1, SEQ ID NO:52.] 3311	100
476	D38549	Homo sapiens	hal025 is new	6533	99
477	AF241230	Homo sapiens	TAK1-binding protein 2	3656	100
478	AL031534	Schizosaccha	putative asparagine synthase	482	40
		romyces	1 3 3 3 3 3 7 1 1 1 1 1 1 1 1 1 1 1 1 1	1 ***	[]
		pombe			
479	L28125	Podospora	beta transducin-like protein	233	26
		anserina			
480	AF161544	Homo sapiens	HSPC059	434	77
481	AJ238248	Homo sapiens		3986	99
482	238061	Saccharomyce		295	23
		s cerevisiae	0.3, AMYH YEAST P08640		
			GLUCOAMYLASE S1 (EC 3.2.1.3)	ł	1
483	AF161381	Homo sapiens	HSPC263	1404	100
484	AF223468	Homo sapiens	AD021 protein	1314	100
485	X57527	Homo sapiens	alpha 1(VIII) collagen	4166	99
488	Y19062 Y73373	Homo sapiens	39k3 protein	2475	100
400	1/33/3	Homo sapiens	HTRM clone 921803 protein	555	56
489	AL021918	Homo	sequence.	<u> </u>	}
103	ADUZISTO	sapiens	b3418.1 (Kruppel related Zinc	4184	100
490	X53773	Rattus	Finger protein 184)		
	3.55775	norvegicus	alpha-c large chain (AA 1- 938)	4675	97
491	U52426	Homo sapiens	GOK		
492	AL359773	Leishmania	possible threonine synthase	1459	59
	1	major	possible inreonine synthase	702	45
493	AF226614	Homo sapiens	ferroportinl	0000	
494	Z93241	Homo sapiens	dJ222B13.1 (novel protein	2929	100
			with some similarity to	513	96
	j j		Drosophila KRAKEN)		:
495	AF036977	Homo sapiens	unknown	1812	100
496	U93564	Homo sapiens	p40	133	45
197	Y91405	Homo sapiens	Human secreted protein	357	100
•		-	sequence encoded by gene 2	337	100
			SEQ ID NO:126.		1
498	AF069781	Drosophila	Bem46-like protein	653	43
		melanogaster	•		"
499	¥16601	Homo sapiens	Human cell-cycle	1658	98
			phosphoprotein CECYP-2.		
500 7	X70944	Homo sapiens	PTB-associated splicing	3883	100
	j		factor	}	
501			putative membrane-associated		36
	AF027503	Mus	baracive membrane-associated	205	JO 1
		musculus	guanylate kinase 1	205	30
502	AF282874	musculus Homo sapiens	guanylate kinase 1 nectin 3; PRR3	2856	99
503	AF282874 AJ249732	Homo sapiens Homo sapiens	guanylate kinase 1 nectin 3; PRR3 G8 protein		
503 504	AF282874 AJ249732 AF208861	Homo sapiens Homo sapiens Homo sapiens	guanylate kinase 1 nectin 3; PRR3 G8 protein BM-019	2856	99
503 504 505	AP282874 AJ249732 AF208861 L09708	musculus Homo sapiens Homo sapiens Homo sapiens Homo sapiens	guanylate kinase 1 nectin 3; PRR3 G8 protein BM-019 complement component C2	2856 669	99 100
503 504 505 507	AF282874 AJ249732 AF208861 L09708 X66285	musculus Homo sapiens Homo sapiens Homo sapiens Homo sapiens Mus musculus	guanylate kinase 1 nectin 3; PRR3 G8 protein BM-019 complement component C2 HC1 ORF	2856 669 1629	99 100 100
503 504 505	AP282874 AJ249732 AF208861 L09708	musculus Homo sapiens Homo sapiens Homo sapiens Homo sapiens	guanylate kinase 1 nectin 3; PRR3 G8 protein BM-019 complement component C2	2856 669 1629 4022	99 100 100

SEQ	ACCESSION	SPECIES	DESCRIPTION	T CM Years	
ID NO:	NUMBER			SMITH- WATERMAN SCORE	IDENTITY
509	Y94971	Homo sapiens	Human secreted protein clone fal71_1 protein sequence SEQ ID NO:148.	2176	100
510	AB019038	Homo sapiens		781	77
511	AB019038	Homo sapiens	beta-1,4 mannosyltransferase	1347	100
512	AB019038	Homo sapiens	beta-1,4 mannosyltransferase	1520	99
513	X84908	Homo sapiens	1	5729	99
514 515	X52851 AF186084	Homo sapiens		650	76
313	AF186084	Homo sapiens	epidermal growth factor repeat containing protein	3046	99
516	G03602	Homo sapiens	Human secreted protein, SEQ ID NO: 7683.	505	99
517	U04706	Bos taurus	50 kDa protein	1749	 77 -
518	G00653	Homo sapiens	Human secreted protein, SEQ	530	100
519	AF161475	Homo sapiens	ID NO: 4734.		<u> </u>
520	¥99366	Homo sapiens	Human PRO1475 (UNQ746) amino	1368 3394	100
]	J Suprem	acid sequence SEQ ID NO:88.	3394	97
521	AF266852	Homo sapiens	PTPLA	1295	100
522	AB000995	Archaeoglobu	chromosome segregation	153	20
523	AF062249	s fulgidus	protein (smcl)	ļ	
524	AJ223830	Homo sapiens	immunoglobulin heavy chain variable region	605	97
		Rattus norvegicus	ARE1	2950	98
525	W01535	Homo sapiens	Cellular homologue of the SV40 large T antigen.	1276	93
526	AF145658	Drosophila melanogaster	BcDNA.GH10229	320	33
527	AF112213	Homo sapiens	putative Rab5-interacting protein	524	79
528	D49387	Homo sapiens	NADP dependent leukotriene b4	1616	100
529	Y30819	Homo sapiens	12-hydroxydehydrogenase Human secreted protein	328	32
530	AL079335	Homo sapiens	encoded from gene 9. dJ132F21.3 (72.1 KDa protein	1050	
		Dupzono	(DKFZP564A032, SBBI88) similar to mouse IFN-gamma induce MG11.)	1059	99
531	Y91506	Homo sapiens	Human secreted protein sequence encoded by gene 56 SEQ ID NO:179.	1159	98
532	X76116	Caenorhabdit	carrier protein (c2)	576	50
533	X76116	is elegans			
534		Caenorhabdit is elegans	carrier protein (c2)	506	50
	X12966	Homo sapiens	3-oxoacyl-CoA thiolase propeptide (424 AA)	1972	100
535	¥09267	Homo sapiens	flavin-containing monooxygenase 2	2486	100
536	Z11773	Homo sapiens	SRE-ZBP	2201	99
537	D84224	Homo sapiens	methionyl tRNA synthetase	4741	99
538 539	D84224 D84224	Homo sapiens	methionyl tRNA synthetase	3887	99
540	D84224	Homo sapiens	methionyl tRNA synthetase	2933	96
541	J03244	Bos taurus	methionyl tRNA synthetase H+ ATPase 31kDa subunit (EC	4529 848	99 77
542	VODETA		3.6.1.3)		''
543	Y92514 AF221712	Homo sapiens	Human OXRE-11.	2301	99
{		Homo sapiens	Smad- and Olf-interacting zinc finger protein	2151	61
544	AE000919	Methanobacte	conserved protein	207	38
1		rium thermoautotr			
545	A06669	ophicum synthetic	DroffCE hotal		
	1	construct	preTGF-betal	2070	99

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
546	Y02698	Homo sapiens	encoded by gene 49 clone	854	98
547	AF112205	Homo sapiens		2275	100
548	X60271	Mus musculus	c-rel	2264	74
549	AC016827	Arabidopsis thaliana	putative GTPase	810	42
550	¥70400	Homo sapiens	Human cell-signalling protein-2.	429	68
551	AB048365	Homo sapiens		8290	99
552	¥57880	Homo sapiens	Human transmembrane protein HTMPN-4.	1112	95
553	AF119855	Homo sapiens	PRO1847	265	67
554	M17236	Homo sapiens	MHC HLA-DQ alpha precursor	1332	100
555	AL078468	Arabidopsis thaliana	putative protein	540	40
556	AC006963	Homo sapiens	similar to Kelch proteins; similar to BAA77027 (PID:g4650844)	515	44
557	AK024487	Homo sapiens	FLJ00086 protein	1623	98
558 559	M12140	Homo sapiens	pol gene protein; Xxx	117	48
	W74825	Homo sapiens	Human secreted protein encoded by gene 97 clone HAQBF73.	225	56
560	X56681	Homo sapiens	junD protein	373	88
561	AF003136	Caenorhabdit is elegans	contains weak similarity to an AMP-binding motif	2926	54
562	AL109839	Homo sapiens	dJ1069P2.3.1 (novel PABPC1 (poly(A)-binding protein)	877	100
563	AF181640	Drosophila melanogaster	BcDNA.GH09817	289	42
564	AF052723	Feline leukemia virus	gag-pol precursor polyprotein gPr80	1547	43
565	AF161472	Homo sapiens	HSPC123	439	44
566	Y28817	Homo sapiens	pt326_4 secreted protein.	3338	100
567	U09848	Homo sapiens	zinc finger protein	1738	100
569	AF155113	Homo sapiens	NY-REN-55 antigen	3603	93
570 571	AF155113	Homo sapiens	NY-REN-55 antigen	3951	99
572	AL032821 M69181	Homo sapiens	dJ55C23.1 (vanin 1)	1821	98
573	M69181	Homo sapiens	non-muscle myosin B	7350	99
574	Y59678	Homo sapiens	non-muscle myosin B	7311	98
575	AL365234	-	Secreted protein 108-008-5-0- E6-PL.	772	100
576		Arabidopsis thaliana	putative protein	788	40
	AL365234	Arabidopsis thaliana	putative protein	788	40
577	X06745	Homo sapiens	DNA polymerase alpha-subunit (AA 1 - 1462)	7619	99
	AB041642	Homo sapiens	PAR-6	1342	100
	D86984	Homo sapiens	similar to yeast adenylate cyclase (956776)	2446	100
	AF165124	Homo sapiens	gamma-aminobutyric acid A receptor gamma 2	2499	99
81	W88812	Homo sapiens	Polypeptide fragment encoded by gene 58.	2339	99
	U82319	Homo sapiens	novel ORF	342	100
	P92219	Homo sapiens	CR1 protein.	11425	99
		(human)			
84	AJ223948	Homo sapiens	RNA helicase	6608	90
84	AJ223948		88kDa nuclear pore complex	6608 3874	99 99
85	AJ223948 Y08612	Homo sapiens Homo sapiens			

TABLE 2

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	
NO:	NUMBER			WATERMAN SCORE	IDENTITY
588	AF131775	Homo sapiens		1929	99
591	AJ250865	Homo sapiens		2348	100
	Z98885	Homo sapiens	containing 1 (similar to peregrin, BR140))	4167	100
592 593	L76571	Homo sapiens		1355	100
593	AF091622	Homo sapiens		9054	100
595	X56807 AL137802	Homo sapiens		4443	100
596	AL022329	Homo sapiens		212	55
597		Homo sapiens	bK407F11.2 (adrenergic, beta, receptor kinase 2)	3653	100
598	AF226048	Homo sapiens		2009	99
598	AJ278112	Homo sapiens] >Y49635 Y49635 21- OCT-1999 15- APR-1998 Human sdp3.5 protein.	putative cell cycle control protein	335	23
599	Y59741	(Homo sapiens			
600		Homo sapiens	Human normal ovarian tissue derived protein 18.	1574	99
601	L36531 Y38458	Homo sapiens		5386	99
602		Homo sapiens	encoded by gene No. 20.	895	100
603	AF218584 Y13115	Homo sapiens	GGA1	3265	100
		Homo sapiens	serine/threonine protein kinase	5071	99
604	AL132776	Homo sapiens	dJ393D12.1 (KIAA0776)	2413	99
	AL034452	Homo sapiens	dJ682J15.1 (novel Collagen triple helix repeat containing protein)	1979	100
606	Y14494	Homo sapiens	aralari	3465	99
607	AJ001981	Homo sapiens	OXA1L	2603	100
608	X86098	Homo sapiens	binds directly to adenovirus type 5 ElA protein	3069	100
610	AF163572	Homo sapiens	Forssman glycolipid synthetase	1865	99
611	AF161503	Homo sapiens	HSPC154	1261	97
612 613	L41834	Ensis minor	nuclear protein	345	30
	¥91954	Homo sapiens	Human cytoskeleton associated protein 9 (CYSKP-9).	3668	100
614	AL022327 X85786	Homo sapiens	dJ355C18.1 (KIAA0027)	361	94
616	Y08319	Homo sapiens	binding regulatory factor	3203	100
617	D12644	Homo sapiens Mus musculus	kinesin-2	3487	99
618	U28789	Mus musculus	KIF2 protein	3609	97
619	Y35914	Homo sapiens	PACT Extended human secreted	5936	89
		nome baptens	protein sequence, SEQ ID NO. 163.	1684	99
620	A9046382	Mus musculus	testis-abundant finger protein	199	23
621	Y00062	Homo sapiens	precursor polypeptide (AA -23 to 1120)	3440	99
622	AF068286	Homo sapiens	HDCMD38P	861	100
623	X98248	Homo sapiens	sortilin		99
624	X61100	Resigna omok	75 kDa subunit NADH dehydrogenase precursor		99
625	S58544	Homo sapiens	75 kda infertility-related sperm protein	2125	99
626	AF151027	Homo sapiens	HSPC193	582	93
627 628	X14968	Homo sapiens	RII-alpha subunit (AA 1-404)		100
020	Y50911	Homo sapiens	Human fetal brain cDNA clone vb7_1 derived protein		100

TABLE 2

SEO	ACCESSION	SPECIES	DESCRIPTION	Ch (Ymy)	
ID NO:	NUMBER	3730133	DESCRIPTION	SMITH- WATERMAN	IDENTITY
629	Y50911	Homo sapiens		SCORE 1694	100
630	AF098786	Ното	vb7_1 derived protein 17 beta-hydroxysteroid	1754	100
631	AL034555	sapiens Homo	dehydrogenase type VII dJ134019.3 (zinc finger		
1	1	sapiens	protein 151 (pHZ-67))	4273	100
632	W74826	Homo sapiens	Human secreted protein	794	96
			encoded by gene 98 clone HAQBT94.	1	
633	AF288288	Homo sapiens		2236	.100
634	AF041429 X66357	Homo sapiens		823	99
L		· -	kinase	1589	100
636	Y11284	Homo sapiens		2571	98
637	AB004884 AJ002303	Homo sapiens		3718	99
639	AJ002304	Homo sapiens	synaptogyrin lc	1020	100
640	AJ002303	Homo sapiens		1002	100
641	D87682	Homo sapiens	similar to a C.elegans	933 2676	94
		nomo ouptens	protein encoded in cosmid	2676	100
642	M14660		T26A5.		i
643	X06661	Homo sapiens	ISG-K54	2473	99
644	AF119900	Homo sapiens	calbindin (AA 1-261) PRO2822	1358	100
645	AB031048	Drosophila	microtubule associated-	185	76
		melanogaster	protein orbit	738	27
646	AF250842	Drosophila melanogaster	multiple asters	834	29
647	X86691	Homo sapiens	Mi-2 protein		
648	U67934	Homo sapiens	44.9 kDa protein C18B11	10110	99
			homolog	""	"
649	AF236061	Oryctolagus cuniculus	RING-finger binding protein	3830	91
650	AL034553	Homo sapiens	dJ914P20.2 (KIAA0784 protein similar to Mus musculus activity-dependent neuroprotective protein (Adnp))	5708	100
653	X14766	Homo sapiens	GABA-A receptor alpha 1 subunit	2388	99
654	AC004614	Homo sapiens	similar to f-spondin proteins AB006086 (PID:g2529225)	3026	99
655	Y57908	Homo sapiens	Human transmembrane protein	608	99
656	634006		HTMPN-32.	1	
658	Z34975 AL050306	Homo sapiens	ldlCp	3733	100
659	W76734	Homo sapiens	dJ475B7.2 (novel protein)	1942	99
		sapiens	Human mDia Rho targeting protein.	781 .	34
660	AF202724	Homo sapiens	Sadl unc-84 domain protein 1	2172	100
661	Z21966	Homo sapiens	mPOU homeobox protein	1529	100
662	AJ242954	Mus musculus	dysferlin	4752	59
663	AF182316	Homo sapiens	myoferlin	6232	99
665	AL161516	Arabidopsis thaliana	hypothetical protein	209	30
667	X59303	Homo sapiens	valyl-tRNA synthetase	3393	99
668	Y13355	Homo sapiens	Amino acid sequence of protein PRO220.	3692	100
669	AB010692	Arabidopsis	contains similarity to endo-		
		thaliana	beta-N-acetylglucosaminidase gene	611	52
671	X56123	Mus musculus	talin	4474	76
672	AB039371	Homo sapiens	mitochondrial ABC transporter	2902	99
673	AF269223	Homo sapiens	TCP11	806	43
674	AF229633	Mus musculus	groucho-related protein 4	4053	99
675	L14463	Rattus	transducin	3619	92

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	* IDENTITY
		norvegicus			
676	AC005757	Homo sapiens	R32611 1	2779	100
677	861069	Homo sapiens	reverse transcriptase	252	65
			homolog=pol (retroviral element)		
678	AF271388	Homo sapiens	CMP-N-acetylneuraminic acid synthase	2273	100
679	X79066	Homo sapiens	ERF-1	1783	100
680	AF118566	Mus musculus	hematopoietic zinc finger protein	769	50
681	Y51415	Homo sapiens	Human wild type pKe83 . protein.	2621	99
682	AL133545	Homo sapiens	bA386Ni4.1 (novel protein similar to a dual specificity phosphatase)	700	68
683	Y86214	Homo sapiens	Nuclear transport protein clone hfb341 protein sequence.	5888	99
684	Y94952	Homo sapiens	Human secreted protein clone fhl16_11 protein sequence SEQ ID NO:110.	354	98
685	AL021878	Homo sapiens	dJ257120.4 (transcription factor 20 (AR1) (KIAA0292) (isoform 2))	154	67
686	AE000198	Escherichia coli	orf, hypothetical protein	628	100
687	M58378	Homo sapiens	synapsin I	3730	99
688	AF039697	Homo sapiens	antigen NY-CO-31	508	98
689	U09355	Oryctolagus cuniculus	protein phosphatase 2A1 B gamma subunit	2356	99
690	AF155106	Homo sapiens	NY-REN-36 antigen	265	50
691	AC004774	Homo sapiens	Dlx-5	1542	100
692	X90530	Homo sapiens	ragB	1926	99
693	X90530	Homo sapiens	ragB	1405	99
694	X90530	Homo sapiens	ragB	1590	85
695	G01563	Homo sapiens	Human secreted protein, SEQ ID NO: 5644.	330	100
696	AC011810	Arabidopsis thaliana	Putative methionine aminopeptidase	669	52
697	AJ250425	Rattus norvegicus	Collybistin I	2455	98
698	AB037901	Homo sapiens	gene amplified in squamous cell carcinoma-1	5364	99
699	Y99401	Homo sapiens	Human PRO1327 (UNQ687) amino acid sequence SEQ ID NO:218.	1386	100
701	AF221712	Homo sapiens	Smad- and Olf-interacting zinc finger protein	6705	100
702	X83573	Homo sapiens	ARSE	3184	99
703 704	AJ243274 Y71262	Homo sapiens	AP-2rep protein Human chondromodulin-like	1697	99
705	Y71262	Homo sapiens	protein, Zchm1. Human chondromodulin-like protein, Zchm1.	1736	99
706	Y41257	Homo sapiens	Amino acid sequence of long human FAIM.	1060	100
707	AL022237	Homo sapiens	bK1191B2.3 (PUTATIVE novel Acyl Transferase similar to C. elegans C50D2.7) (isoform 1))	2030	100
708	AJ006266	Homo sapiens	AND-1 protein	5942	100
709	G01571	Homo sapiens	Human secreted protein, SEQ ID NO: 5652.	777	99
710	Y08698	Homo sapiens	ranbp3	2849	98
711	Y68770	Homo sapiens	Amino acid sequence of a human phosphorylation effector PHSP-2.	754	99

SEQ	ACCESSION) SPECIES	DESCRIPTION	SMITH-	7
ID	NUMBER			WATERMAN	IDENTITY
NO:		1		SCORE	
712	U93574	Homo sapiens	putative p150	799	59
713	AC004531	Homo sapiens	Gene with similarity to DEAD	2715	99
			box helicases		
714	D89016	Homo sapiens	Neuroblastoma	538	48
715	Y92175	Homo sapiens	Human cardiovascular system	734	98
			associated protein tyrosine	į.	
716			phosphatase 2.		
716	AL137013	Homo sapiens	bA311P8.3 (probable uracil phosphoribosyltranferase)	862	100
717	AB035123	Mus musculus	GD1 alpha/GT1a alpha/GQ1b	1	
'-'	ABUSSIES	Mus musculus	alpha synthase	1696	93
718	Y96290	Homo >P40254	Human IGFAM-2 immunoglobulin.	2345	B5
]	P40254 25-	Admin 101741-2 1/mining10bd1111.	2343	0.5
· ·	į	OCT-1984 09-	1		1
	į	APR-1983	i	ļ	
		Human IgD.			l .
	1	[Homo			1
l	ļ	sapiens		į]
719	X07979	Homo sapiens	integrin beta 1 subunit	4347	99
			precursor	1	
720	AJ224819	Homo sapiens	tumor suppressor	2149	99
721	Y07595	Homo sapiens	transcription factor TFIIH	2373	100
722	W41565	Homo	Human calpain.	1591	99
		sapiens)			
}		>W41564		1	
ì		N41564 08-		ł	l
		OCT-1997 05- APR-1996			}
	•	Human			ì
ļ		calpain.	'	ļ	}
	İ	(Homo		ļ	
		sapiens			•
723	AF161341	Homo sapiens	HSPC078	1097	98
724	AF187318	Homo sapiens	F-box protein Fbx2	1607	100
725	AC006708	Caenorhabdit	contains simlarity to	1143	46
725	AC006708	Caenorhabdit is elegans	Saccharomyces cerevisiae pre-	1143	46
725	AC006708		Saccharomyces cerevisiae pre- mRNA splicing protein PRP31	1143	46
		is elegans	Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB: 272876)		46
725	AC006708	is elegans	Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:272876) contains simlarity to	988	46
		is elegans	Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:272876) contains simlarity to Saccharomyces cerevisiae pre-		
		is elegans	Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:272876) contains simlarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31		
726	AC006708	is elegans Caenorhabdit is elegans	Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876) contains simlarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876)	988	45
		is elegans Caenorhabdit is elegans Caenorhabdit	Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876) contains simlarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876) contains similarity to Pfam		
726	AC006708	is elegans Caenorhabdit is elegans	Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876) contains similarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876) contains similarity to Pfam family PF00400 (WD domain,	988	45
726	AC006708	is elegans Caenorhabdit is elegans Caenorhabdit	Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:272876) contains similarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:272876) contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8,	988	45
726	AC006708	is elegans Caenorhabdit is elegans Caenorhabdit	Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876) contains similarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876) contains similarity to Pfam family PF00400 (WD domain,	988	46
726	AC006708	is elegans Caenorhabdit is elegans Caenorhabdit is elegans	Saccharomyces cerevisiae premRNA splicing protein PRP31 (GB:272876) contains similarity to Saccharomyces cerevisiae premRNA splicing protein PRP31 (GB:Z72876) contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3	988	45
726	AC006708 AC024818 AJ005897	is elegans Caenorhabdit is elegans Caenorhabdit is elegans	Saccharomyces cerevisiae premRNA splicing protein PRP31 (GB:272876) contains simlarity to Saccharomyces cerevisiae premRNA splicing protein PRP31 (GB:272876) contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3 JMS	988	44
726 727 . 728 729	AC006708 AC024818 AJ005897 Y45377	is elegans Caenorhabdit is elegans Caenorhabdit is elegans	Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876) contains simlarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876) contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3 JMS Human secreted protein	988	44
726	AC006708 AC024818 AJ005897	is elegans Caenorhabdit is elegans Caenorhabdit is elegans	Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876) contains simlarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876) contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3 JMS Human secreted protein fragment encoded from gene	988	44
726 727 . 728 729	AC006708 AC024818 AJ005897 Y45377 G03931	is elegans Caenorhabdit is elegans Caenorhabdit is elegans Homo sapiens Homo sapiens Homo sapiens	Saccharomyces cerevisiae premRNA splicing protein PRP31 (GB:272876) contains similarity to Saccharomyces cerevisiae premRNA splicing protein PRP31 (GB:Z72876) contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3 JMS Human secreted protein fragment encoded from gene 27. Human secreted protein, SEQ ID NO: 8012.	988 950 831 908	44
726 727 . 728 729	AC006708 AC024818 AJ005897 Y45377	is elegans Caenorhabdit is elegans Caenorhabdit is elegans Homo sapiens Homo sapiens Homo sapiens Oncorhynchus	Saccharomyces cerevisiae premRNA splicing protein PRP31 (GB:Z72876) contains similarity to Saccharomyces cerevisiae premRNA splicing protein PRP31 (GB:Z72876) contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3 JMS Human secreted protein fragment encoded from gene 27.	988 950 831 908	44
726 727 . 728 729 730 731	AC006708 AC024818 AJ005897 Y45377 G03931 AB012720	is elegans Caenorhabdit is elegans Caenorhabdit is elegans Homo sapiens Homo sapiens Homo sapiens Oncorhynchus masou	Saccharomyces cerevisiae premRNA splicing protein PRP31 (GB:Z72876) contains simlarity to Saccharomyces cerevisiae premRNA splicing protein PRP31 (GB:Z72876) contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3 JMS Human secreted protein fragment encoded from gene 27. Human secreted protein, SEQ ID NO: 8012. GTP-binding protein	998 950 831 908 578 3865	44 47 97 100
726 727 . 728 729	AC006708 AC024818 AJ005897 Y45377 G03931	is elegans Caenorhabdit is elegans Caenorhabdit is elegans Homo sapiens Homo sapiens Homo sapiens Oncorhynchus	Saccharomyces cerevisiae premRNA splicing protein PRP31 (GB:Z72876) contains simlarity to Saccharomyces cerevisiae premRNA splicing protein PRP31 (GB:Z72876) contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3 JMS Human secreted protein fragment encoded from gene 27. Human secreted protein, SEQ ID NO: 8012. GTP-binding protein	988 950 831 908	44 47 97
726 727 728 729 730 731 732	AC006708 AC024818 AJ005897 Y45377 G03931 AB012720 W73404	is elegans Caenorhabdit is elegans Caenorhabdit is elegans Homo sapiens Homo sapiens Homo sapiens Oncorhynchus masou Homo sapiens	Saccharomyces cerevisiae premRNA splicing protein PRP31 (GB:Z72876) contains simlarity to Saccharomyces cerevisiae premRNA splicing protein PRP31 (GB:Z72876) contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3 JMS Human secreted protein fragment encoded from gene 27. Human secreted protein, SEQ ID NO: 8012. GTP-binding protein Human secreted protein encoded by Gene No. 8.	998 950 831 908 578 3865	44 47 97 100 76
726 727 . 728 729 730 731	AC006708 AC024818 AJ005897 Y45377 G03931 AB012720	is elegans Caenorhabdit is elegans Caenorhabdit is elegans Homo sapiens Homo sapiens Homo sapiens Oncorhynchus masou	Saccharomyces cerevisiae premRNA splicing protein PRP31 (GB:Z72876) contains simlarity to Saccharomyces cerevisiae premRNA splicing protein PRP31 (GB:Z72876) contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3 JMS Human secreted protein fragment encoded from gene 27. Human secreted protein, SEQ ID NO: 8012. GTP-binding protein Human secreted protein encoded by Gene No. 8. Human secreted protein, SEQ	998 950 831 908 578 3865	44 47 97 100
726 727 728 729 730 731 732 733	AC006708 AC024818 AJ005897 Y45377 G03931 AB012720 W73404 G02650	is elegans Caenorhabdit is elegans Caenorhabdit is elegans Homo sapiens Homo sapiens Homo sapiens Oncorhynchus masou Homo sapiens Homo sapiens	Saccharomyces cerevisiae premRNA splicing protein PRP31 (GB:272876) contains simlarity to Saccharomyces cerevisiae premRNA splicing protein PRP31 (GB:Z72876) contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3 JMS Human secreted protein fragment encoded from gene 27. Human secreted protein, SEQ ID NO: 8012. GTP-binding protein Human secreted protein encoded by Gene No. 8. Human secreted protein, SEQ ID NO: 6731.	988 950 831 908 578 3865 862 644	44 47 97 100 76 97
726 727 728 729 730 731 732	AC006708 AC024818 AJ005897 Y45377 G03931 AB012720 W73404	is elegans Caenorhabdit is elegans Caenorhabdit is elegans Homo sapiens Homo sapiens Homo sapiens Oncorhynchus masou Homo sapiens Homo sapiens Caenorhabdit	Saccharomyces cerevisiae premRNA splicing protein PRP31 (GB:272876) contains simlarity to Saccharomyces cerevisiae premRNA splicing protein PRP31 (GB:272876) contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3 JMS Human secreted protein fragment encoded from gene 27. Human secreted protein, SEQ ID NO: 8012. GTP-binding protein Human secreted protein encoded by Gene No. 8. Human secreted protein, SEQ ID NO: 6731. Hypothetical protein	998 950 831 908 578 3865	44 47 97 100 76
726 727 728 729 730 731 732 733 734	AC006708 AC024818 AJ005897 Y45377 G03931 AB012720 W73404 G02650 AC024813	is elegans Caenorhabdit is elegans Caenorhabdit is elegans Homo sapiens Homo sapiens Homo sapiens Oncorhynchus masou Homo sapiens Homo sapiens Caenorhabdit is elegans	Saccharomyces cerevisiae premRNA splicing protein PRP31 (GB:Z72876) contains simlarity to Saccharomyces cerevisiae premRNA splicing protein PRP31 (GB:Z72876) contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3 JMS Human secreted protein fragment encoded from gene 27. Human secreted protein, SEQ ID NO: 8012. GTP-binding protein Human secreted protein encoded by Gene No. 8. Human secreted protein, SEQ ID NO: 6731. Hypothetical protein Y54F10AL.a	998 950 831 908 578 3865 862 644 152	44 47 97 100 76 97 97
726 727 728 729 730 731 732 733	AC006708 AC024818 AJ005897 Y45377 G03931 AB012720 W73404 G02650	is elegans Caenorhabdit is elegans Caenorhabdit is elegans Homo sapiens Homo sapiens Homo sapiens Oncorhynchus masou Homo sapiens Homo sapiens Caenorhabdit	Saccharomyces cerevisiae premRNA splicing protein PRP31 (GB:Z72876) contains simlarity to Saccharomyces cerevisiae premRNA splicing protein PRP31 (GB:Z72876) contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3 JMS Human secreted protein fragment encoded from gene 27. Human secreted protein, SEQ ID NO: 8012. GTP-binding protein Human secreted protein encoded by Gene No. 8. Human secreted protein, SEQ ID NO: 6731. Hypothetical protein Y54F10AL.a dJ967N21.6 (novel CDP-alcohol	988 950 831 908 578 3865 862 644	44 47 97 100 76 97
726 727 728 729 730 731 732 733 734	AC006708 AC024818 AJ005897 Y45377 G03931 AB012720 W73404 G02650 AC024813	is elegans Caenorhabdit is elegans Caenorhabdit is elegans Homo sapiens Homo sapiens Homo sapiens Oncorhynchus masou Homo sapiens Homo sapiens Caenorhabdit is elegans	Saccharomyces cerevisiae premRNA splicing protein PRP31 (GB:Z72876) contains simlarity to Saccharomyces cerevisiae premRNA splicing protein PRP31 (GB:Z72876) contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3 JMS Human secreted protein fragment encoded from gene 27. Human secreted protein, SEQ ID NO: 8012. GTP-binding protein Human secreted protein encoded by Gene No. 8. Human secreted protein, SEQ ID NO: 6731. Hypothetical protein y54Fl0AL.a dJ967N21.6 (novel CDP-alcohol phosphatidyltransferase	998 950 831 908 578 3865 862 644 152	44 47 97 100 76 97 97
726 727 728 729 730 731 732 733 734 735	AC006708 AC024818 AJ005897 Y45377 G03931 AB012720 W73404 G02650 AC024813 AL035461	is elegans Caenorhabdit is elegans Caenorhabdit is elegans Homo sapiens Homo sapiens Homo sapiens Oncorhynchus masou Homo sapiens Caenorhabdit is elegans Homo sapiens	Saccharomyces cerevisiae premRNA splicing protein PRP31 (GB:272876) contains similarity to Saccharomyces cerevisiae premRNA splicing protein PRP31 (GB:Z72876) contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3 JMS Human secreted protein fragment encoded from gene 27. Human secreted protein, SEQ ID NO: 8012. GTP-binding protein Human secreted protein encoded by Gene No. 8. Human secreted protein, SEQ ID NO: 6731. Hypothetical protein Y54F10AL.a dJ967N21.6 (novel CDP-alcohol phosphatidyltransferase family member protein)	998 950 831 908 578 3865 862 644 152	44 47 97 100 76 97 97 24
726 727 728 729 730 731 732 733 734	AC006708 AC024818 AJ005897 Y45377 G03931 AB012720 W73404 G02650 AC024813	is elegans Caenorhabdit is elegans Caenorhabdit is elegans Homo sapiens Homo sapiens Homo sapiens Oncorhynchus masou Homo sapiens Caenorhabdit is elegans Homo sapiens Caenorhabdit is elegans Caenorhabdit	Saccharomyces cerevisiae premRNA splicing protein PRP31 (GB:272876) contains simlarity to Saccharomyces cerevisiae premRNA splicing protein PRP31 (GB:Z72876) contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3 JMS Human secreted protein fragment encoded from gene 27. Human secreted protein, SEQ ID NO: 8012. GTP-binding protein Human secreted protein encoded by Gene No. 8. Human secreted protein Human secreted protein, SEQ ID NO: 6731. Hypothetical protein Y54F10AL.a dJ967N21.6 (novel CDP-alcohol phosphatidyltransferase family member protein) similar to S. cerevisiae YJU2	998 950 831 908 578 3865 862 644 152	44 47 97 100 76 97 97
726 727 728 729 730 731 732 733 734 735	AC006708 AC006708 AC024818 AJ005897 Y45377 G03931 AB012720 W73404 G02650 AC024813 AL035461 U00033	is elegans Caenorhabdit is elegans Caenorhabdit is elegans Homo sapiens Homo sapiens Homo sapiens Oncorhynchus masou Homo sapiens Caenorhabdit is elegans Homo sapiens Caenorhabdit is elegans Caenorhabdit is elegans	Saccharomyces cerevisiae premRNA splicing protein PRP31 (GB:272876) contains simlarity to Saccharomyces cerevisiae premRNA splicing protein PRP31 (GB:272876) contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3 JMS Human secreted protein fragment encoded from gene 27. Human secreted protein, SEQ ID NO: 8012. GTP-binding protein Human secreted protein, SEQ ID NO: 6731. Hypothetical protein y54F10AL.a dJ967N21.6 (novel CDP-alcohol phosphatidyltransferase family member protein) similar to S. cerevisiae yJU2 protein	998 950 831 908 578 3865 862 644 152 1562	44 44 47 97 100 76 97 97 24 98
726 727 728 729 730 731 732 733 734 735	AC006708 AC024818 AJ005897 Y45377 G03931 AB012720 W73404 G02650 AC024813 AL035461	is elegans Caenorhabdit is elegans Caenorhabdit is elegans Homo sapiens Homo sapiens Homo sapiens Oncorhynchus masou Homo sapiens Caenorhabdit is elegans Homo sapiens Caenorhabdit is elegans Caenorhabdit	Saccharomyces cerevisiae premRNA splicing protein PRP31 (GB:272876) contains simlarity to Saccharomyces cerevisiae premRNA splicing protein PRP31 (GB:Z72876) contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3 JMS Human secreted protein fragment encoded from gene 27. Human secreted protein, SEQ ID NO: 8012. GTP-binding protein Human secreted protein encoded by Gene No. 8. Human secreted protein Human secreted protein, SEQ ID NO: 6731. Hypothetical protein Y54F10AL.a dJ967N21.6 (novel CDP-alcohol phosphatidyltransferase family member protein) similar to S. cerevisiae YJU2	998 950 831 908 578 3865 862 644 152	44 47 97 100 76 97 97 24

TABLE 2

SEQ	ACCESSION	SPECIES	DESCRIPTION	1 CHYMII	
ID	NUMBER	SPECIES	DESCRIPTION	SMITH-	*
NO:	NUMBER			WATERMAN	IDENTITY
			·	SCORE	
738	AJ131712	Homo sapiens	nucleolar RNA-helicase	.2793	100
739	AJ133115	Homo sapiens	TSC-22-like protein	2054	99
740	X98258	Homo sapiens	M-phase phosphoprotein 9	953	100
741	X98258	Homo sapiens	M-phase phosphoprotein 9	564	74
742	U97191	Caenorhabdit	strong similarity to the YPT1	960	85
ĺ	1	is elegans	sub-family of RAS proteins	1 200	100
743	X76057	Homo sapiens	phosphomannose isomerase	2191	1
744	G03209		phosphomatmose isomerase		100
/44	G03209	Homo sapiens	Human secreted protein, SEQ	496	98
L			ID NO: 7290.	1	
745	X97064	Homo sapiens	Sec23 protein	4034	99
746	W93946	Homo sapiens	Human regulatory molecule	994	100
	1		HRM-2 protein.		
747	¥73388	Homo sapiens	HTRM clone 3376404 protein	1565	99
1		name supreme	Sequence.	1 2003	1 22
74B	M19529	Sus scrofa	l •	l	
			follistatin A	1906	98
749	AJ249457	Trichomonas	centrin, putative	183	28
	1	vaginalis	j	1	i
750	AC004410	Homo sapiens	fos39554 1	2094	100
751	AF074968	Homo sapiens	p47ING3 protein	2167	100
752	AF252284	Homo sapiens	transcription specificity	4005	100
1		Jane Saptemb	factor Sp1	1 2003	1 100
753	10040600				
/53	AB049629	Homo sapiens	phospholysine	1375	99
1			phosphohistidine inorganic	1	ì
L	!	· ·	pyrophosphate phosphatase	}	
754	D79205	Homo sapiens	ribosomal protein L39	160	77
755	AB008430	Homo sapiens	CDEP	142	29
758	L32162	Homo sapiens	transcription factor	574	80
759	AF037204	Homo sapiens	RING zinc finger protein	295	
760	Y44250	Homo sapiens	RING ZINC linger protein		54
/60	144250		Human cell signalling	625	100
L	<u> </u>	sapiens	protein-13.	1	İ
761	AF218586	Homo sapiens	Cide-b	1136	100
762	U38934	Gallus	histone H2A	625	97
		gallus			- '
763	AF226053	Homo sapiens	HSKM-B	606	32
764	X13403	Homo sapiens	Oct-1 protein (AA 1 - 743)	3626	100
765	D87446		Similar to a C.elegans		
/65	D8/446	.Homo sapiens		568	38
	}	1	protein encoded in cosmid		1
			C27F2 (U40419)	ł	ļ
766	AL023828	Caenorhabdit	Y17G7B.14	200	27
		is elegans		1	
767	¥82777	Homo sapiens	Human chordin related protein	2551	99
			(Clone dw665 4).	****	,,,
768	X92475	Homo sapiens	ITBA1		
769	Y42752			1429	100
709	142/52	Homo sapiens	Human calcium binding protein	1426	100
			3 (CaBP-3).	I	
770	X51416	Homo sapiens	hormone receptor hERR1 (AA 1-	2641	97
			521)	<u> </u>	
771	AJ006591	Homo sapiens	cysteine-rich protein	1793	100
772	A08695	Homo sapiens	rap2	935	100
773	Z12173	Homo sapiens	N-acetylglucosamine-6-		
		sapiens		2970	100
774	V01050	**	Sulphatase		
774	Y91950	Homo sapiens	Human cytoskeleton associated	565	43
			protein 5 (CYSKP-5).	į l	
776	AL023799	Homo sapiens	dJ322P7.1 (zinc finger)	855	56
777	AL023799	Homo sapiens	dJ322P7.1 (zinc finger)	855	56
778	G01880	Homo sapiens	Human secreted protein, SEQ	849	98
			ID NO: 5961.	""	·
779	AJ012590	Homo garadana			
_		Homo sapiens	glucose 1-dehydrogenase	4155	99
780	AL078582	Homo sapiens	dJ130E4.2 (KIAA0796)	1321	68
781	275955	Caenorhabdit	similar to mitochondrial	384	34
		is elegans	carrier protein		ļ
782	AL109965	Homo	dJ1121G12.2 (SCAN domain-	900	100
		sapiens	containing 1 protein)		~~~
783	AF061262	Mus			
			semaF cytoplasmic domain	1316	83
704	- AA20-18	musculus	associated protein 2		
784	G03873	Homo sapiens	Human secreted protein, SEQ	649	95

TABLE 2

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	3
ID	NUMBER	3.55.55	DESCRIPTION	WATERMAN	IDENTITY
NO:				SCORE	IDENTITI
	 	 	ID NO: 7954.		
785	Y84441	Homo sapiens	Amino acid sequence of a	2074	100
•		1	human RNA-associated		
	1		protein.		
786	Y00918	Homo sapiens	Human Rab protein, RABP-1,	1048	99
	1		protein sequence.	1	1
787	Z97029	Homo sapiens	ribonuclease HI large subunit	1548	99 .
788	AB035384	Homo sapiens	SRp25 nuclear protein	962	94
789	AF024631	Homo sapiens	ANG2	2644	100
790	AJ006710	Rattus	phosphatidylinositol 3-kinase	4508	97
	1	norvegicus			* .
792	V00638	bacteriophag	reading frame eal0	600	100
	1	e lambda			
793	AF049103	Homo sapiens	Huntingtin interacting	819	100
		1	protein		
795	Z26317	Homo sapiens	desmoglein 2	4810	99
796	Y76884	Homo sapiens	Retinoblastoma binding	5080	99
	1		protein-7sequence.	Ì	
797	U15155	Gallus	trypsinogen	372	37
	<u> </u>	gallus		į	
798	U97189	Caenorhabdit	strong similarity to thw	227	28
	}	is elegans	P13/P14 family of kinases	ľ	
799	AF112201	Homo sapiens	neuronal protein NP25	1053	100
800	AF234765	Rattus	serine-arginine-rich splicing	958	63
		norvegicus	regulatory protein SRRP86	1	
801	AF267852	Homo sapiens	placental protein 13-like	743	99
	<u></u> .	İ	protein	1	
802	AF208851	Homo sapiens	BM-009	766	80
803	281097	Caenorhabdit	Similarity to Human	152	27
		is elegans	retinoblastoma-binding		ļ
)	protein RBAP46 yk662d12.5		J
			comes from this gene		ł
804	G02113	Homo sapiens	Human secreted protein, SEQ	496	98
005			ID NO: 6194.		L
805 806	AL121673	Homo sapiens	bA305P22.1 (novel protein)	1160	100
806	AC013483	Arabidopsis	putative GTPase activator	264	30
807	AC013483	thaliana	protein		
807	AC013483	Arabidopsis thaliana	putative GTPase activator	264	3C
808	AB013885	Homo sapiens	protein		
809	AF078842	Homo sapiens	beta-ureidopropionase	1494	100
810	AF161421	Homo sapiens	HOTTL protein	1581	99
811	AF261689			2134	96
011	AF261689	Homo sapiens	DNA polymerase epsilon p17 subunit	734	100
812	274029	Caenorhabdit	Similarity to C.elegans		
	274023	is elegans	alcohol dehydrogenase comes	610	71
		15 cregans	from this gene		
813	273497	Homo sapiens	cU240C2.2 (Core histone	324	
		nomo saprens	H2A/H2B/H3/H4)	324	100
814	W87689	Homo	Human HTXFT19 polypeptide.	1484	00
		sapiens	porypeptide.	7.40.4	99
815	X16282	Homo	zinc finger protein (217 AA)	1109	99
		sapiens	(1 is 2nd base in codon)	2207) 5
816	Z92539	Mycobacteriu	pth	300	36
	-	m	F	300	36
	ļ	tuberculosis			
818	AB030483	Mus musculus	B9	197	27
819	AL117555	Homo sapiens	hypothetical protein	321	94
820	AC005328	Homo sapiens	R26660 2, partial CDS	865	97
821	G03951	Homo sapiens	Human secreted protein, SEO	700	99
- 1	-		ID NO: 8032.	,,,,	27
822	L34807	Musca	transposase	174	20
j		domestica		1/3	20
823	G02928	Homo sapiens	Human secreted protein, SEQ	558	78
	-		ID NO: 7009.	550	, 0
824	Z99531	Schizosaccha	caffeine-induced death	184	29

SEO	ACCESSION	SPECIES	DESCRIPTION	- CHYMIL	
ID NO:	NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
		romyces	protein 1	SCORE	
825	AJ006692	Homo sapiens	ultra high sulfer keratin	693	68
826	U23037	Oryctolagus cuniculus	eIF-2Bepsilon	3406	90
827	G03412	Homo sapiens	Human secreted protein, SEQ ID NO: 7493.	464	100
828	Y30327	Homo sapiens	Human secreted protein encoded from gene 17.	113	44
829	Y32199	Homo sapiens	Human receptor molecule (REC) encoded by Incyte clone 2022379.	1012	100
830	W78279	Homo sapiens	Fragment of human secreted protein encoded by gene 33.	1264	99
832	AB011542	Homo sapiens	MEGP9	2097	100
833	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 6720.	223	70
834	AF119664	Homo sapiens	transcriptional regulator protein HCNGP	1574	100
835	AF119664	Homo sapiens	transcriptional regulator protein HCNGP	1144	89
836	AF119664	Homo sapiens	transcriptional regulator protein HCNGP	1448	94
837	X12517	Homo sapiens	C protein (AA 1-159)	918	100
838	U32865	Drosophila melanogaster	linotte protein	164	24
839	AF067730	Homo sapiens	TLS-associated protein TASR-2	631	56
840	U27831	Homo sapiens	striatum-enriched phosphatase	2840	98
841	AF286366	Homo sapiens	CamKI-like protein kinase	1796	100
842	G02309	Homo sapiens	Human secreted protein, SEQ ID NO: 6390.	278	98
843	AE003615	Drosophila melanogaster	ade3 gene product	113	48
844	G01350	Homo sapiens	Human secreted protein, SEQ ID NO: 5431.	629	100
845	U27838	Mus musculus	glycosyl-phosphatidyl- inositol-anchored protein homolog	3305	96
847	Y87788	Homo sapiens	Human RBP-26 protein.	2026	100
848	AF164794	Homo sapiens	Diff33 protein homolog	2398	100
849	U41315	Homo sapiens	ZNF127-Xp	2458	93
850	AF192784	Homo sapiens	makorin 1	2062	97
851	Y58628	Homo sapiens	Protein regulating gene expression PRGE-21.	1548	100 .
852	Z22968	Homo sapiens	M130 antigen	6205	100
853 854	222971	Homo sapiens	M130 antigen extracellular variant	6380	100
	G03362	Homo sapiens	Human secreted protein, SEQ ID NO: 7443.	330	96
855	G03362	Homo sapiens	Human secreted protein, SEQ ID NO: 7443.	203	100
856 857	AF285118	Homo sapiens	CGI-203	452	100
857	AC006069	Arabidopsis thaliana	putative cleavage and polyadenylation specifity factor	1383	55
858	AL021546	Homo sapiens	Cytochrome C Oxidase Polypeptide VIa-liver precursor (EC 1.9.3.1)	593	100
859	L02956	Xenopus laevis	ribonucleoprotein	1664	85
860	AF201947	Homo sapiens	MEK binding partner 1	616	100
861	L31783	Mus musculus	uridine kinase	1266	92
862	AF161472	Homo sapiens	HSPC123	602	73
863	Z49068	Caenorhabdit is elegans	mitochondrial carrier protein	370	43
864	AF154108	Homo sapiens	tumor necrosis factor type 1	3559	99

SEQ	ACCESSION	SPECIES			
ID	NUMBER	SPECIES	DESCRIPTION	SMITH-	*
NO:			1	WATERMAN	IDENTITY
			receptor associated protein	SCORE	
865	AE001530	Helicobacter	putative	230	32
<u> </u>		pylori J99			1
866	X57807	Homo sapiens		699	91
			chain	}	
867	AL031673	Homo sapiens		4066	99
ļ	1		KRAB box protein with 18 C2H2		į
868	Y11652	 	type Zinc finger domains)		1
869	AF192968	Homo sapiens		238	1.00
1 005	AF 192900	Homo sapiens	high-glucose-regulated	3041	99
870	AB020648	Homo sapiens	KIAA0841 protein		
871	AL031427	Homo sapiens		3237	59
872	AF151534	Homo sapiens	core histone macroH2A2.2	1608	100
873	AL021331	Homo sapiens	dJ366N23.1 (putative C.	1866	100
			elegans UNC-93 (protein 1,	1129	100
İ	ł	1	C46F11.1) LIKE protein)		
874	X14608	Homo sapiens	propionyl-CoA carboxylase	3579	100
875	AL117334	Homo sapiens	dJ687F11.1 (nove) protein	306	100
	ĺ	1	(part of translation of cDNA	1000	1.00
-			DKFZp434N061, Em:AL110249))		1
876	X79489	Saccharomyce	E-925 protein	446	35
877		B cerevisiae			
877	Y53001	Homo sapiens	Human secreted protein clone	811	100
			dn834_1 protein sequence SEQ		
878	AF281064	Homo sapiens	ID NO:8.	<u>i </u>	i
879	X79417	Sus scrofa	CHMP1.5	957	100
880	AF001317	Saccharomyce	40S ribosomal protein S12 Soilp	687	100
		5 cerevisiae	Soilb	478	28
881	Y87275	Homo sapiens	Human signal peptide	8848	
			containing protein HSPP-52	2547	100
_			SEQ ID NO:52.	į	
882	M14036	Homo sapiens	C1-inhibitor	598	77
883	AB041261	Homo sapiens	calcium-independent	2903	100
		<u> </u>	phospholipase A2	1	100
884	AF020313	Mus musculus	proline-rich protein 48	999	84
886	Y10936 AF073997	Homo sapiens	hypothetical protein	1104	99
000	AF0/399/	Mus musculus	myotubularin related protein	866	36
887	Y57893	Homo sapiens	1	<u>L</u>	
•••	137033	nous saptens	Human transmembrane protein	1099	94
888	AL117635	Homo sapiens	hypothetical protein		
889	AF210317	Homo sapiens	facilitative glucose	929	99
		areans capacing	transporter family member	2046	99
		ł	GLUT9		j
890	Y36031	Homo sapiens	Extended human secreted	583	100
			protein sequence, SEQ ID NO.	,	100
			416.]	i
891	¥36031	Homo sapiens	Extended human secreted	192	57
			protein sequence, SEQ ID NO.]	1
892	DE227621		416.	[1
032	AF237631	Homo sapiens	ubiquitous tropomodulin U-	1798	100
893	AF090929	Wana and	Tmod		
894	AL031228	Homo sapiens	PR00477p	653	99
		Homo sapiens	dJ1033B10.2 (WD40 protein	3196	100
		1	BING4 (similar to S.		
] [ſ	cerevisiae YERO82C, M. sexta	1	-1
895	AL031228	Homo sapiens	MNG10 and C. elegans F28D1.1) dJ1033B10.2 (WD40 protein		•
	MD031228 I		WATARIA INDAO BLOCGIU	2825	96
	AL031228				
	AL031228		BING4 (similar to S.		i
		_	BING4 (similar to S. cerevisiae YER082C, M. sexta		
396	AF171102		BING4 (similar to S. cerevisiae YER082C, M. sexta MNG10 and C. elegans F28D1.1)	·	95
	AF171102 AE003551	Homo sapiens	BING4 (similar to S. cerevisiae YER082C, M. sexta	1302	95

TABLE 2

SEQ	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN	IDENTITY
NO:				SCORE	
898	AJ237946	Homo sapiens	DEAD Box Protein 5	2443	100
899	Z97184	Homo sapiens	EKE2	624	100
900	297184	Homo sapiens	HKE2	409	98
901	AJ245587	Homo sapiens	Kruppel-type zinc finger	1942	100
902	AF091034	Homo sapiens	GTP-binding protein RAB22A	1011	100
903	R95953	Homo sapiens	Eukaryotic cell growth	414	96
	1		inhibiting factor.		
904	L04733	Homo sapiens	kinesin light chain	1936	72
905	AE003540	Drosophila	CG10984 gene product	446	33
		melanogaster	1	ł	
906	И55542	Homo sapiens	guanylate binding protein isoform I	2993	98
907	И55542	Homo sapiens	guanylate binding protein	2901	96
908	W84085	Homo sapiens	Human membrane fusion protein	1889	100
909	AF168676	Homo	WDProl.	<u> </u>	
909	WL108010		TNF intracellular domain-	647	100
910	AB029150	sapiens	interacting protein	ļ	
		Homo sapiens	KRAB zinc finger protein HFB101L	2196	100
911	G02871	Homo sapiens	Human secreted protein, SEQ ID NO: 6952.	521	100
912	G03162	Homo sapiens	Human secreted protein, SEQ ID NO: 7243.	387	87
913	AJ243721	Homo	dTDP-4-keto-6-deoxy-D-glucose	1710	100
		sapiens)	4-reductase	1 - 1 - 1	
		>Y92508		J]
		Y92508 13-			
		APR-2000 06-		ļ	
		OCT-1998		Ì	}
		Human OXRE-		ŀ	
		5. [Homo		İ	
		sapiens		1	
914	U24189	Caenorhabdit	hypothetical protein 1207-1;	244	41
		is elegans	Method: conceptual		
		1	translation supplied by		
			authors	1	
915	Y02591	Homo sapiens	A human progesterone receptor	843	99
			complex p23-like protein.	1 725	1
916	AE000984	Archaeoglobu	dinitrogenase reductase	171	26
		s fulgidus	activating glycohydrolase	-/-	
010			(draG)		
918	M23159	Cricetus	DHFR-coamplified protein	163	30
		cricetus			L
919	L12018	Caenorhabdit	putative	1232	41
920	AF102177	is elegans			
		Homo sapiens	tumor antigen SLP-8p	1260	97
921	λL096712	Homo sapiens	dJ744I24.2 (similar to a	1017	78
			novel human gene mapping to	i	
022	77761405	**************************************	Activator)		
922	AL161495	Arabidopsis	putative WD-repeat protein	866	42
	3012122	thaliana		<u> </u>	
923	AL161495	Arabidopsis thaliana	putative WD-repeat protein	442	36
924	U97001	Caenorhabdit	similar to	605	51
		is elegans	Schizosaccharomyces pombe	~~~	J.
925	X71978	Mus musculus	Fif	1503	95
926	M92288	Drosophila	beta-spectrin	290	51
-		melanogaster	TTTT UPOCOCASI		
927	Y27575	Homo sapiens	Human secreted protein	1392	100
	.=	nobicity	encoded by gene No. 9.	2226	100
928	Y22499	Homo sapiens	Human secreted protein	2249	100
		Cabielle	sequence clone mh703 1.	6477	100
930	AJ224326	Homo sapiens	ribulose-5-phosphate-	912	100
		sebtang	epimerase	316	100
931	U28991	Caenorhabdit	coded for by C. elegans cDNA	660	55
		-acitornapare	coded for DA C. effedage CDMV	660	22

TABLE 2

SEQ	ACCESSION	SPECIES	DESCRIPTION		
ID	NUMBER	OF DCIES	DESCRIPTION	SMITH-	*
NO:				WATERMAN SCORE	IDENTITY
		is elegans	cm21c7	SCORE	 _
932	AL080065	Homo sapiens		210	25
933	G01884	Homo sapiens		767	98
	1	•	ID NO: 5965.	1 ""	1 3%
934	AJ276485	Homo sapiens	integral membrane transporter	1200	100
ı		-	protein	1	100
935	AL035681	Homo sapiens	dJ756G23.3 (novel protein	1142	80
ĺ	1		similar to drosophila		""
			transcriptional repressor)		
936	AB026808	Mus musculus	synaptotagmin XI	2142	95
937	AB015345	Homo sapiens		2601	99
938	X65724	Homo sapiens	ORF2	498	100
939	W89024	Homo sapiens	Polypeptide fragment encoded	1487	100
	1	1	by gene 156.		100
940	G04047	Homo sapiens		117	100
L			ID NO: 8128.	1	1 200
941	AF094583	Homo sapiens	putative HIV-1 infection	452	100
		1	related protein		100
942	AC024200	Caenorhabdit	contains similarity to	350	69
	1	is elegans	several zinc finger proteins	1	1 33
	1	_	but not to the zinc finger	1	1
	.1		domains		1
943	AF129756	Homo sapiens	G5c	273	100
944	M23765	Rattus	alpha-tropomyosin	133	96
	i	norvegicus			1 30
945	AC009917	Arabidopsis	Contains similarity to	583	47
		thaliana			1 * ′
946	AF223468	Homo sapiens	AD021 protein	551	44
947	AF055473	Homo sapiens	GAGE-8	273	51
948	X75756	Homo sapiens	protein kinase C mu	2019	68
949	AP143956	Mus musculus	corcnin-2	2300	93
950	Y36729	Homo	Human PG1 protein sequence.	1861	99
	<u> </u>	sapiens	1		
951	W49041	Homo sapiens	Human low density lipoprotein	202	67
			binding protein LBP-2.		١ ٠٠
952	AB016881	Arabidopsis	gene_id:MXC17.7~	203	46
		thaliana			
953	Y01785	Homo sapiens	Human ubiquitin-conjugating	365	100
	}		enzyme >Y25341 Y25341 01-JUL-	ł l	
			1999 12-AUG-1998 Human NCE-2		
954	3944555		protein.		
954	AF145615	Drosophila	BcDNA.GH03377	823	46
955	U09410	melanogaster		, ,	
956	i .	Homo sapiens	zinc finger protein ZNF131	2483	99
955	U09410 AF195623	Homo sapiens	zinc finger protein ZNF131	1853	99
J3 /	WE 132953	Homo sapiens	cholinephosphotransferase 1	2126	99
958	X94917	Dec	alpha	<u> </u>	
,,,,	V342T1	Drosophila	head-elevated expression in	155	32
959	U54807	melanogaster	0.9 kb		1
,,,	034007	Rattus	GTP-binding protein	1167	97
960	AF058807	norvegicus	Comp.		
961	G03244	Bos taurus	GTP-binding protein rah	606	97
207	GU3244	Homo sapiens	Human secreted protein, SEQ	471	100
962	NEO-TO-F-C	TV-	ID NO: 7325.		į
963	AF078850	Homo sapiens	steroid dehydrogenase homolog	583	40
202	AP001754	Homo sapiens	transient receptor potential-	317	30
1		İ	related channel 7, a novel	ĺ	1
964	AT 035/30		putative Ca2+ channel protein		
-04	AL035419	Homo sapiens	dJ1100H13.1 (putative novel	1129	100
965	VC1261	N-F-	protein)		1
203	X61381	Rattus	interferon-induced protein	202	46
966	D3 91 60	rattus			İ
200	D38169	Homo	inositol 1,4,5-trisphosphate	3278	100
967	AL031432	sapiens	3-kinase isoenzyme		
- "	VTA37	Homo	dJ465N24.2.1 (PUTATIVE novel	893	100
		sapiens	protein) (isoform 1)		1

SEQ	ACCESSION	SPECIES	2242		
ID NO:	NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
968	U79275	Homo sapiens	unknown	611	100
969	AJ011306	Homo sapiens	guanine nucleotide exchange factor (long isoform)	2752	99
970	AF281134	Homo sapiens		1186	100
971	U53336	Caenorhabdit		536	23
	Ì	is elegans	region to myosin heavy chain	1 330	23
972	AC018749	Leishmania major	L8840.12	589	53
973	AF188504	Mus musculus	LNV	544	85
974	U25801	Homo sapiens	Taxl binding protein	852	98
975	AP049523	Homo sapiens	huntingtin-interacting protein HYPA/FBP11	1390	97
976	AF161530	Homo sapiens	HSPC182	1040	100
977	G04020	Homo sapiens	Human secreted protein, SEQ ID NO: 8101.	626	100
978	AP164797	Homo sapiens	ribosomal protein L17 isolog	908	100
979	U94991	Xenopus laevis	transcription factor XLMO1	795	97
980	S73775	Homo sapiens	calmitine; calsequestrine	2029	100
981	Y94888	Homo sapiens	Human protein clone HP01462.	2501	100
982	AJ243191	Homo sapiens	heat shock protein	827	96
983	X65020	Bos taurus	PSST subunit of the NADH:	964	85
984	AJ249207		ubiquinone oxidoreductase complex		
		Rhodococcus sp. AD45	putative racemase	351	43
985	Z30093	Homo sapiens	basic transcription factor 2, 35 kD subunit	1576	99
986	AB030835	Homo sapiens	contains two glutamine rich domains, three zinc-finger domains, and matrin 3 homologous domain 3 (MH3)	4697	99
987	AF227258	Bos taurus	RPGR-interacting protein-1	1262	38
988	AL022238	Homo sapiens	dJ1042K10.2 (supported by GENSCAN, FGENES and GENEWISE)	4048	99
989	AL022238	Homo sapiens	dJ1042K10.2 (supported by GENSCAN, FGENES and GENEWISE)	2321	99
990	AF161426	Homo sapiens	HSPC308	448	92
991	AF161426	Homo sapiens	HSPC308	448	92
992	AF161426	Homo sapiens	HSPC308	453	92
993	AL023859	Schizosaccha romyces pombe	trna-splicing endonuclease subunit	172	42
994	AL049631	Homo sapiens	dJ513M9.1 (novel Homeobox domain protein)	241	47
995	AC005253	Homo sapiens	R26445 1	902	100
996	AF265206	Homo sapiens	MOG1 isoform A .	974	100
997	AJ248285	Pyrococcus abyssi	sarcosine oxidase, subunit beta (soxB)	195	28
998	AE003641	Drosophila melanogaster	BG:DS00941.3 gene product	218	58
999	W69343	Homo sapiens	Secreted protein of clone CR930 1.	1340	98
1000	AY007135	Homo sapiens	similar to bovine ADP/ATP translocase T1 mRNA with GenBank Accession Number M24102.1	1543	100
1001	Y73381	Homo sapiens	HTRM clone 1877278 protein sequence.	1668	100
1002	AF208844	Homo sapiens	BM-002	428	100
1003	AE004944	Pseudomonas aeruginosa	hypothetical protein	134	35
1004	AL031431	Homo sapiens	dJ462023.2 (novel protein)	2058	100
1005	S45367	Canis	centractin	1949	100
- 1	1	familiaris			

SEQ	ACCESSION	SPECIES	DESCRIPTION	T AVERT	
ID	NUMBER	JEECI DO	DESCRIPTION	SMITH- WATERMAN	IDENTITY
NO:			1	SCORE	IDBNILLA
1006	\$45367	Canis familiaris	centractin	1315	98
1007	AB022158	Mus	chaperonin containing TCP-1	2649	96
1008	Y76332	musculus	epsilon subunit		1
		Homo sapiens	Fragment of human secreted protein encoded by gene 38.	1282	97
1009	AB011414	Homo sapiens	Kruppel-type zinc finger protein	1671	58
1010	Z68218	Caenorhabdit is elegans		269	67
1011	AB011414	Homo sapiens	Kruppel-type zinc finger protein	1671	58
1012	214000	Homo sapiens		2017	100
1013	G02841	Homo sapiens	Human secreted protein, SEQ ID NO: 6922.	332	93
1014	AF145659	Drosophila melanogaster	BcDNA.GH10333	1244	52
1015	Y02860	Homo sapiens	Fragment of human secreted protein encoded by gene 65.	664	67
1016	Y02591	Homo sapiens	A human progesterone receptor complex p23-like protein.	772	97
1017	Y99448	Homo sapiens	Human PRO1759 (UNQ832) amino	2323	100
1018	X67250	Rattus	acid sequence SEQ ID NO:374.	1710	97
1019	AF183417	norvegicus Homo	microtubule-associated	631	100
		sapiens	proteins 1A/1B light chain 3		
1020	AF164795	Homo sapiens	sex-regulated protein janus-a	674	100
1021	AF190625	Coturnix coturnix	qdgl-1	638	96
1022	AL133363	Arabidopsis thaliana	putative protein	155	37
1023	AB034912	Homo sapiens	WD-repeat like sequence	2483	100
1024	AY007091	Homo sapiens	similar to Homo sapiens mammalian inositol hexakisphosphate kinase 2 (IP6K2) mRNA with Ge	2243	100
1025	X69910	Homo sapiens	P63 protein	2958	99
1026	V80736	Homo sapiens	CAGF9	1657	100
1027	AB029333	Halocynthia	HrPET-1	1048	54
_		roretzi	,	1030	3
1028	AB032931	Homo sapiens	ubiquitin-conjugating enzyme isolog	1045	100
1029	G01797	Homo sapiens	Human secreted protein, SEQ ID NO: 5878.	749	98
1030	G01797	Homo sapiens	Human secreted protein, SEQ ID NO: 5878.	749	98 .
1031	AF193795	Homo sapiens	vacuolar sorting protein VPS29/PEP11	960	100
1032	AJ222968	Mus musculus	L-periaxin	120	30
1033	281317	Schizosaccha	DNA2-NAM7 helicase family	685	31
		romyces pombe	protein		
1034	¥41519	Homo sapiens	Fragment of human secreted protein encoded by gene 75.	1321	99
1035	AJ276004	Mus musculus	Paxneb protein	1709	77
1036	AF025459	Caenorhabdit is elegans	H14A12.3 gene product	190	30
1037	U37251	Homo sapiens	Description: KRAB zinc finger protein; this is a splicing supplied by author	196	43
1038	W74580	Homo sapiens	Human membrane protein BA0306.	1921	97
1039	U88173	Caenorhabdit	weak similarity to	331	80
		is elegans	Arabidopsis thaliana ubiquitin-like protein 8	-31	

SEO	ACCESSION	SPECIES	DESCRIPTION	- CHY MIL	· · · · · · · · · · · · · · · · · · ·
ID	NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN	IDENTITY
NO:				SCORE	IDENTITY
1040	AF290204	Homo sapiens	blood group carrier molecule	1637	99
1041	Y96730	Homo sapiens	PRO539, a Costal-2 homologue.	162	22
1042	AF140683	Mus musculus	F-box protein FWD2	2397	98
1043	AF151023	Homo sapiens	HSPC189	1104	100
1044	AF181631	Drosophila melanogaster	BcDNA.GH04929	204	37
1045	Y77985	Homo sapiens	Human collectin amino acid sequence.	1940	100
1046	AJ243972	Homo sapiens	6-phosphogluconolactonase	1317	100
1047	AB035863	Homo sapiens	ATP specific succinyl CoA synthetase beta subunit precursor	2324	99
1048	AL034550	Homo sapiens	dJl184F4.2 (novel protein similar to nucleolar protein 4 (NOL4) (NOLP))	981	92
1049	AF163825	Homo sapiens	pre-B lymphocyte protein 3	634	100
1050	AF201949	Homo sapiens	60S ribosomal protein L30 isolog	868	100
1051	AF190624	Mus musculus	mdgl-1	236	85
1052	AE003529	Drosophila melanogaster	CG6151 gene product	160	44
1053	G01191	Homo sapiens	Human secreted protein, SEQ ID NO: 5272.	646	98 ·
1054	AL162756	Neisseria meningitidis	Glu-tRNA(Gln) amidotransferase subunit A	682	44
1055	AF181856	Rattus norvegicus	tRNA selenocysteine associated protein	1525	99
1056	U89649	Chlamydomona s reinhardtii	Mr19,000 outer arm dynein light chain	244	34
1057	AF159141	Homo sapiens	breast cancer metastasis- suppressor l	663	53
1058	AF230929	Homo sapiens	keratinocyte annexin-like protein pemphaxin	1710	99
1059	AJ270952	Homo sapiens	putative membrane protein	1363	100
1050	AF224263	Heterodontus francisci	HoxDB	742	83
1061	X63417	Homo sapiens	IRLB	1037	100
1062	AL079345	Streptomyces coelicolor A3(2)	hypothetical protein	143	27
1063	Y71112	Homo sapiens	Human Hydrolase protein-10 (HYDRL-10).	2547	100
1064	AF263614	Homo sapiens	acetyl-CoA synthetase	3493	99
1065	Y13356	Homo sapiens	Amino acid sequence of protein PRO221.	1363	100
	AC006153	Homo sapiens	similar to Aquifex aeolicus GTP-binding protein; similar to AE000771 (PID:g2984292)	662	98
1067	Y18930	Sulfolobus solfataricus	hypothetical protein	162	29
1068	R65969	Homo sapiens T98G	Glioblastoma-derived polypeptide.	887	100
1069	Y07964	Homo sapiens	Human secreted protein fragment	863	96
1070	AF177476	Rattus norvegicus	CDK5 activator-binding protein	1995	86
1071	AF245505	Homo sapiens	adlican	3109	99
1072	U92794	Mus musculus	alpha glucosidase II, beta subunit	147	36
1073	G03889	Homo sapiens	Human secreted protein, SEQ ID NO: 7970.	698	98
1074	U15779	Homo sapiens	p70	380	28
1075	Y13392	Homo sapiens	Amino acid sequence of	1271	91

SEQ	ACCESSION	SPECIES	DESCRIPTION	1 0147	
ID	NUMBER	3786725	DESCRIPTION	SMITH- WATERMAN	IDENTITY
NO:	1	1	}	SCORE	IDENTILI
			protein PRO328.	- SCOKE	-
1076	AF161457	Homo sapiens		571	100
1077	Y79509	Homo sapiens		2151	98
		-	protein CRBAP-5.		1
1078	AF223466	Homo sapiens	HT015 protein	831	66
1079	AL132965	Arabidopsis	putative WD-40 repeat-protein	286	29
		thaliana			
1080	AB024937	Homo sapiens	LUNX	1284	100
1081	Y14768	Homo sapiens		579	100
	1		protein	1	ł
1092	AF016416	Caenorhabdit	F29A7.4 gene product	141	31
	<u> </u>	is elegans		_	
1083	L13291	Homo sapiens	ADP-ribosylarginine hydrolase	802	45
1084	AB041541	Mus musculus	unnamed protein product	151	44
1085	G01922	Homo sapiens	Human secreted protein, SEQ	202	97
1000	*****		ID NO: 6003.	<u>L</u>	i
1086	AB030814	Homo sapiens		833	100
1087	AF151638	Homo sapiens	phosphatidylcholine transfer	1142	100
1088	Y84432	ļ	protein		
1000	104432	Homo sapiens	Amino acid sequence of a	2783	100
		ł	human RNA-associated	1	ļ
1089	Y94867	Ното	protein. Human protein clone HP10563.	<u> </u>	
	134007	sapiens	Adman process clone HP10563.	613	100
1090	AK023982	Homo sapiens	unnamed protein product	130	
1091	AB041586	Mus musculus	unnamed protein product	1103	49
1092	Y71277	Homo sapiens	Human Zlipo3 protein.	606	100
1093	U34973	Mus musculus	protein tyrosine phosphatase-	1131	95
			like	1231	33
1094	Y66677	Homo	Membrane-bound protein	522	56
		sapiens	PRO828.		1 20
1095	Y87276	Homo sapiens	Human signal peptide	1029	99
	•		containing protein HSPP-53		1
			SEQ ID NO:53.	1]
1096	Y87276	Homo sapiens	Human signal peptide	863	98
			containing protein HSPP-53		
1097	N 1 2 1 1 2 2 1 1 2 2 1 1 2 2 1 1 2 2 1 2		SEQ ID NO:53.		
1098	AF161455 U80029	Homo sapiens	HSPC337	742	98
1030	080029	Caenorhabdit is elegans	similar to thioredoxin	242	39
1099	AJ005866	Homo sapiens	3 1 1		
1100	AJ005866	Homo sapiens	Sqv-7-like protein Sqv-7-like protein	1321	99
1101	AJ005866	Homo sapiens	Sqv-7-like protein	1118	99
1102	AJ005866	Homo sapiens	Sqv-7-like protein	891	99
1103	AL110244	Homo sapiens	hypothetical protein	1016	99
1104	AF242194	Drosophila	brakeless-B	299	31
	1	melanogaster	DIAKCIESS-B	147	52
1105	AL031010	Homo sapiens	dJ422F24.1 (PUTATIVE novel	968	100
		Duptons	protein similar to C. elegans	308	100
			CO2C2.5)		
1106	U28016	Mus musculus	parathion hydrolase	1624	87
			(phosphotriesterase) -related	1023	· ° ′
			protein		
1107	AJ278150	Homo sapiens	putative lipid kinase	2207	99
1108	G03733	Homo sapiens	Human secreted protein, SEQ	495	98
{		-	ID NO: 7814.		
1109	AF217287	Drosophila	G protein RhoBTB	834	54
		melanogaster		-	
1110	Y28921	Homo	Human regulatory protein	941	48
		sapiens	HRGP-7.	•	1
1111	Y28921	Homo	Human regulatory protein	1331	51
		sapiens	HRGP-7.	ľ	ļ
1112	AF176704	Homo sapiens	F-box protein FBX9	2027	99
1113	AF182076	Homo	glioma tumor suppressor	2418	100
1114	004036	sapiens	candidate region protein 2		}
4	G04039	Homo sapiens	Human secreted protein, SEQ	475	96

TABLE 2

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	
ID	NUMBER	0.00.00	DESCRIPTION	WATERMAN	IDENTITY
NO:		1	1	SCORE	1DEWIIII
			ID NO: 8120.		
1115	AF229439	Mus musculus		1697	91
1116	L40357	Homo sapiens	thyroid receptor interactor	509	100
1117	L40357	Homo sapiens	thyroid receptor interactor	404	85
1118	A12155	Homo sapiens	Human X5L cDNA.	1673	100
1119	AL161542	Arabidopsis	isomerase like protein	607	53
		thaliana	-	ſ	1
1120	AL023754	Homo sapiens	dJ272L16.1 (Rat	2341	98
			Ca2+/Calmodulin dependent	1	
			Protein Kinase LIKE protein)		1
1121	Y57901	Homo sapiens	Human transmembrane protein	321	36
	<u> </u>	<u> </u>	ETMPN-25.		
1122	214122	Xenopus	XLCL2	455	77
 		laevis		1	1
1123	AF225418	Homo sapiens	lipase	1531	97
1124	Y06518	Homo sapiens	Zen GTPase interacting	3227	100
			protein ZIP.	1	
1125	AL035690	Homo sapiens	dJ202I21.1 (novel protein)	952	100
1126	AJ000217	Homo sapiens	CL1C2	1286	99
1127	AB030505	Mus musculus	UBE-1c2	1069	79
1128	¥73375	Homo sapiens	HTRM clone 1427838 protein	874	100
	-		sequence.		
1129	Y78941	Homo sapiens	Cyclophilin-type peptidyl	877	100
			prolyl cis/trans isomerase	}	
			amino acid sequence.		
1130	AL023553	Homo sapiens	dJ347H13.4 (novel protein)	557	100
1131	Y91945	Homo sapiens	Human chaperone protein 6	1408	100
1132	268197	<u> </u>	(HCHP-6).		
1132	200197	Schizosaccha	putative nuclear pore protein	596	39
		romyces			
1133	268197	Schizosaccha		1	
1133	40019/		putative nuclear pore protein	389	35
	1	romyces pombe	ĺ	1	
1134	AF180681	Homo sapiens			
1131	74 100001	nomo sapiens	guanine nucleotide exchange factor	3597	100
1135	AF079765	Mus musculus	enhancer of polycomb	264	
1136	M62419	Mus musculus	clathrin-associated protein	2189	41
1137	AJ006219	Drosophila	clathrin-associated protein	1254	99
		melanogaster	crachin-associated protein	1454	78
1138	Y76218	Homo sapiens	Human secreted protein	440	98
		, nome capacing	encoded by gene 95.	940	98
1139	W88104	Homo	A Rab protein designated	1065	99
		sapiens	HRABS-2.	1003	99
1140	Y13401	Homo sapiens	Amino acid sequence of	3979	98
			protein PRO339.	3373	30
1141	W85026	Chimeric -	Green fluorescent protein-	3309	100
	1	Homo sapiens	Zap70 fusion product.		-00
1142	Y13402	Homo sapiens	Amino acid sequence of	1694	99
		•	protein PRO310.		
1143	G03875	Homo sapiens	Human secreted protein, SEO	660	99
]		ID NO: 7956.		
1144	Y12917	Homo sapiens	Amino acid sequence of a	750	98
			human secreted peptide.	'	
1145	Y12917	Homo sapiens	Amino acid sequence of a	1096	100
		- 1	human secreted peptide.	<i>-</i>	
1146	AL022157	Homo sapiens	SPIN (SPINDLIN HOMOLOG	1233	100
		·	(PROTEIN DXF34))		
1147	AL022157	Homo sapiens	SPIN (SPINDLIN HOMOLOG	1233	100
		•	(PROTEIN DXF34))		
1148	G02548	Homo sapiens	Human secreted protein, SEQ	370	98
		• •	ID NO: 6629.	- ' -	
1149	Y73338	Homo sapiens	HTRM clone 2019742 protein	1492	100
		-	sequence.		
1150	W74841	Homo sapiens	Human secreted protein	228	55
		- 1	encoded by gene 113 clone		
					

TABLE 2

SEO	ACCESSION	SPECIES	DESCRIPTION	I ONTER	
ID	NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN	IDENTITY
NO:				SCORE	IDENTITE
	 		HEAAR60.		
1151	AF044201	Rattus	neural membrane protein 35;	1570	92
L	<u> </u>	norvegicus	NMP35	_l	
1152	AF156774	Homo	lysophosphatidic acid	1855	99
1153	AL118501	sapiens	acyltransferase-gammal dJ1191N16.1 (A novel protein		
1133	ALLIBSOI	Homo sapiens	(translation of the cDNA	872	64
	1		DKFZp566A0946, Em:AL050069))	1	ļ
1154	AF131852	Homo sapiens	Unknown	473	100
1155	Y41705	Homo	Human PRO352 protein	1381	97
_		sapiens	sequence.		
1156	G04036	Homo sapiens	Human secreted protein, SEQ	607	99
1.55	ļ		ID NO: 8117.		L
1157	AF112444	Lupinus luteus	L-asparaginase	287	43
1158	AF151848	Homo sapiens	CGI-90 protein	232	32
1159	AJ272267	Homo sapiens	choline dehydrogenase	2449	100
1160	AB001773	Clona	PEM-6	196	33
		savignyi			"
1161	Y87330	Homo sapiens	Human signal peptide	746	83
	1		containing protein HSPP-107		ł
1162	W07770	<u> </u>	SEQ ID NO:107.		<u> </u>
1102	Y87330	Homo sapiens	Human signal peptide containing protein HSPP-107	746	83
		•	SEQ ID NO:107.		
1163	AF113534	Homo sapiens	HPI-BP74 protein	2723	96
1164	AF232226	Danio rerio	Dedd1	191	41
1165	AL118501	Homo sapiens	dJ1191N16.1 (A novel protein	1051	71
			(translation of the cDNA		
1166	59110501		DKFZp566A0946, Em:AL050069))		
1100	AL118501	Homo sapiens	dJ1191N16.1 (A novel protein	945	76
			(translation of the cDNA DKFZp566A0946, Em:AL050069))	1	
1167	AF187733	Homo sapiens	syntaphilin	831	42
1168	AB019435	Homo sapiens	phospholipase	951	55
1169	AF064604	Homo sapiens	KE03 protein	324	33
1170	Y01164	Homo sapiens	Polypeptide fragment encoded	1191	100
1171			by gene 6.		
11/1	L03188	Saccharomyce s cerevisiae	putative	180	22
1172	AF113751	Mus musculus	nuclear pore membrane	3941	81
		dodocaras	glycoprotein POM210	3941	9.1
1173	AJ245417	Homo sapiens	G5b protein	794	100
1174	AL022238	Homo sapiens	dJ1042K10.3 (novel protein)	1285	100
1175	U41278	Caenorhabdit	F33G12.3 gene product	332	28
	1005515	is elegans			
1176	M35617	Homo sapiens	T-cell receptor V-alpha-J-	284	83
1177	AC012680	Arabidopsis	alpha region	209	<u> </u>
	ACULZUU	thaliana	putative protein phosphatase 2C; 55455-56414	209	37
1178	G01345	Homo sapiens	Human secreted protein, SEQ	692	99
			ID NO: 5426.	1	
1179	AL096767	Homo sapiens	dJ579N16.3 (novel protein	1342	100
			similar to worm, Arabidopsis	į i	
1180	AF039716	Caenorhabdit	and pine proteins)	1.55	
7700	ער עט ארי דער איזיי	is elegans	similar to ATP synthase B	496	55
1181	Y11710	Homo sapiens	collagen type XIV	1048	97
1182	X82240	Homo	T cell leukemia/lymphoma 1	617	100
		sapiens]			
ļ		>R94974		j í	1
İ		R94974 09-			
	!	MAY-1996 27- OCT-1994			.
}		Human TCL-1			
j	[polypeptide.			- 1
	·			L	

TABLE 2

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	*
ID	NUMBER	1		WATERMAN	IDENTITY
NO:	- -	[Homo		SCORE	
	ł	Sapiens		ł	
1183	U42841	Caenorhabdit	short region of weak	161	33
	1	is elegans	similarity to collagen	101	
1185	AJ131613	Homo sapiens	dicarboxylate carrier protein	1470	199
1186	L27645	Danio rerio	growth-associated protein	130	36
1187	Y02738	Homo sapiens	Human secreted protein	636	100
			encoded by gene 89 clone		1
1188	AF217544	Xenopus	HLHFP03. ornithine decarboxylase-2		
	1117,544	laevis	officialitie decarboxytase-2	1459	60
1189	AL136307	Homo sapiens	dJ380B8.2 (Neuritin, a	182	33
			protein which promotes	1 -02 .	33 .
			neurite outgrowth)		1
1190	X89602	Homo sapiens	rTSbeta	197	100
1191	U32828	Haemophilus	ribosomal protein S6	268	31
		influenzae Rd	modification protein (rimK)	1	
1192	AF154831	Rattus	PV-1	1403	60
	123.032	norvegicus	1 **-1	1403	60
1193	Y50926	Homo sapiens	Human fetal brain cDNA clone	918	100
		-	vc16 1 derived protein.		1 200
1194	AF026530	Rattus	stathmin-like-protein splice	1093	97
1195		norvegicus	variant RB3''		
1195	U35244	Rattus	vacuolar protein sorting	2981	96
1196	Y70470	norvegicus Homo sapiens	homolog r-vps33a Human p53 target molecule,		
	1	Tiono saptens	PRG3 protein.	1680	100
1197	AF157318	Homo sapiens	AD-017 protein	912	47
1198	AF125443	Caenorhabdit	contains similarity to S.	460	39
		is elegans	pombe phosphatidyl synthase		1
1100	******	<u> </u>	(GB: 228295)		1
1199	AF201934 AL031775	Homo sapiens	DC12	1649	88
1200	MP031//2	Homo sapiens	dJ30M3.3 (novel protein	1902	100
	-		similar to C. elegans Y63D3A.4)		
1201	M21103	Ovis aries	BIIIB4 high-sulfur keratin	484	82
1202	285986	Homo sapiens	dJ108K11.3 (similar to yeast	1143	75
			suppressor protein SRP40)		
1203	U18762	Rattus	retinol dehydrogenase type I	890	52
1204	U35730	norvegicus Mus musculus			
1205	AB002327	Homo sapiens	jerky KIAA0329	2235	76
1206	AB019233	Arabidopsis	ubiquinone/menaquinone	151 762	24 56
		thaliana	biosynthesis	/62	56
			methyltransferase-like		
1207	AL136307	Homo sapiens	dJ380B8.2 (Neuritin, a	742	100
	ļ		protein which promotes		
1208	AP207000	Vana and	neurite outgrowth)		
-EVO .	AF207989	Homo sapiens	orphan G-protein coupled receptor	2326	100
1209	297630	Homo sapiens	dJ466N1.4 (novel protein	181	44
		January Supremo	similar to ANK3 (ankyrin 3,	***	44
			node of Ranvier (ankyrin]
			G)))		İ
1210 1211	U21549	Mus musculus	Ac39/physophilin	1280	68
1211	Y27700	Homo sapiens	Human secreted protein	1267	100
1212	AF117814	Mus musculus	encoded by gene No. 12. odd-skipped related 1 protein		
1213	AF277233	Naegleria	calcineurin B	945	66
i		fowleri	omedinentin b	222	39
1214	D14849	Mus musculus	meiosis-specific nuclear	1950	77
			structural protein 1		
1215	G03022	Homo sapiens	Human secreted protein, SEQ	590	100
1216	272510	Canantal	ID NO: 7103.		
	2/2310	Caenorhabdit	similarity to yeast UTR3	634	49

TABLE 2

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	\$
ID NO:	NUMBER			WATERMAN SCORE	IDENTITY
		is elegans	protein (Swiss Prot accession yk677hl1.5 comes from this gene		
1217	Z49703	Saccharomyce s cerevisiae	unknown	134	22
1218	AC013430	Arabidopsis thaliana	F3F9.18	199	29
1219	L10910	Homo sapiens	splicing factor	1026	71
1220	270750	Caenorhabdit	similar to vanadate	965	58
		is elegans	resistance protein transmembranous comes from this gene		
1221	AL163815	Arabidopsis thaliana	putative protein	653	61
1222	AF155100	Homo sapiens	zinc finger protein NY-REN-21 antigen	2261	100
1223	J05071	Bos taurus	GTP-binding regulatory protein gamma-6 subunit	356	100
1224	¥73364	Homo sapiens	HTRM clone 2765991 protein sequence.	1169	99
1225	AL050170	Homo sapiens	hypothetical protein	714	100
1226	X64002	Homo sapiens	RAP74	2661	99
1227	X04085	Homo sapiens	catalase	2846	100
1228	AJ005620	Mus musculus	skeletal muscle-specific gene	1416	90
	AF045564	Rattus norvegicus	development-related protein	1715	93
1230 1231	X97571 L08239	Mus musculus	HCMV-interacting protein	479	96
1232	AF121863	Homo sapiens	located at OATL1 sorting nexin 14	2274	100
1233	AF121863	Homo sapiens	sorting nexin 14	1964	100
1234	AC024805	Caenorhabdit	contains similarity to	1203 744	84
1235	AC006634	is elegans	TR:004595]	
1235	AC008634	Caenorhabdit is elegans	contains similarity to Saccharomyces cerevisiae probable membrane protein YLR418C (GB:U20162)	357	33
1236	Y18101	Mus musculus	macrophage actin-associated- tyrosine-phosphorylated protein	1559	87
1237	AB042646	Homo sapiens	TGIF2	1224	100
1238	AB026264	Homo sapiens	IMPACT	1694	100
1239	AB026264	Homo saplens	IMPACT	1123	100
1240	G00429	Homo sapiens	Human secreted protein, SEQ ID NO: 4510.	324	100
1241	Y76144	Homo sapiens	Human secreted protein encoded by gene 21.	1363	53
1242	AL035602	Arabidopsis thaliana	putative protein	499	28
1243	X76483	Gallus gallus	Yes-associated protein (65kDa)	574	48
1244	AF220186	Homo sapiens	uncharacterized hypothalamus protein HT012	503	100
1245 1246	AL021453 AJ276003	Homo sapiens	dJ821D11.3 (PUTATIVE protein)	856	100
1247	Y57910	Homo sapiens	GAR1 protein	1216	100
1248		Homo sapiens	Human transmembrane protein HTMPN-34.	1369	98
	AC004874	Homo sapiens	similar to N- acetylgalactosaminyltransfera se; similar to Q07537 (PID:g1171989)	957	100
1249	AF199597	Homo sapiens	A-type potassium channel modulatory protein 1	1139	100
1250	Y13148	Rattus norvegicus	PAG608	1350	88
1251	M24852	Rattus	neuron-specific protein PEP-	124	46

TABLE 2

SEQ	ACCESSION	SPECIES	DESCRIPTION	Chieffer	
ID NO:	NUMBER	0.2020	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
1252	AF146738	Rattus norvegicus	testis specific protein	771	83
1253	G02725	Homo sapiens	Human secreted protein, SEQ ID NO: 68C6.	419	97
1254	W44375	Homo sapiens	Human ubiquitin-conjugating enzyme polypeptide.	1045	99
1255	AC006538	Homo sapiens	BC41195_1	831	78
1256	AB004316	Bos taurus	mitochondrial methionyl-tRNA transformylase	1556	88
1257	235094	Homo sapiens	SURF-2	1354	97
1258	Y13362	Homo sapiens	Amino acid sequence of protein PRO214.	2383	100
1259	AC006014	Homo sapiens	similar to RFP transforming protein; similar to P14373 (PID:q132517)	1299	100
1260	AC005099	Homo sapiens	match to AI222572 (NID:g3804775)	469	100
1261	V00507	Homo sapiens	coding sequence of DHFR (1 is 1st base in codon) (561 is 3rd base in codon)	984	100
1262	X15443	Rattus sp.	gamma-glutamyltranspeptidase (AA 1-568)	697	32
1263	AF173871	Mus musculus	neuronal PAS3	977	94
1264	AF178983	Homo sapiens	Ras-associated protein Rap1	433	97
1265	¥70473	Homo sapiens	Human cyclic nucleotide- associated protein-1 (CNAP- 1).	2785	99
1266	Y41738	Homo sapiens	Human PRO541 protein sequence.	1622	100
1267	AF061346	Mus musculus	Edpl protein	1077	64
1268	U97006	Caenorhabdit is elegans	C13F10.4 gene product	154	23
1269	AF233582	Mus musculus	GTPase Rab37	942	95
1270	AF195951	Homo sapiens	signal recognition particle 68	3127	98
1271	AL031177	Homo sapiens	dJ889M15.3 (novel protein)	1150	55
1272	AF201933	Homo sapiens	DC11	650	100
1273 1274	AF201933	Homo sapiens	DC11	346	98
1275	AL021710	Arabidopsis thaliana	putative protein	348	49
1275	AC004449 Y86295	Homo sapiens	R33683_3	556	100
1276	Y71111	Homo sapiens	Human secreted protein HL2AG87, SEQ ID NO:210.	1920	100
1278	S94421	Homo sapiens	Human Hydrolase protein-9 (HYDRL-9).	1576	99
1278	Y66695	Homo sapiens	T cell receptor eta-exon	478	100
1280		sapiens	Membrane-bound protein PR01344.	1909	100
1280	AF161380 Y48610	Homo sapiens	HSPC262	772	100
1282		Homo sapiens	Human breast tumour- associated protein 71.	779	100
	AC015446	Arabidopsis thaliana	Similar to AIG1 protein	406	35
1283 1284	AK024432	Homo sapiens	FLJ00022 protein	403	35
	W96153	Homo sapiens	Human FADD-interacting protein (FIP).	1825	81
1285	AJ001019	Homo sapiens	ring finger protein	1301	100
1286	AE003823	Drosophila melanogaster	CG13178 gene product	195	29
1287	AF178632	Homo sapiens	FEM-1-like death receptor binding protein	3261	100
1288	AC006033	Homo sapiens	similar to MLN 64; similar to I38027 (PID:g2135214)	1195	100
1289	AC006033	Homo sapiens	similar to MLN 64; similar to 138027 (PID:g2135214)	668	93
1290	AB023811	Homo sapiens	TU3A	351	54

TABLE 2

SEO	ACCESSION	SPECIES	DESCRIPTION		-
ID	NUMBER	J. D. L. C. L. S.	DESCRIPTION	SMITH- WATERMAN	IDENTITY
NO:			1	SCORE	IDENTITY
1291	Z73424	Caenorhabdit is elegans	C44B9.1	235	36
1292	Y94871	Homo sapiens	Human protein clone HP02551.	1222	100
1293	AF190425	Homo sapiens	protein RAP140	489	29
1294	G03856	Homo sapiens	Human secreted protein, SEQ ID NO: 7937.	538	99
1295	AF133670	Mus musculus		367	51
1296	AJ249735	Homo sapiens	claudin-6	1142	100
1297	X57560	Escherichia coli	pspE protein	535	100
1298	AF169284	Homo sapiens	LIM and cysteine-rich domains protein 1	1997	100
1299	U41023	Caenorhabdit is elegans	yk61f1.3; coded for by C. yk109h8.5	324	29
1300	AB024523	Homo sapiens	basic kruppel like factor	1206	100
1301	X55989	Homo sapiens	eosinophil cationic-related protein	737	99
1302	AF007151	Homo sapiens	unknown	1481	100
1303	X52904	Escherichia coli	open reading frame (AA 1-65)	359	100
1304	U19577	Escherichia coli	galactonate dehydratase	242	93
1305	AF266508	Mus musculus	NELF protein	1409	97
1306	Y57901	Homo sapiens	Human transmembrane protein HTMPN-25.	932	100
1307	U58750	Caenorhabdit is elegans	similar to the mitochondrial carrier family	365	54
1308	AF044774	Homo sapiens	breakpoint cluster region	2681	99
1309	AL078593	Homo sapiens	dJ210B1.1 (KIAA0680)	267	34
1310	X82693	Homo sapiens	E48 antigen	620	96
1311	282263	Caenorhabdit is elegans	C47A4.1	283	35
1312	AF131218	Homo sapiens	chromosome 16 open reading frame 5	1493	100
1313	Y41763	Homo sapiens	Human PRO938 protein sequence.	1636	100
1314	AF196972	Homo sapiens	JM24 protein	2239	100
1315	AF053356	Homo sapiens	insulin receptor substrate like protein	228	97
1316	Y66695	Homo sapiens	Membrane-bound protein PR01344.	1909	100
1317	AF153127	Gallus gallus	SAPK interacting protein	2442	89
1318	AF153127	Gallus gallus	SAPK interacting protein	1477	83
1319	AF153127	Gallus gallus	SAPK interacting protein	1651	86
1320	X56932	Homo sapiens	23 kD highly basic protein	1044	100
1321	AF174605	Homo	F-box protein Fbx25	467	70
		sapiens) > X83086 Y83086 09- MAR-2000 28- AUG-1998 P- box protein FBP-18. [Homo sapiens	·		
1322	M61732	Trypanosoma cruzi	neuraminidase	214	24
1323	Y17013	porcine	pol	304	64
		endogenous			

SEQ	ACCESSION	SPECIES	DECORYDATAN	- CN/Tm/T	· · · · · · · · · · · · · · · · · · ·
ID	NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN	IDENTITY
NO:	I WONDER			SCORE	IDENTITY
		retrovirus		DCOAL	
1324	AL138655	Arabidopsis	putative protein	1174	37
		thaliana] Factoria Protocu		- '
1325	AL138655	Arabidopsis	putative protein	946	35
		thaliana	1		
1326	AL133215	Homo sapiens	bA108L7.2 (novel protein	1322	99 1
			similar to rat tricarboxylate	1	
			carrier)		
1327	AF161541	Homo sapiens	HSPC056	1357	99
1328	Y73346	Homo sapiens	HTRM clone 619699 protein	785	96
	l		sequence.		1
1329	L10910	Homo sapiens	splicing factor	912	82
1330	AF146568	Homo sapiens	MIL1 protein	1936	100
1331	W87772	Homo sapiens	Human serum glucocorticoid-	232	39
			regulated kinase (H-SGK2)		
			polypeptide.		
1332	Y41741	Homo	Human PRO704 protein	1860	100
		sapiens	sequence.		
1333	AF295096	Homo sapiens	zinc-finger protein ZBRK1	411	91
1334	282271	Caenorhabdit	Similarity to Mouse kinensin-	578	44
		is elegans	like protein KIF4 comes from		1
1225	AROSSOS	Nach-	this gene		
1335	AE000810	Methanobacte	conserved protein	290 .	43
		rium			İ
		thermoautotr			l
1336	Y68779	ophicum Homo sapiens			ļ
1236	168//9	Homo sapiens	Amino acid sequence of a	1019	91
			human phosphorylation effector PHSP-11.		
1337	AB027003	Mus musculus		1.72	<u> </u>
1338	U64856	Caenorhabdit	protein phosphatase weak similarity to TPR	378	84
1330	004030	is elegans	domains	215	40
1339	AE001394	Plasmodium	protein of the YMR7 family	170	
1339	MEGGT334	falciparum	process of the sak/ samssy	170	29
1340	X76717	Homo sapiens	MT-11 protein	204	89
1341	AC011914	Arabidopsis	putative mutT protein; 68398-	289	45
		thaliana	6788]	1	1.0
1342	AJ276171	Homo sapiens	ASPIC	2122	100
1343	AF187016	Homo sapiens	myosin regulatory light chain	2303	99
		_	interacting protein MIR		
1344	AC006963	Homo sapiens	similar to Kelch proteins;	894	35
			similar to BAA77027	ļ	ļ
			(PID:g4650844)	}	
1345	AF257466	Homo sapiens	N-acetylneuraminic acid	1880	99
			phosphate synthase]
1346	Y25896	Homo sapiens	Human secreted protein	1148	100
		İ	fragment encoded from gene	Į.	
3345	* *****		64.		
1347	AJ272073	Torpedo	male sterility protein 2-like	1664	58
1240	NB161546	marmorata	protein	<u> </u>	
1348	AF161548	Homo sapiens	HSPC063	1018	98
1349	W78128	Homo sapiens	Human secreted protein	1117	100
			encoded by gene 3 clone	İ	
1351	C02144	Home access	HOSBI96.		
1721	G02144	Homo sapiens	Human secreted protein, SEQ	418	100
1352	D90869	Fachenia	ID NO: 6225.		
1334	£00067	Escherichia coli	similar to	2047	100
1353	A12029	HOmo sapiens	MDD 14		4.00
1354			MRP-14	613	100
1	AC005328	Homo sapiens	R26660_1, partial CDS	870	74
1355	AC024876	Caenorhabdit	contains similarity to	829	61
1356	NP027224	is elegans	SW:RPB1_CRIGR		
1356 1359	AF077226 AF217188	Homo sapiens	Copine III	1876	64
1	AC074331	Mus musculus Homo sapiens	YIP1B ZNF234	801	63
1360 1361	AL163279	Homo sapiens	homolog to cAMP response	3869 5035	100 99

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	2
ID NO:	NUMBER			WATERMAN SCORE	IDENTITY
			element binding and beta transducin family proteins		
1362	Z48475	Homo sapiens	glucokinase regulator	3160	99
1363	248475	Homo sapiens	glucokinase regulator	2682	97
1364	AF195764	Homo sapiens	megakaryocyte-enhanced gene transcript 1 protein; MEGT1	2055	99 ,
15.66	1	ļ 	protein		
1365 1366	AF116609 AF116609	Homo sapiens	PRO0915	581	100
1366	AL117352	Homo sapiens		581	100
1367	ALII/352	Homo sapiens	dJ876B10.3 (novel protein similar to C. elegans T19B10.6 (Tr:Q22557))	2581	99
1368	Y34124	Homo sapiens	Human potassium channel K+Hnov15.	1342	100
1369	AJ245621	Homo sapiens	CTL2 protein	3728	99
1370	AF008220	Bacillus subtilis	YtaG	429	45
1371	X05562	Homo sapiens	alpha-2 chain precursor (AA - 25 to 1018) (3416 is 2nd base in codon)	5908	99
1372	Z98048	Homo sapiens	dJ408N23.4 (novel DnaJ domain protein)	1296	99
1373	AF154415	Homo sapiens	FLASH	10253	100
1374	U20286	Rattus norvegicus	lamina associated polypeptide 1C	1567	69
1376	U53445 AL117337	Homo sapiens	DOC1	1645	46
1377	AC005328	Homo sapiens Homo sapiens	bA393J16.1 (zinc finger protein 33a (KOX 31))	250	60
1378	U35113	Homo sapiens	R26660_1, partial CDS metastasis-associated gene	1126	100
1379	L15313	Caenorhabdit is elegans	putative putative	1823 858	69 58
1380	Y25756	Homo sapiens	Human secreted protein encoded from gene 46.	1508	100
1381	AB037360	Homo sapiens	ANKHZN	5734	95
1382	AB037360	Homo sapiens	ANKHZN	959	97
1383	AF237676	Mus musculus	G beta-like protein GBL	1721	96
1384	AF237676	Mus musculus	G beta-like protein GBL	1043	70
1385	Y58793	Homo sapiens	Human calcium regulatory protein CaREG-1.	715	100
1386	AF212162 AL031685	Homo sapiens	ninein	10369	99
1388	AC004890	Homo sapiens Homo sapiens	dJ963K23.2 (novel protein) similar to zinc finger	337	33
1300	AC004890	Nomb saprens	proteins; similar to BAA24380 >W06316 W06316 03-OCT-1996 27-APR-1995 TRP-1 protein.	542	86
1389	AF187989	Homo sapiens	zinc finger protein ZNF223	2665	99
1390 .	AC035150	Homo sapiens	Zinc finger protein ZNF221	3459	100
1391	AF287894	Homo sapiens	PIST	1410	97
1392	AF282265	Homo sapiens	inner centromere protein INCENP	1794	99
1393	X90840	Homo sapiens	axonal transporter of synaptic vesicles	4584	99
	AF076249	Homo sapiens	zinc finger protein SBBIZ1	3208	99
1395	G02224	Homo sapiens	Human secreted protein, SEQ ID NO: 6305.	299	75
	AC004809	Arabidopsis thaliana	Similar to	130	34
1398	AF242519	Homo sapiens	zinc finger protein SBZF3	181	66
1399	AL133396 Y48611	Homo sapiens	dJ1068H6.4 (prion protein like protein doppel)	962	100
1400	AC004472	Homo sapiens	Human breast tumour- associated protein 72.	817	99
1402	X91489	Homo sapiens Saccharomyce	P1.11659_5 putative HMG box	280	54
		s cerevisiae	Paractive UNO DOX	164	27

TABLE 2

SEQ	ACCESSION	SPECIES	DESCRIPTION	T SMITH-	- E
ID	NUMBER		DESCRIPTION	WATERMAN	IDENTITY
NO:				SCORE	IDENTITY
1403	Y79222	Homo	Human transferasc TRNSPS-14.	2842	100
1	1	sapiens		2012	1 -00
1404	X81058	Mus musculus	tex261	1010	99
1405	AB012084	Mus musculus		194	29
1406	AB030251	Homo sapiens		3233	99
1407	AJ010585	Rattus	PTB-like protein	2684	3
	1.202000	rattus	FIB-LIKE PLOCETU	2684	99
1408	X75760	Drosophila	LRR47	364	29
		melanogaster	IIIII 7	1 384	29
1409	076618	Mus musculus	N-RAP	804	48
1410	AC005578	Homo sapiens	P20887_1, partial CDS	835	
1411	AE000284	Escherichia	orf, hypothetical protein.	360	63
		coli	orr, mypochecical process.	360	100
1412	X01563	Escherichia	L5 (rplE) (aa 1-179)	911	
	1.02303	coli	13 (1912) (ad 1-1/9)	311	100
1413	W78279	Homo sapiens	Fragment of human secreted	1222	
1	11,02,7	supicina	protein encoded by gene 33.	1264	99
1414	AB031051	Homo sapiens	organic anion transporter	1 2022	
	1.2032032	momo Bapiens	OATP-E	3832	100
1415	M17466	Homo sapiens	coagulation factor XII	3455	-
1416	AF097994	Homo	L-kynurenine/alpha-	I	100
	111 05 7554	sapiens	aminoadipate aminotransferase	2202	99
1417	AF151077	Homo sapiens	HSPC243	1262	
1418	Y09945	Rattus	putative integral membrane	1	99
	10000	norvegicus	transport protein	1098	61
1419	U13152	Mesocricetus	guanine nucleotide-binding	2179	
]	023232	auratus	protein beta 5	21/9	76
1420	AL162458	Homo sapiens	bA465L10.5 (KIAA1176 (novel	5696	
		nomo saptens	protein, presumed ortholog	5696	100
1	ļ		of mouse K-Cl cotransporter	1	l i
			(KCC2))	ĺ	İ
1421	Y99426	Homo sapiens	Human PRO1604 (UNQ785) amino	152	29
)		acid sequence SEQ ID NO:308.	132	29
1422	Y94923	Homo sapiens	Human secreted protein clone	4039	99
ł			qs14_3 protein sequence SEQ	1 2000	33
1	ļ		ID NO:52.		!
1423	AF177388	Homo	cancer-amplified	10748	99
1		sapiens	transcriptional coactivator		"
	į	-	ASC-2		!
1424	Y48517	Homo sapiens	Human breast tumour-	1851	99
1	1		associated protein 62.		"
1425	AF208848	Homo sapiens	BM-006	1454	89
1426	AF208848	Homo sapiens	BM-006	853	79
1427	AF112886	Bos taurus	differentiation enhancing	4693	95
į	İ	Ì	factor 1	1000	
1428	U41387	Homo sapiens	Gu protein	1372	63
1429	AF161534	Homo sapiens	HSPC049	2853	78
1430	AF125043	Mus musculus	bisphosphate 3'-nucleotidase	275	30
1431	Y66718	Homo	Membrane-bound protein	1886	100
İ		sapiens	PRO1106.		
1432	AF193613	Homo sapiens	cell recognition molecule	568	100
L		, i	Caspr2		
1433	AB044560	Mus musculus	Gliacolin	192	34
1434	R99900	Homo sapiens	NTII-1 nerve protein,	707	51
		_ ·	facilitates regeneration of		
			nerve cells.		- 1
1435	AF220530	Homo sapiens	myo-inositol 1-phosphate	2904	100
		_	synthase Al		
1436	X70944	Homo sapiens	PTB-associated splicing	1261	72
			factor		
1437	AF271732	Homo sapiens	bridging integrator-3	1282	100
1438	Y30811	Homo sapiens	Human secreted protein	595	98
		_	encoded from gene 1.		
1439	AJ293659	Homo sapiens	mucolipidin	628	97
1440	AF219138	Homo sapiens	GGA3 long isoform	3083	100
1441	AF219138	Homo sapiens	GGA3 long isoform	3346	100

SEQ	ACCESSION	SPECIES	DECORTORION	T AUTON	
ID	NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN	IDENTITY
NO:	I IIII	1		SCORE	IDENTITY
1442	AB039669	Homo sapiens	ALEX3	1944	100
1443	AF237711	Drosophila	Diablo	191	27
		melanogaster		131	"
1444	AJ011896	Homo sapiens	Nafl beta protein	439	39
1445	X73874	Homo sapiens	phosphorylase kinase	6233	98
1446	AF214114	Homo sapiens	breast carcinoma-associated	3999	99
] -	antigen BCAA		"
1447	AF003924	Homo sapiens	ANC 2H01	2645	99
1448	AF003136	Caenorhabdit	contains weak similarity to	2843	52
	1	is elegans	an AMP-binding motif	1	1
1449	AF155112	Homo sapiens	NY-REN-50 antigen	1184	89
1450	Y95004	Homo sapiens	Human secreted protein	985	100
	}		vc54_1, SEQ ID NO:48.		
1451	AF107203	Homo sapiens	ataxin 2-binding protein	688	57
1452	AF107203	Homo sapiens	ataxin 2-binding protein	456	78
1453	Z38011	Mus musculus	DMR-N9	882	56
1454	X90568	Homo sapiens	Protein sequence and	510	28
			annotation available soon via		
		<u></u>	LABEIT@EMBL-Heidelberg.DE	1	
1455	AL035409	Homo sapiens	dJ564M11.3 (similar to	1356	100
			sialyltranferase)		
1456	D44480	Mus musculus	MATH-2 protein	272	100
1458	AF141326	Homo sapiens	RNA helicase HDB/DICE1	478	45
1459	AF242552	Gallus	retinovin	945	34
		gallus	<u>L</u>	1	
1460	U11036	Homo sapiens	Ibd1	724	84
1461	AB025258	Mus musculus	granuphilin-a	545	39
1462	Y08134	Homo sapiens	acid sphingomyelinase-like	2428	99
			phosphodiesterase		
1463	AC004997	Homo sapiens	match to ESTs 243979 (NID:g573097), R19699 (NID:g774333)	869	98
1464	AC004997	Homo sapiens	match to ESTs 243979 (NID:g573097), R19699 (NID:g774333)	869	98
1465	U32743	Haemophilus influenzae	fucose operon protein (fucU)	315	50
1466	Y09022	Homo sapiens	Not56-like protein		
1467	AC003034	Homo sapiens	Homolog of rat kidney-	2342	100
	110003034	nono saprens	specific (KS) gene	1072	99
1468	AF071544	Spinacia	ribulose-1,5-bisphosphate	333	26
		oleracea	carboxylase/oxygenase small	333	26
		1	subunit N-methyltransferase I		
1469	Y57930	Homo sapiens	Human transmembrane protein HTMPN-54.	1053	100
1470	AF032666	Rattus	rsec5	4504	93
		norvegicus		"50"	13
1471	Y70467	Homo sapiens	Human membrane channel protein-17 (MECHP-17).	452	74
1472	27.027.527	77	C321D2.1 (Ribosomal Large	1.604	100
	AL031033	Homo sapiens	Subunit Pseudouridine	1694	100
		•	Subunit Pseudouridine Synthase protein)		
1473	AF177292	Homo sapiens	Subunit Pseudouridine Synthase protein) genethonin 3	4026	98
1473 1474	AF177292 S45936	Homo sapiens	Subunit Pseudouridine Synthase protein) genethonin 3 HTS1	4026 1101	98 50
1473 1474 1475	AF177292 S45936 Y86241	Homo sapiens Homo sapiens Homo sapiens	Subunit Pseudouridine Synthase protein) genethonin 3 HTS1 Human secreted protein HOABR60, SEQ ID NO:156.	4026	98
1473 1474 1475	AF177292 S45936 Y86241 AJ010317	Homo sapiens	Subunit Pseudouridine Synthase protein) genethonin 3 HTS1 Human secreted protein	4026 1101	98 50
1473 1474 1475	AF177292 S45936 Y86241	Homo sapiens Homo sapiens Homo sapiens	Subunit Pseudouridine Synthase protein) genethonin 3 HTS1 Human secreted protein HOABR60, SEQ ID NO:156. Sand coded for by C. elegans cDNA yk99b4.3; similar to human transforming protein	4026 1101 1879	98 50 98
1473 1474 1475	AF177292 S45936 Y86241 AJ010317	Homo sapiens Homo sapiens Homo sapiens Fugu rubripes Caenorhabdit is elegans	Subunit Pseudouridine Synthase protein) genethonin 3 HTS1 Human secreted protein HOABR60, SEQ ID NO:156. Sand coded for by C. elegans cDNA yk99b4.3; similar to human transforming protein (PIR:S22157)	4026 1101 1879 1278	98 50 98 68
1473 1474 1475 1476	AF177292 S45936 Y86241 AJ010317 U42831	Homo sapiens Homo sapiens Homo sapiens Fugu rubripes Caenorhabdit	Subunit Pseudouridine Synthase protein) genethonin 3 HTS1 Human secreted protein HOABR60, SEQ ID NO:156. Sand coded for by C. elegans cDNA yk99b4.3; similar to human transforming protein	4026 1101 1879	98 50 98 68

TABLE 2

SEO	ACCESSION	SPECIES		·	
ID NO:	NUMBER		DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
1481	AL078599	Homo sapiens	dJ991C6.1 (novel protein similar to C. elegans F55Al2.9 (Tr:P91086))	1274	65
1482	298977	Schizosaccha romyces pombe	putative vacuolar protein	256	29
1483	AB005662	Mus musculus	JNK/SAPK-associated protein-1	4968	92
1484	AL050120	Homo sapiens	hypothetical protein	716	100
1485	M27878	Homo sapiens	DNA binding protein	1006	53
1486	Y69161	Homo sapiens	Amino acid sequence of a partial protein kinase.	575	99
1487	X84156	Saccharomyce s cerevisiae	ATHI	341	29
1488	AP038963	Homo sapiens		446	34
1489	U56966	Caenorhabdit is elegans	yk30b3.5; coded for by C. elegans cDNA vk30b3.3	620	42
1490	AE000989	Archaeoglobu s fulgidus	enoyl-CoA hydratase (fad-4)	533	46
1491	M80633	Rattus norvegicus	adenylyl cyclase type IV	707	95
1492	Y73342	Homo sapiens	HTRM clone 2709055 protein sequence.	3513	99
1493	Y17220	Homo sapiens	Human secreted protein (clone fj283-11).	462	37
1494	AF133670	Mus musculus	ARL-6 interacting protein-2	701	97
1495	Y94897	Homo sapiens	Human protein clone HP10574.	1371	100
1496	AL049699	Homo sapiens	dJ747H23.2 (novel protein)	1550	100
1497	AF037447	Homo sapiens	ribosomal S6 protein kinase	2427	100
	AL445067	Thermoplasma acidophilum	putative target YPL207w of the HAP2 transcriptional complex related protein	269	35
1.499	AB039947	Homo sapiens	X11L-binding protein 51	227	36
1500 1501	AJ277750	Homo sapiens	UBASH3A protein	3509	100
1501	AL050333	Homo sapiens	dJ93K22.1 (novel protein (contains DKFZP564B116))	2439	100
1503	AF178948	Homo sapiens	TALE homeobox protein Meis2b	1140	100
1504	X53005	Homo sapiens	TALE homeobox protein Meis2a Human secreted protein clone	1177	100
		nomo saprens	pm749_8 protein sequence SEQ ID NO:16.	1442	99
1505	X82494	Homo sapiens	fibulin-2	3580	99
1506	X98296	Homo sapiens	ubiquitin hydrolase	783	42
1507	AL034548	Homo sapiens	dJ1103G7.6 (novel protein)	1098	100
1509	Y76144 AF220182	Homo sapiens	Human secreted protein encoded by gene 21.	1736	100
1510	U64601	Homo sapiens	uncharacterized hypothalamus protein HT008	1181	98
1511	AL356192	Caenorhabdit is elegans	Gene probably begins in the next cosmid	415	58
1512	D17629	Neurospora crassa	related to MDM1 protein	196	29
1513		Homo sapiens	N-acetylgalactosamine 6- sulfate sulfatase (GALNS)	1829	100
1514	AF168717 AJ243531	Homo sapiens	x 009 protein	694	99
1515	AC003672	Homo sapiens Arabidopsis	nM15 protein	735	100
1516		thaliana	putative C3HC4-type RING zinc finger protein	407	30
1516	AF115435	Rattus norvegicus	syntaxin 17	1374	90
	AF003140	Caenorhabdit is elegans	C44E4.5 gene product	274	31
1518	AB002584 AL121764	Rattus norvegicus	beta-alanine-pyruvate aminotransferase	2238	82
2023	AD121/04	Schizosaccha	yeast atpl2 protein precursor	270	30

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	1
ID	NUMBER			WATERMAN	IDENTITY
NO:		<u> </u>		SCORE	
		romyces pombe	homolog		
1520	AF255910	Homo	vascular endothelial	547	100
		sapiens	junction-associated molecule	347	100
1521	D31764	Homo sapiens	KIAA0064	170	27
1522	Y66634	Homo	Membrane-bound protein	985	100
		sapiens	PRO190.		
1523	Y94450	Homo sapiens	Human inflammation associated	250	43
1524	AC000107	Arabidopsis	protein		1
1324	ACCOUNTE	thaliana	F17F8.22	277	37
1525	AF109377	Mus musculus	ldlBp	1277	
1526	AL031427	Homo sapiens		1432	83 99
1527	Y08135	Mus musculus	acid sphingomyelinase-like	1496	79
		i	phosphodiesterase	1	' '
1528	AK024423	Homo sapiens	FLJ00012 protein	611	100
1529	AF154502	Homo sapiens	1 man promise	679	100
1530	AF205598	 	dipeptidase		
1531	AF251039	Homo sapiens	transposase-like protein	1368	100
1532	W74805	Homo sapiens	putative zinc finger protein	1420	50
2000	"71003	nomo saptens	Human secreted protein encoded by gene 77 clone	493	57
1533	AF039023	Homo sapiens	HOEAS24.		
	Ar 039023	nomo sapiens	Ran-GTP binding protein; RanBP6	5707	99
1534	AC007190	Arabidopsis	F23N19.9	374	
		thaliana	123,13.3	3/4	37
1535	AB027564	Homo sapiens	DINB1	4482	100
1536	Y36178	Homo sapiens	Human secreted protein	377	87
1537	¥50907	Homo sapiens	Human fetal brain cDNA clone	3693	99
1538	AF017368		vb3_1 derived protein.		
1230	AF01/368	Mus musculus	faciogenital dysplasia	177	47
1539	AF266756	Homo sapiens	protein 2 sphingosine kinasc ·	2011	
1540	Z48804	Homo sapiens	OA1	2238	99 100
1541	AF000195	Caenorhabdit	Contains similarity to Pfam	379	42
		is elegans	domain: PF00169 (PH),		~~
			Score=20.6, E-value=1.9e-05,		
1542	Y71159	Homo sapiens	N=1	<u> </u>	<u> </u>
1342	1/1139	Homo Bapiens	Human phosphodiesterase interacting protein,	9415	99
	l	•	myomegalin.		
1543	X76092	Homo sapiens	DNA binding protein RFX3	3327	100
1544	AB015330	Homo sapiens	HRIHFB2007	631	50
1545	AF198487	Homo sapiens	transcription factor LBP-1b	2822	100
1546	AF016417	Caenorhabdit	Similar to BZIP transcription	518	42
1547	X55885	is elegans	factor		
1548		Homo sapiens	KDEL receptor	1106	100
	AB035495	Carassius auratus	ubiquitin-activating enzyme B1	836	42
1549	AL021707	Homo sapiens	dJ508115.4 (KIAA0668)	2600	
1550	AJ223978	Bacillus	YvqK protein	3688 292	100
		subtilis	Bunnalus		7.4
1551	AF145615	Drosophila	BcDNA.GH03377	822	44
		melanogaster			ļ
1552	AL157734	Schizosaccha	putative mannosyltransferase	435	37
		romyces pombe	involved in N-glycosylation		Į
1553	AF079527	Mus musculus	IER5		
1554	AB026291	Rattus	acetoacetyl-CoA synthetase	691	63
İ		norvegicus	accounterly con synthetase	1099	88
1555	Y44722	Homo sapiens	Human immune system molecule.	1780	99
			ISMO-3.		
1556	AF116553	Drosophila	antennal-specific short-chain	277	32
1557	Y71056	melanogaster	dehydrogenase/reductase		
	1,1030	Homo sapiens	Human membrane transport	1975	99

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	£
ID	NUMBER			WATERMAN	IDENTITY
NO:				SCORE	<u> </u>
	<u> </u>		protein, MTRP-1.		
1558	Y71056	Homo sapiens	Human membrane transport	1975	99
			protein, MTRP-1.	<u> </u>	<u> </u>
1559	Y71056	Homo sapiens	Human membrane transport	1894	97
1560	7.5000050		protein, MTRP-1.		
1560	AF092050	Mus musculus	beta-1,3-N-	262	44
			acetylglucosaminyltransferasc	<u> </u>	<u> </u>
1561	AL109827	Homo sapiens	dJ309K20.2 (acrosomal protein	1607	97
			ACRSS (similar to rat sperm	1	
1562	AJ131890	Homo sapiens	antigen 4 (SPAG4)))	L	
1563	AL035424		DNA polymerase lambda dA22D12.1 (novel protein	3002	100
1303	AL035424	Homo sapiens	similar to Drosophila Kelch	3015	100
	ſ		proteins)		
1564	AC002400	Homo sapiens	Gene product with similarity	2790	
1204	AC002400	ansiqua omon	to Ubiquitin binding enzyme	2790	100
1565	AC005306	Homo sapiens	R27216 1	919	
1566	AF000195	Caenorhabdit	Contains similarity to Pfam	550	82
1300	AF000133	is elegans	domain: PF00169 (PH),	550	45
		15 eregans	Score=20.6, E-value=1.9e-05.	1	
		İ	N=1	ľ	
1567	AB033281	Нопо	F-box and WD-repeats protein	2879	100
,		sapiens	beta-TRCP2 isoform C	2019	100
1568	D19173	Mus musculus	truncated form of Sox17	1047	78
1569	AK025270	Homo sapiens	unnamed protein product	210	91
1570	X75756	Homo sapiens	protein kinase C mu	4797	99
1571	AF145713	Homo sapiens	SCHIP-1	2388	100
1572	AE003831	Drosophila	CG18445 gene product	180	31
	1	melanogaster	Coro442 dewe bindadi	180	31
1573	AF074603	Streptomyces	NonF	205	38
		griseus	, ,,,,,,,	205	30
	,	subsp.		1	
		griseus			1
1574	U28993	Caenorhabdit	F22D3.3 gene product	144	27
		is elegans	Jan game		
1575	AF129507	Homo sapiens	transcription factor ICBP90	287	68
1576	X64878	Homo sapiens	oxytocin receptor	2002	100
1577	AF237711	Drosophila	Diablo	421	54
		melanogaster			
1578	G00975	Homo sapiens	Human secreted protein, SEQ	480	100
		-	ID NO: 5056.		
1579	AF248744	Cryptosporid	thrombospondin-related	123	33
		ium parvum	adhesive protein	ļ	
1580	AL121782	Homo sapiens	dJ585I14.2 (novel protein	663	100
			(translation of cDNA		ł
			Em:AK000219))		[
1581	AF041853	Homo sapiens	kinesin family member protein	345	33
			KIF3A		
1582	AF025441	Homo sapiens	Opa-interacting protein OIP5	1198	100
1583	AE001803	Thermotoga	glycerate kinase, putative	349	34
		maritima	<u> </u>	L	
1584	AF252283	Homo sapiens	Kelch-like 1 protein	3973	100
1585	AF169675	Homo	leucine-rich repeat	3494	99
1505		sapiens	transmembrane protein FLRT1		
1586	AF118274	Homo sapiens	DNb-5	2628	97
1587	X79440	Homo sapiens	NADP+-dependent malic enzyme	3167	99
1588	X99802	Homo sapiens	ZYG homologue	3966	99
1589	AF169803	Homo sapiens	flavohemoprotein b5+b5R	2563	100
1590	Y29861	Homo sapiens	Human secreted protein clone	181	47
156			cb98_4.		
1591	225535	Homo sapiens	nuclear pore complex protein	7567	99
			hnup153		
1592	X13293	Homo sapiens	B-myb protein (AA 1-700)	3678	99
1593	M74027	Homo sapiens	mucin	242	27
	AL139314	Schizosaccha	hypothetical protein	235	54
1594	12222214	romyces	JF F		

SEO	ACCESSION	SPECIES	DISCON Y DITTON	T GUYENI	·
ID	NUMBER	SPECIES	DESCRIPTION	SMITH-	*
NO:	NONDER			WATERMAN	IDENTITY
10.	 	pombe		SCORE	
1595	W78324	Homo sapiens	Fragment of human secreted	1318	98
2020	,	nomo Bapieno	protein encoded by gene 81.	1318	98
1596	Y94906	Homo sapiens	Human secreted protein clone	2236	98
1	1	nomo suprems	rb649_3 protein sequence SEQ	2236	98
		}	ID NO:18.		
1597	AF174605	Homo sapiens	F-box protein Fbx25	1408	ļ.,,
1598	AB032254	Homo sapiens	bromodomain adjacent to zinc		99
1330	70032234	sapiens	finger domain 2A	9676	98
1599	X73114	Homo sapiens	slow MvBP-C	5568	
1600	X82200	Homo sapiens	gpStaf50	1	95
1601	Y00876	Homo sapiens		2305	100
1001	100070	sapiens	Human LAPH-1 protein	1149	98
1602	AJ223351	Homo sapiens	sequence. HIRA-interacting protein 3		ļ.,,
1603	AJ222801	Homo sapiens		2821	99
1604	AJ222801		neutral sphingomyelinase	2268	99
1605	AF185576	Homo sapiens	neutral sphingomyelinase	1601	99
.1605	AF1855/6	Mus musculus	POZ/zinc finger transcription	3435	97
1606	AF093744	 	factor ODA-8		
1607	A12142	Homo sapiens	unknown	131	100
1,001	A12142		IFN-pseudo-omega 2	800	98
1608	¥57949	construct			
1008	25/949	Homo sapiens	Human transmembrane protein	1868	100
1609	N 171 C 1 C 1		HTMPN-73.		
1610	AF151044	Homo sapiens	HSPC210	681	97
1611	X15218	Homo sapiens	ski protein (AA 1 - 728)	3765	100
1611	¥08200	Homo sapiens	rab geranylgeranyl	2976	100
1612	AF220560		transferase		
1613		Homo sapiens	B/K protein	2486	99
1013	AC004481	Arabidopsis thaliana	nodulin-like protein	371	26
1614	Y09501				
1615	Y15521	Homo sapiens	NADH-cytochrome-b5 reductase	1607	100
1616	AJ010750	Homo sapiens	start position 1	3150	97
1010	A0010750	Rattus	Castration induced prostatic	890	62
		norvegicus	apoptosis related protein-1,	ļ	İ
1617	X58079	77	(CIPAR-1)		
1618	Y66678	Homo sapiens	S100 alpha protein	481	100
1010	1000/0	1	Membrane-bound protein	967	100
1619	AJ242973	sapiens Homo sapiens	PRO1009.		
1013	AU242973	nomo sapiens	peptide methionine sulfoxide	929	100
1620	AF150733	Homo sapiens	reductase	,	
1621	AJ007509	Homo sapiens	AD-014 protein	288	100
1622	X64177	Homo sapiens	E1B-55kDa-associated protein	4646	98
1623	AE001045		metallothionein	380	100
1023	AEUUIU45	Archaeoglobu s fulgidus	A. fulgidus predicted coding	240	36
1624	AL355013	Schizosaccha	region AF0859		
1024	AB333013	romyces	mitochondrial carrier protein	403	34
		pombe			
1625	¥66746	Homo	Mombrano bound	1100	
		sapiens	Membrane-bound protein PRO1198.	1184	100
1626	D90053	Sus scrofa	destrin		100
1627	Y35954	Homo sapiens	Extended human secreted	863	100
		adbreits		756	100
i			protein sequence, SEQ ID NO. 203.		
1628	AL031775	Homo sapiens	dJ30M3.2 (novel protein)	420	100
1629	AF132484	Mus musculus	unknown	470	100
1630	AF017096	Drosophila		286	68
		melanogaster	similar to C. elegans	493	61
	!	c.zuioyaster	R10H10.6 and S. cerevisiae	ļ	ļ
1631	X03077	Homo sapiens	YD8419.03c lactate dehydrogenase-A	1774	
1632	AF151084	Homo sapiens		1704	100
1633	AJ001874		HSPC250	763	100
1634	AC012187	Homo sapiens	orf	255	97
702.1	UCAT5181	Arabidopsis	Contains weak similarity to	143	38
		thaliana	GATA-6 DNA-binding protein		İ
		j	gb H36135, gb Z26200 come	ł	
		i	from this gene.	f	- 1

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	
ID NO:	NUMBER	SPECIES	DESCRIPTION	WATERMAN SCORE	IDENTITY
1635	AF026246	Homo sapiens	HERV-E integrase	111	90
1636	Y50943	Homo sapiens	Human adult brain cDNA clone	1126	95
			ve8_1 derived protein.	1	1 - 3
1637	AF134593	Homo sapiens		2068	99
1638	AJ238247	Mus musculus	putative phosphatase subunit	1948	96
1639	Y94942	Homo sapiens	Human secreted protein clone	1320	100
			yk251_1 protein sequence SEQ ID NO:90.		
1640	AF235030	Homo sapiens	BM88 antigen	766	99
1641	AF233288	Drosophila melanogaster	WDS	358	26
1642	М19351	Mus musculus	immunoglobulin heavy chain binding protein	145	34
1643	¥70452	Homo sapiens	Human membrane channel protein-2 (MECHP-2).	1352	100
1644	AF176520	Mus musculus	WD repeat-containing F-box protein FBW5	2676	88
1645	W67816	Homo sapiens	Human secreted protein encoded by gene 10 clone HCEMU42.	1156	100
1646	X67155	Homo sapiens	mitotic kinase-like protein-l	4456	99
1647	M63180	Homo sapiens		1040	61
1648	Y87342	Homo sapiens	Human signal peptide containing protein HSPP-119 SEQ ID NO:119.	1566	93
1649	R95332	Homo sapiens	Tumor necrosis factor receptor 1 death domain ligand (clone 3TW).	4137	100
1650	AC007136	Homo sapiens	Putative map kinase interacting kinase	856	99
1651	AB015346	Homo sapiens	Eps15R	4464	99
1652	AL161576	Arabidopsis thaliana	putative protein	1341	48
1653	AC005313	Arabidopsis thaliana	putative calmodulin	288	28
1654	AL031428	Homo sapiens	dJ184J9.1 (KIAA0601 protein)	3526	100
1655	AL031428	Homo sapiens	dJ184J9.1 (KIAA0601 protein)	3526	100
1656	AB017910	Dictyosteliu m discoideum	туом	297	32
1657	Y28919	Homo sapiens	Human regulatory protein HRGP-5.	2251	99
1658	AF056191	Homo sapiens	TPA inducible protein	2744	98
1659	U76846	Arabidopsis thaliana	ubiquitin-specific protease	137	35
1660	AL078627	Schizosaccha romyces pombe	actin-like protein; (2 actin domains)	320	34
1662	X52022	Homo sapiens	collagen type VI, alpha 3 Chain	16274	99
1663	AF300648	Homo sapiens	guanine nucleotide binding protein beta subunit 4	1811	100
1664	AF214736	Homo sapiens	EH domain containing protein	2774	100
1665	Z48613	Saccharomyce s cerevisiae	unknown	138	26
1666	AF177385	Homo sapiens	cytochrome c oxidase assembly protein isoform 2	1395	99
1667	AC007842	Homo sapiens	BC331191_1	1581	47
1668	S67513	Borna disease virus BDV, WT-1, Halle Bl/91, horse brain, field isolate,		397	43
		Peptide, 370			

SEQ ID	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-	*
NO:	NOMBER	aa		WATERMAN SCORE	IDENTITY
1669	Z99753	Schizosaccha	putative NOL1-NOP2-sun family	7.20	
		romyces pombe	nucleolar protein	569	47
1670	G03130	Homo sapiens	ID NO: 7211.	427	97
1671	M96625	Gallus gallus	cardiac muscle tensin	1185	54
1673	AF174482 Y51846	Homo sapiens		2005	99
1674	AF255334	Homo sapiens	fragment.	233	29
1675	Y94867	Homo sapiens	EXP35	152	29
1676		Homo sapiens	Human protein clone HP10563.	109	30
	Y25712	Homo sapiens	Human secreted protein encoded from gene 2.	3043	99
1677	Y25712	Homo sapiens	Human secreted protein encoded from gene 2.	1580	91
1678	AF163151	Homo sapiens	dentin sialophosphoprotein precursor	170	17
1679	AF163151	Homo sapiens	dentin sialophosphoprotein precursor	170	17
1680	AK024453	Homo sapiens	FLJ00045 protein	1349	100
1681	AF019236	Dictyosteliu m discoideum	TipD	613	34
1682	AJ243459	Leishmania major	proteophosphoglycan	153	26
1683	Z69369	Schizosaccha romyces pombe	putative GTP-binding protein	560	46
1684	X94910	Homo sapiens	ERp28	1334	100
1685	AF286475	Takifugu	retinitis pigmentosa GTPase	196	19
1686	177-01-0	rubripes	regulator-like protein] **
1687	AF191298 AJ275986	Homo sapiens	vacuolar sorting protein 35	4087	100
1688	AJ275986	Homo sapiens	transcription factor	2958	100
1689	X07311	Drosophila	transcription factor heat shock protein	1886	88
1690	AF240463	melanogaster Rattus		138	43
1691	AJ272078	norvegicus Homo sapiens	LIS1-interacting protein NUDE1	1383	83
1692	AJ272079	Homo sapiens	APOBEC-1 stimulating protein	1256	68
1693	AF177942	Xenopus laevis	APOBEC-1 stimulating protein katanin p60	1336 1664	60 66
1694	AF263539	Homo sapiens	arginine N-methyltransferase	1774	
1695	AF222689	Homo sapiens	protein arginine N- methyltransferase 1-variant 2	1182	81
1696	AK000193	Homo sapiens	unnamed protein product	1060	100
1697	AB041035	Homo sapiens	kidney superoxide-producing NADPH oxidase	3122	100
1698	AB041035	Homo sapiens	kidney superoxide-producing NADPH oxidase	2181	100
1699	AF025772	Homo sapiens	C2H2 zinc finger protein	488	54
1700	Y44676	Homo sapiens	Human ARF-Related Protein-1 (HARP-1).	938	97
1701	AX022407	Homo sapiens	unnamed protein product	315	00
1702	AB024574	Homo sapiens	GTP-binding like protein 2	1172	98 100
1703	AF055078	Homo sapiens	zinc finger protein 42	421	52
704	AF198092	Mus musculus	RP42	1057	77
1705	AE003573	Drosophila melanogaster	CG12474 gene product	161	33
1706	AB036345	Drosophila melanogaster	aquaporin	164	24
L707	Y55927	Homo sapiens	Human STLK2 protein.	2146	100
708	027121		G12		47
.709	AL391710	Arabidopsis	putative protein		50

TABLE 2

SEO	ACCESSION	SPECIES	DEGGD Y DETGO		
ID	NUMBER	SPECIES	DESCRIPTION	SMITH-	*
NO:				WATERMAN SCORE	IDENTITY
	 	thaliana		SCORE	
1710	B01311	Homo sapiens	Human PRO241 polypeptide.	1649	97
1711	U40750	Mus musculus	formin binding protein 30	4561	85
1712	AJ011118	Mus musculus	skeletal muscle and cardiac	1490	89
	ļ	1	protein	1 - 1 - 1	1 03
1713	AF255303	Homo	membrane-associated nucleic	4416	99
		sapiens	acid binding protein	1	
1714	AF255303	Homo	membrane-associated nucleic	2960	100
4845		sapiens	acid binding protein		
1715	U08227	Rattus	Ras-related protein	511	51
1716	AF168795	norvegicus			
1/16	AF168795	Rattus	schlafen-4	1129	44
1717	AF196304	norvegicus Homo sapiens	- Cinio		
1718	AL355737	Homo sapiens	SUMO-1-specific protease	5804	99
1719	AB029333	Halocynthia	HrPBT-1	1782	100
	ADV25333	roretzi	HTPBT-I	1069	46
1720	AF071317	Mus musculus	COP9 complex subunit 7b		
1721	AJ272215	Homo sapiens	HEYL protein	1297	97
1722	G01982	Homo sapiens	Human secreted protein, SEO	1681	99
			ID NO: 6063.	718	100
1723	AL032643	Caenorhabdit	similar to Uncharacterized	825	
_		is elegans	protein family UPF0034,	023	41
1724	G01972	Homo sapiens	Human secreted protein, SEQ	586	92
			ID NO: 6053.	366	92
1725	Y94441	Homo	Human Adipose Specific	1231	100
		sapiens	Protein 1.	1 2 2 2	100
1726	AF255443	Homo sapiens	CGI-201 protein	4397	99
1727	AF183426	Homo sapiens	HT004 protein	1810	99
1728	D10884	Bos taurus	neurocalcin	1002	99
1729	Z18529	Gallus	tensin	1411	84
1000		gallus	<u> </u>		[
1730	273423	Caenorhabdit	cDNA EST EMBL: Z14908 comes	233	41
	r	is elegans	from this gene-cDNA EST this		
1732	AF090891	Homo sapiens	9ene PR00105		
1733	AJ277724	Homo sapiens	histone deacetylase 8	470	30
1734	G04050	Homo sapiens	Human secreted protein, SEQ	2015	100
	1	bupicing	ID NO: 8131.	503	95
1735	D45913	Mus musculus	leucine-rich-repeat protein	3531	94
1736	AF096709	Drosophila	failed axon connections	276	32
		virilis	protein	2.0	32
1737	AF195120	Homo sapiens	dynactin p62 subunit	2417	99
1738	L15314	Caenorhabdit	contains similarity to Pfam	206	37
		is elegans	family PF01772 N=1]	
1739	X54618	Listeria	phosphadidylinositol specific	134	27
		monocytogene	phospholipase C]	J
1746	NI OZZICEO	5		<u> </u>	
1740	AL031658	Homo sapiens	dJ310013.4 (novel protein	123	31
ļ			similar to predicted C.		1
- 1			elegans an C. intestinalis] [1
1741	Y35924	Homo sapiens	proteins)		
		sabrana	Extended human secreted protein sequence, SEQ ID NO.	1013	99
J	1	ļ	173.	ļ	
1742	AC013354	Arabidopsis	F15H18.15	202	
l		thaliana		***	32
1743	W75771	Ното	Human GTP binding protein	1932	59
	į	sapiens	APDO8.	2556	55
1744	W75771	Homo	Human GTP binding protein	1854	61
	<u> </u>	sapiens	APDO8.	-054	· ·
1745	AF221098	Homo	Ral guanine nucleotide	1224	70
		sapiens	exchange factor RalGPS1A	·	1
1746	Y99372	Homo sapiens	Human PRO1430 (UNQ736) amino	1332	99
747	V04004		acid sequence SEQ ID NO:116.		1
L747	Y94294	Homo sapiens	Human coenzyme A-utilising	842	100

TABLE 2

SEO	ACCESSION	SPECIES			· .
ID	NUMBER	SEECTES	DESCRIPTION	SMITH-	\$
NO:		1		WATERMAN	IDENTITY
			enzyme CoAEN-2.	SCORE	
1748	AK024436	Homo sapiens	FLJ00026 protein	1619	
1749	AE000877	Methanobacte	conserved protein	231	36
		rium	process	231	36
1		thermoautotr	-	1	
L		ophicum		·	
1750	AF101361	Drosophila	Abnormal X segregation	193	33
		melanogaster	·]	1 233	33
1751	Y15067	Homo sapiens		889	100
1752	AF251038	Homo sapiens	GAP-like protein	822	100
1753	AC003093	Homo sapiens	OXYSTEROL-BINDING PROTEIN:	352	57
1			45% similarity to P22059	1 332	31
			(PID:g129308)	1	1
1754	X69089	Homo sapiens	165kD protein	5703	99
1755	AL049795	Homo sapiens	dJ622L5.3 (novel protein)	1039	100
1756	AL031393	Homo sapiens	dJ733D15.1 (Zinc-finger	2765	100
			protein)	2,03	100
1757	AB040672	Homo sapiens	UDP-GalNAc: polypeptide N-	2020	99
	1		acetylgalactosaminyltransfera	2020	1 33
		}	se		
1758	AL022238	Homo sapiens	dJ1042K10.4 (novel protein)	776	43
1759	AF117653	Homo sapiens	double homeobox protein	375	54
1760	¥12065	Homo sapiens	hNop56	2959	99
1761	AL049712	Homo sapiens	dJ686C3.2 (nucleolar protein	2595	99
		1	hNop56)	2333	33
1762	AC002394	Homo	Gene product with similarity	1542	51
		sapiens	to dynein beta subunit	1342	31
1763	AF169017	Homo sapiens	formiminotransferase	877	100
		<u></u>	cyclodeaminase	• · ·	1 200
1764	U91541	Homo sapiens	human formiminotransferase	596	100
ļ	ļ		cyclodeaminase (ftcd)protein,	1 .	1 -00
1765	-		carboxy-terminal end	1	
1765	AB013365	Bacillus	YlqF	350	34
1766	W2 6 4 6 7	halodurans	<u> </u>		"
1/00	Y38421	Homo sapiens	Human secreted protein	145	71
1767	AC009176		encoded by gene No. 36.		
1,0,	ACOUST /6	Arabidopsis	putative ribulose-1,5-	216	27
}	1	thaliana	bisphosphate	1	
			carboxylase/oxygenase small	.]	
1768	AK000647	Homo sapiens	subunit N-methyltransferase I		
1769	AJ238982	Homo sapiens	unnamed protein product	737	99
1770	U73522	Homo sapiens	VNN3 protein	2665	99
1771	U89435	Mus musculus	AMSH	1214	56
1772	\$70011	Rattus sp.	unknown	829	86
1773	AL035086	Homo sapiens	tricarboxylate carrier	1604	95
1774	Y99426	Homo sapiens	dJ44A20.2 (novel protein)	2036	100
-		sabtens	Human PRO1604 (UNQ785) amino	1057 .	99
1775	AF110330	Homo sapiens	acid sequence SEQ ID NO:308. glutaminase		
1776	AJ269529	Homo sapiens	glycarol 3 sheets	3146	100
1777	Z81579	Caenorhabdit	glycerol 3-phosphate permease cDNA EST yk76f1.5 comes from	2787	100
		is elegans	this gene	232	31
1778	AY007239	Homo sapiens	monooxygenase X	1000	
1779	AL109608	Schizosaccha	oxysterol-binding protein	1875	99
		romyces	family	644	38
	J	pombe		ļ	
1780	AF254260	Homo sapiens	tuftelin 1 ·	1726	
1781	L07924	Mus musculus	guanine nucleotide	1729	100
	İ		dissociation stimulator	247	50
1782	AF295773	Homo	ral guanine nucleotide		
	1	sapiens	dissociation stimulator	142	49.
1783	AK024475	Homo sapiens	FLJ00068 protein	4333	
1784	AK024475		FLJ00068 protein		100
1785			Human secreted protein, SEQ		93
		- 1	ID NO: 8014.	570	100
1786	S82637		Ig lambda-like gene/beta-	247	
				441	100

TABLE 2

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	*
ID	NUMBER		f	WATERMAN	IDENTITY
NO:				SCORE	
			glucuronidase exon 11 homolog		

TRADOCS:1416280.1(%CT4011.DOC)

TABLE 3

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
2	BL00240	Receptor tyrosine kinase	BL00240B 24.70 8.250e-
3	PR00109	class III proteins. TYROSINE KINASE CATALYTIC DOMAIN	12 157-181 PR00109D 17.04 8.085e- 13 358-381
4	BL00028	SIGNATURE Zinc finger, CZH2 type, domain proteins.	BL00028 16.07 9.400e- 10 1129-1146 BL00028 16.07 1.257e-09 820- 837
5	BL00023	Type II fibronectin collagen-binding domain proteins.	BL00023 24.31 8.920e- 33 413-450 BL00023 24.31 4.545e-27 353- 390
6	BL00023	Type II fibronectin collagen-binding domain proteins.	BL00023 24.31 8.920e- 33 413-450 BL00023 24.31 4.545e-27 353- 390
7	BL00023	Type II fibronectin collagen-binding domain proteins.	BL00023 24.31 8.920e- 33 413-450 BL00023 24.31 4.545e-27 353- 390
8	BL00023	Type II fibronectin collagen-binding domain proteins.	BL00023 24.31 8.920e- 33 413-450 BL00023 24.31 4.545e-27 353- 390
9	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 5.119e- 09 863-917
10	PR00464	B-CLASS P450 GROUP II SIGNATURE	PR00464D 17.40 6.182e- 12 294-312 PR00464G 12.41 4.231e-11 377- 393
11	PR00734	GLYCOSYL HYDROLASE FAMILY 7 SIGNATURE	PR00734I 11.46 4.296e-
12	PF00023	Ank repeat proteins.	PF00023B 14.20 6.500e- 10 89-99 PF00023B 14.20 2.636e-09 56-66
14	DM00031	IMMUNOGLOBULIN V REGION.	DM00031B 15.41 3.848e- 09 79-113
15	PR00208	GLIADIN AND LMW GLUTENIN SUPERFAMILY SIGNATURE	PR00208A 12.59 9.868e- 10 517-535 PR00208A 12.59 2.233e-09 520- 538
17	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 8.200e- 14 282-295 PD00066 13.92 9.400e-14 477- 490 PD00066 13.92 6.500e-13 505-518 PD00066 13.92 9.500e- 13 254-267 PD00066 13.92 1.429e-12 393- 406 PD00066 13.92 6.571e-12 421-434
18	BL00845	CAP-Gly domain proteins.	BL00845 16.43 2.200e- 25 55-80
20	BL00487	IMP dehydrogenase / GMP reductase proteins.	BL00487E 16.12 5.737e- 26 154-199 BL00487F 18.79 8.984e-22 235- 276 BL00487G 26.82 4.082e-12 287-329
21	BL00487	IMP dehydrogenase / GMP reductase proteins.	BL00487E 16.12 5.737e- 26 154-199 BL00487F 18.79 8.984e-22 235- 276 BL00487G 26.82 4.082e-12 348-390
22	BL00107	Protein kinases ATP- binding region proteins.	BL00107A 18.39 3.250e- 26 302-333

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
	NO.		
23	BL00107	Protein kinases ATP-	BL00107A 18.39 3.250e-
25	-	binding region proteins.	26 302-333
23	BL00115	Bukaryotic RNA	BL00115T 8.45 7.273e-
į		polymerase II heptapeptide repeat	29 1208-1242 BL00115Q
	•	proteins.	18.08 2.776e-21 953-
		processa.	983 BL00115Y 11.86 8.000e-17 1604-1650
}		1	BL00115M 19.19 8.130e-
		<u> </u>	16 731-774 BL00115H
			14.34 9.392e-16 463-
			496 BL00115A 15.44
			7.414e-15 43-82
		· į	BL00115R 6.50 6.128e-
	1	· ·	14 983-1010 BL00115J
		1	16.71 9.289e-14 591-
	1		617 BL00115I 8.33
			4.336e-13 535-590 BL00115L 12.25 5.939e-
		1	13 662-694 BL00115G
			11.65 6.011e-13 435-
	1	1	463 BL00115K 15.03
			3.417e-10 617-659
			BL001150 16.76 5.805e-
			10 863-913 BL00115P
			11.54 7.538e-10 913-
			953 BL00115S 18.24
			7.968e-10 1010-1052
•			BL00115U 10.34 4.475e- 09 1242-1265
26	BL00420	Speract receptor repeat	BL00420A 20.42 4.109e-
		proteins domain	11 81-110 BL00420A
		proteins.	20.42 8.820e-10 84-113
27	BL00050	Ribosomal protein L23	BL00050A 23.71 9.250e-
	1	proteins.	27 94-127 BL00050B
	İ		14.81 8.125e-12 133-
28	PR00925	NONHISTONE CHROMOSOMAL	147
		PROTEIN HMG17 FAMILY	PR00925B 3.73 3.089e-
	İ	SIGNATURE	20 12 01
29	PF30756	Putative esterase.	PF00756C 14.12 1.108e-
			09 486-516
32	BL00557	FMN-dependent alpha-	BL00557D 17.76 5.065e-
		hydroxy acid	37 274-316 BL00557A
		dehydrogenases proteins.	35.08 8.909e-29 24-73
			BL00557C 15.59 1.000e-
			28 227-257 BL00557B 21.27 8.898e-22 130-
			169
34	PR00629	SHC PHOSPHOTYROSINE	PR00629E 9.90 5.886e-
		INTERACTION DOMAIN	35 299-328 PR00629F
		SIGNATURE	10.95 8.364e-32 334-
			361 PR00629B 13.66
			3.786e-27 224-247
		1	PR00629A 13.45 8.364e-
			21 206-222 PR00629C
f			3.80 4.000e-12 249-261
ļ		1	PR00629D 12.45 3.739e-
35	PD01270	RECEPTOR FC	PD01270A 17.22 1.000e-
İ		IMMUNOGLOBULIN AFFIN.	40 39-79 PD01270B
			22.18 2.875e-38 94-131
1			PD01270D 24.66 3.700e-
1			34 171-207 PD01270C
ļ			19.54 3.455e-30 137-
36	PD01270	i promove	166
	01210	RECEPTOR FC	PD01270A 17.22 1.000e-
ļ		IMMUNOGLOBULIN AFFIN.	40 39-79 PD01270B
J		<u> </u>	22.18 2.875e-38 94-131

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			PD01270D 24.66 3.700e- 34 171-207 PD01270C 19.54 3.455e-30 137- 166
37	BL00412	Neuromodulin (GAP-43) proteins.	BL00412C 10.28 9.241e- 10 264-298
38	BL00412	Neuromodulin (GAP-43) proteins.	BL00412C 10.28 9.241e- 10 264-298
39	BL00412	Neuromodulin (GAP-43) proteins.	BL00412C 10.28 9.241e- 10 264-298
40	PR00380	KINESIN HEAVY CHAIN SIGNATURE	PR00380B 12.64 7.366e- 14 342-360 PR00380C 13.18 6.927e-13 375- 394 PR00380D 9.93 2.180e-12 429-451 PR00380A 14.18 5.154e- 12 143-165
44	BL00345	Ets-domain proteins.	BL00345B 21.28 1.000e- 40 239-290 BL00345A 13.96 2.452e-14 204- 223
45	BL00345	Ets-domain proteins.	BL00345B 21.28 1.000e- 40 215-266 BL00345A 13.96 2.452e-14 180- 199
46	DM01551	kw OSTEOINDUCTIVE YOPM MEMBRANE OUTER.	DM01551A 15.63 3.53Be- 26 172-202 DM01551C 14.62 3.571e-17 232- 252 DM01551B 8.84 4.750e-11 214-226
47	PR00876	NEMATODE METALLOTHIONEIN SIGNATURE	PR00876B 7.66 9.328e- 11 246-260
48	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 4.231e- 33 6-45
	BL00972	Ubiquitin carboxyl- terminal hydrolases family 2 proteins.	BL00972D 22.55 7.750e- 19 994-1019 BL00972A 11.93 7.120e-18 216- 234 BL00972E 20.72 9.471e-14 1020-1042 BL00972C 16.48 7.000e- 13 360-375 BL00972B 9.45 8.269e-10 302-312
51	BL00972	Ubiquitin carboxyl- terminal hydrolases family 2 proteins.	BL00972D 22.55 7.750e- 19 990-1015 BL00972A 11.93 7.120e-18 216- 234 BL00972E 20.72 9.471e-14 1016-1038 BL00972C 16.48 7.000e- 13 360-375 BL00972B 9.45 8.269e-10 302-312
52	BL01115	GTP-binding nuclear protein ran proteins.	BL01115A 10.22 3.063e- 14 10-54
53	PR00988	URIDINE KINASE SIGNATURE	PR00988A 6.39 8.500e- 17 20-38 PR00988F 12.23 7.828e-15 196- 210 PR00988C 13.64 6.108e-14 104-120 PR00988E 8.27 3.872e- 11 174-186 PR00988D 5.95 6.878e-10 160-171 PR00988B 11.60 2.915e- 09 57-69
55	PR00762	CHLORIDE CHANNEL SIGNATURE	PR00762C 9.29 4.682e- 21 294-314 PR00762D 11.29 4.103e-19 509- 530 PR00762A 14.22 9.333e-18 199-217

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
	1.0.		PR00762P 15.12 3.100e- 16 563-583 PR00762B
			12.12 6.063e-16 230- 250 PR00762E 12.07
			2.286e-15 545-562 PR00762G 14.13 6.276e-
56	BL00216	Sugar transport	13 601-616 BL00216B 27.64 8.800e-
58	PF00791	Domain present in ZO-1	10 153-203 PF00791B 28.49 2.049e-
		and Unc5-like netrin receptors.	10 1080-1135
59	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791B 28.49 2.049e- 10 1062-1117
61	PD01929	KINASE TYPE RESISTANCE ANTIBIOTIC TRANSFERASE AM.	PD01929E 10.76 9.018e- 09 206-221
68	PR00360	C2 DOMAIN SIGNATURE	PR00360A 14.59 7.395e-
69	PR00360	C2 DOMAIN SIGNATURE	PR00360A 14.59 7.395e- 09 670-683
70	PF00651	BTB (also known as BR- C/Ttk) domain proteins.	PF00651 15.00 8.714e- 10 51-64
72	DM00179	w KINASE ALPHA ADHESION T-CELL.	DM00179 13.97 5.304e- 09 108-118
73	BL00239	Receptor tyrosine kinase class II proteins.	BL00239B 25.15 7.075e- 12 118-166
74	BL00790	Receptor tyrosine kinase class V proteins.	BL00790N 13.25 6.116e-
76	DM00471	0 PROKARYOTIC DNA TOPOISOMERASE I.	DM00471A 11.73 9.357e- 13 53-66 DM00471B 8.45 4.857e-12 70-81
80	PD02876	DECARBOXYLASE PHOSPHATIDYLSERINE.	PD02876C 8.80 2.723e- 13 223-236 PD02876D 12.13 2.588e-12 334- 351
81	PD02876	DECARBOXYLASE PHOSPHATIDYLSERINE.	PD02876C 8.80 2.723e- 13 282-295 PD02876D 12.13 2.588e-12 393- 410
83	BL00708	Prolyl endopeptidase family serine proteins.	BL00708B 24.91 7.197e- 12 570-601
84	PR00014	FIBRONECTIN TYPE III REPEAT SIGNATURE	PR00014C 15.44 8.043e- 09 985-1004
86	PR00678	PI3 KINASE P85 REGULATORY SUBUNIT SIGNATURE	PROD678H 9.13 1.379e- 09 246-269
89	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320C 13.01 8.200e- 09 264-279 PR00320B 12.19 8.650e-09 264- 279
93	BL00455	Putative AMP-binding domain proteins.	BL00455 13.31 2.588e- 14 316-332
95	BL00107	Protein kinases ATP- binding region proteins.	BL00107A 18.39 4.000e- 10 123-154
96	BL00107	Protein kinases ATP- binding region proteins.	BL00107A 18.39 4.000e- 10 212-243
97	PR00081	GLUCOSE/RIBITOL DEHYDROGENASE FAMILY SIGNATURE	PR00081B 10.38 6.318e- 13 134-146 PR00081A
98	.PR00380	KINESIN HEAVY CHAIN SIGNATURE	10.53 2.500e-12 54-72 PR00380A 14.18 5.500e- 24 401-423 PR00380D 9.93 7.188e-20 613-635 PR00380B 12.64 7.517e- 16 529-547 PR00380C 13.18 2.756e-13 560- 579

NO. PR00300 ATP-DEPENDENT CLP PR07EASE APP-SHIDING SUBDATY SIGNATURE SUBDA	SEQ ID NO:	ACCESSION	DECOTOTON	T 000-11-11-11-11-11-11-11-11-11-11-11-11-
PROTEASE ATP-BINDING 14 289-308 15 38-308 15 38		NO.	DESCRIPTION	RESULTS*
SUBNIT SIGNATURE	102	PR00300		PR00300A 9.56 7.545e-
BL00479				14 289-308
diacylglycerol binding 18 288-314 BL00679 19.86 4.310e-13 272-255 178 BL004798 19.86 4.300e-13 272-255 178 BL004798 19.86 4.300e-13 272-255 180 BL004798 12.57 6.29 12 181-19 19.86 4.300e-13 272-255 180 BL001798 13.20 8.01 19	104	BL00479		BL00479B 12 57 6 7869-
Description				
A.300e-13 272-295			domain proteins.	19.86 4.913e-16 155-
BL0019 ADP-ribosylation factors 12 181-197 12 181-197 12 181-197 13 181-197 14 181-197 15 491-197 16 401-197 16 401-197 16 401-197 16 401-197 16 401-197 16 401-197 16 401-197 16 401-197 16 401-197 17 181-197 16 401-197 17 181-197 16 401-197 17 181				178 BL00479A 19.86
106 BL01019 ADP-ribosylation factors BL01019A 13.20 8.01	j		}	
106 BL01019 ADP-ribosylation factors EL01019A 13.20 8.01				BL00479B 12.57 6.294c-
Second Color Seco	106	BL01019	ADP-ribosylation factors	RL010192 22 20 9 0125
ENDOSOMAL III. 16 403-416 16 403-416 17 18 10 18 17 18 19 11 13 17 18 19 11 13 17 18 19 11 13 17 18 19 18 19 18 19 18 19 18 19 18 19 18 19 18 19 18 19 18 19 18 19 18 19 18 19 18 18			family proteins.	
Nosomal III. 16 403-416	107	DM01970	0 kw ZK632.12 YDR313C	DM01970B 8.60 5.000e-
heme-binding domain proteins. 11.37 6.447e-17 182 204	100	-		
Proteins	108	BL00191	Cytochrome b5 family,	
109				
PRO1066			process.	
SINDING NU. Scorpion short toxins BL01138A 10.96 8.29 10.38-50 10.33-19.100e-14 225-241 117 BL00214 Cytosolic fatty-acid BL00214B 26.51 1.00 10.33 19.100e-14 225-241 117 BL00214 Cytosolic fatty-acid BL00214B 26.51 1.00 10.38-30 10.38-30 10.38-56 10.38-56 10.38-56 10.38-56 10.38-56 10.38-56 10.38-56 10.38-56 10.38-57 10.38-56 10.38-57 10.3	109	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 4.938e-
BL01138 Scorpion short toxins BL01138A 10.96 8.29 10.38-50 10.38-50 10.38-50 10.38-50 10.38-50 10.38-50 10.38-50 10.38-50 10.38-50 10.38-50 10.38-50 10.38-50 10.38-50 10.38-50 10.38-50 10.38-50 10.38-50 10.33.1 9.100e-14 225-241 117 BL00214 Cytosolic fatty-acid BL00107A 18.39 8.56 10.100e-14 225-11 5-3: 10.100e-14			ZINC-FINGER METAL-	
Proteins 10 38-50	110	1		1
BL00107 Protein kinases ATP-binding region proteins 23 156-187 BL001071 21 313 19 100e-14 225-241 225-241 225-241 225-241 240-241 240-241 241-241	110	Br01138		BL01138A 10.96 8.297e-
BL00214 Cytosolic fatty-acid BL00214 225. 241 13.31 9.100e-14 225. 241 13.31 9.100e-14 225. 241 13.31 9.100e-14 225. 241 13.31 9.100e-14 225. 241 13.31 9.100e-14 225. 241 13.31 9.100e-14 225. 241 13.31 9.100e-14 225. 241 13.31 9.100e-14 225. 241 13.31 9.100e-14 225. 241 14.51	113	BL-00107	Protein kingge amp	
13.31 9.100e-14 225. 241		EBOOTO /	binding region proteins	
117 BL00214 Cytosolic fatty-acid binding proteins. 17 46-91 BL00214B 26.51 1.001 binding proteins. 17 46-91 BL00214A 21.17 7.052e-11 5-3:			region processis.	
Dinding proteins 17 46-91 BL00214A 21.17 7.052e-11 5-3; 100 17 46-91 BL00214A 21.17 7.052e-11 5-3; 119 PR00529 GONADOTROPHIN RELEASING RR00529C 11.03 7.506 10 158-177 10 158-177 10 475-496 10 158-177 10 475-496 10 158-177 10 475-496 10 158-177 10 475-496 10 158-177 10 475-496 10 158-177 10 158-17		<u></u>		
118 BL00107 Protein kinases ATP- binding region proteins. 13 dc-67	117	BL00214		BL00214B 26.51 1.000e-
BL00107		ì	binding proteins.	
Dinding region proteins. 13 36-67	118	B1.00107	Protein kinases ATB	
PR00529 GONADOTROPHIN RELEASING HORMONE RECEPTOR SIGNATURE 10 158-177 10 15		2200107		
HORMONE RECEPTOR 10 158-177	119	PR00529		
PR00320 G-PROTEIN BETA WD-40 PR00320C 13.01 9.400 REPEAT SIGNATURE 09 80-95 REPEAT SIGNATURE 09 80-95 REPEAT SIGNATURE 09 80-95 REPEAT SIGNATURE 09 80-95 BL00215 Mitochondrial energy BL00215A 15.82 7.156 transfer proteins. 13 216-241 128 BL01032 Protein phosphatase 2C BL01032C 6.14 3.1956 12 147-157 BL0032E 8.33 8.932e-11 282-296 BL01032I 10.42 8.902 09 379-389 BL01310 ATPIGI / PLM / MAT8 BL01310 14.74 6.694e family proteins. 26 28-64 PR00990B 12.32 9.534 15 47-67 PR00990A 16.23 5.500e-14 20-4 PR00990C 12.62 2.412 09 119-133 BL00880 Acyl-CoA-binding BL00880 T.52 5.575e PR00990B 12.32 9.534 Tegion RNP-1 proteins. 14 18-37 PR00990B 12.32 9.308 Tegion RNP-1 proteins. 14 18-37 PR00215C 13.98 6.779 136 BL01310 ATPIGI / PLM / MAT8 BL00030A 14.39 9.308 Tegion RNP-1 proteins. PR00215C 13.98 6.779 136 BL01310 ATPIGI / PLM / MAT8 BL01310 14.74 2.432e Tegion RNP-1 proteins. PR00215C 13.98 6.779 136 BL0028 Tegion RNP-1 PLM / MAT8 BL01310 14.74 2.432e Tegion RNP-1 PLM / MAT8 BL01310 14.74 2.432e Tegion RNP-1 PLM / MAT8 BL01310 14.74 2.432e Tegion RNP-1 PLM / MAT8 BL01310 14.74 2.432e Tegion RNP-1 PLM / MAT8 BL01310 14.74 2.432e Tegion RNP-1 PLM / MAT8 Tegion RNP-1 PLM / MAT8 BL01310 14.74 2.432e Tegion RNP-1 PLM / MAT8 Tegion RNP-1 PLM / MAT8 BL01310 14.74 2.432e Tegion RNP-1 PLM / MAT8 Tegion RNP-1 PLM / MA		•		
REPEAT SIGNATURE 09 80-95	120	DD 0000		
PR00320 G-PROTEIN BETA WD-40 PR00320C 13.01 9.400 REPEAT SIGNATURE 09 80-95	120	PR00320		
REPEAT SIGNATURE 09 80-95 127 BL00215 Mitochondrial energy BL00215A 15.82 7.158 13 216-241 13 216-241 13 216-241 13 216-241 128 BL01032 Protein phosphatase 2C BL01032C 6.14 3.1956 12 147-157 BL01032E 11.25 5.680e-11 318 331 BL01032G 8.33 8.932e-11 282-296 BL01032I 10.42 8.902 09 379-389 BL01032I 10.42 8.902 09 379-389 BL01032I 10.42 8.902 09 379-389 BL01032I 10.42 8.902 130 PR00990 RIBOKINASE SIGNATURE PR00990B 12.32 9.534 15 47-67 PR00990A 16.23 5.500e-14 20-4 PR00990C 12.62 2.412 09 119-133 BL00880 Acyl-CoA-binding BL00880 17.52 5.5756 26 72-122 134 BL00030 Eukaryotic RNA-binding BL00030A 14.39 9.308 region RNP-1 proteins 14 18-37 14 18-37 155 PR00215 NEUROMODULIN SIGNATURE PR00215C 13.98 6.779 10 475-496 BL01310 ATP1G1 / PLM / MAT8 BL01310 14.74 2.432e 29 71-107 2 inc finger, C2H2 type, BL00028 16.07 7.882e 14 214-231 BL00028 16.07 9.471e-14 102-	121	PR00320		
Transfer proteins. 13 216-241 158 15 216-241 17 216 17		ļ		
BL01032 Protein phosphatase 2C BL01032C 6.14 3.195e 12 147-157 BL01032E 11.25 5.680e-11 318-331 BL01032G 8.33 8.932e-11 282-296 BL01032I 10.42 8.902 09 379-389 129 BL01310 ATPIGI / PLM / MAT8 BL01310 14.74 6.694e family proteins. 26 28-64 28-64 PR00990B 12.32 9.534 15 47-67 PR00990A 16.23 5.500e-14 20-4 PR00990C 12.62 2.412 09 119-133 133 BL00880 Acyl-coa-binding BL00880 17.52 5.575e 26 72-122 134 BL0030 Eukaryotic RNA-binding BL0030A 14.39 9.308 27 2-122 135 PR00215 NEUROMODULIN SIGNATURE PR00215C 13.98 6.779 10 475-496 136 BL01310 ATPIGI / PLM / MAT8 BL0032B 16.07 7.882e domain proteins. 14 214-231 BL00028 16.07 9.471e-14 102-	127	BL00215		BL00215A 15.82 7.158e-
proteins. 12 147-157 BL01032E 11.25 5.680e-11 318-331 BL01032G 8.33 8.932e-11 282-296 BL01310 ATP1G1 / PLM / MAT8 BL01310 14.74 6.694e family proteins. 26 28-64 130 PR00990 RIBOKINASE SIGNATURE PR00990B 12.32 9.534 15 47-67 PR00990A 16.23 5.500e-14 20-4 PR00990C 12.62 2.412 133 BL00880 Acyl-CoA-binding BL00880 17.52 5.575e protein. 26 72-122 134 BL00030 Eukaryotic RNA-binding BL0030A 14.39 9.308 region RNP-1 proteins. 14 18-37 135 PR00215 NEUROMODULIN SIGNATURE PR00215C 13.98 6.779 10 475-496 BL01310 ATP1G1 / PLM / MAT8 BL0032B 14.74 2.432e family proteins. 29 71-107 140 BL00028 Zinc finger, C2H2 type, BL00028 16.07 7.882e domain proteins. 14 214-231 BL00028 16.07 9.471e-14 102-	120	57.01.00	transfer proteins.	
11.25 5.680e-11 318- 331 BL01032G 8.33 8.932e-11 282-296 BL01032I 10.42 8.902 09 379-389 129 BL01310 ATPIGI / PLM / MAT8 BL01310 14.74 6.694e family proteins. 26 28-64 130 PR00990 RIBOKINASE SIGNATURE PR00990B 12.32 9.534 15 47-67 PR00990A 16.23 5.500e-14 20-4 PR00990C 12.62 2.412 09 119-133 133 BL00880 Acyl-CoA-binding BL00880 17.52 5.575e protein. 26 72-122 134 BL00030 Eukaryotic RNA-binding region RNP-1 proteins. 14 18-37 135 PR00215 NEUROMODULIN SIGNATURE PR00215C 13.98 6.779 10 475-496 BL01310 ATPIGI / PLM / MAT8 BL01310 14.74 2.432e family proteins. 29 71-107 140 BL00028 Zinc finger, C2H2 type, BL00028 16.07 7.882e domain proteins. 14 214-231 BL00028 16.07 9.471e-14 102-	120	BF01035		
331 BL01032G 8.33 8.932e-11 282-296 BL01032I 10.42 8.902 09 379-389 BL01310 ATPIGI / PLM / MAT8 BL01310 14.74 6.694e family proteins. 26 28-64 26 28-64 26 28-64 27-67 PR00990B 12.32 9.534 15 47-67 PR00990B 12.32 15 47-67 PR00990B 12.32 15 47-67 PR00990B 12			proceins.	
S.932e-11 282-296		1		
129 BL01310 ATPIGI / PLM / MAT8 BL01310 14.74 6.694e family proteins. 26 28-64				8.932e-11 282-296
BL01310				BL01032I 10.42 8.902e-
Section	129	BI-01310	ATDICI / DIM / Mario	
130 PR00990 RIBOKINASE SIGNATURE PR00990B 12.32 9.534 15 47-67 PR00990A 16.23 5.500e-14 20-4 PR00990C 12.62 2.412 09 119-133 BL00880 Acyl-CoA-binding BL00880 17.52 5.575e protein. 26 72-122 134 BL00030 Eukaryotic RNA-binding Region RNP-1 proteins. 14 18-37 135 PR00215 NEUROMODULIN SIGNATURE PR00215C 13.98 6.779 10 475-496 BL01310 ATP1G1 / PLM / MAT8 BL01310 14.74 2.432e family proteins. 29 71-107 140 BL00028 Zinc finger, C2H2 type, BL00028 16.07 7.882e domain proteins. 14 214-231 BL00028 16.07 9.471e-14 102-		-201310		
15 47-67 PR00990A 16.23 5.500e-14 20-4 PR00990C 12.62 2.412 09 119-133 BL00880 Acyl-CoA-binding BL00880 17.52 5.575e 26 72-122 27 -122 27 -122 28 -122 2	130	PR00990		PR00990B 12.32 9.534e-
PR00990C 12.62 2.412		l	1	15 47-67 PR00990A
133 BL00880 Acyl-CoA-binding BL00880 17.52 5.575e protein. 26 72-122			1	16.23 5.500e-14 20-42
BL00880 Acyl-CoA-binding BL00880 17.52 5.575e 26 72-122			İ	PR00990C 12.62 2.412e-
Protein. 26 72-122	133	BL00880	Acvl-CoA-binding	
BL00030 Eukaryotic RNA-binding region RNP-1 proteins. 14 18-37 135 PR00215 NEUROMODULIN SIGNATURE PR00215C 13.98 6.779 10 475-496 BL01310 ATP1G1 / PLM / MAT8 BL01310 14.74 2.432e family proteins. 29 71-107 140 BL00028 Zinc finger, C2H2 type, domain proteins. 14 214-231 BL00028 16.07 9.471e-14 102-				
region RNP-1 proteins. 14 18-37 PRO0215 NEUROMODULIN SIGNATURE PRO0215C 13.98 6.779 10 475-496 BL01310 ATP1G1 / PLM / MAT8 BL01310 14.74 2.432e family proteins. 29 71-107 Zinc finger, C2H2 type, BL00028 16.07 7.882e domain proteins. 14 214-221 BL00028 16.07 9.471e-14 102-	134	BL00030		BL00030A 14.39 9.308e-
136 BL01310 ATP1G1 / PLM / MAT8 BL01310 14.74 2.432e family proteins. 29 71-107 140 BL00028 Zinc finger, C2H2 type, domain proteins. 14 214-231 BL00028 16.07 9.471e-14 102-	132	Doce	region RNP-1 proteins.	14 18-37
136 BL01310 ATP1G1 / PLM / MAT8 BL01310 14.74 2.432e family proteins. 29 71-107 140 BL00028 Zinc finger, C2H2 type, domain proteins. BL00028 16.07 7.882e-14 214-231 BL00028 16.07 9.471e-14 102-	133	FK00215	NEUROMODULIN SIGNATURE	PR00215C 13.98 6.779e-
family proteins. 29 71-107 140 BL00028 Zinc finger, C2H2 type, BL00028 16.07 7.882e domain proteins. 14 214-231 BL00028 16.07 9.471e-14 102-	136	BL01310	ATPICI / DIM / MAME	
140 BL00028 Zinc finger, C2H2 type, BL00028 16.07 7.882e domain proteins. 14 214-231 BL00028 16.07 9.471e-14 102-				
domain proteins. 14 214-231 BL00028 16.07 9.471e-14 102-	140	BL00028		
16.07 9.471e-14 102-				
	ļ			16.07 9.471e-14 102-
				119 BL00028 16.07
2.800e-13 18-35				2.800e-13 18-35

SEQ ID NO	: ACCESSION	DESCRIPTION	DECIT TO
250 10 80	NO.	DESCRIPTION	RESULTS*
			BL00028 16.07 5.500e-
		· ·	13 74-91 BL00028
		1	16.07 9.100e-13 186-
		1	203 BL00028 16.07
			8.043e-12 46-63
			BL00028 16.07 8.435e-
		1	12 130-147 BL00028
	<u> </u>		16.07 9.217e-12 270-
		· ·	287 BL00028 16.07
		ľ	6.192e-11 242-259
			BL00028 16.07 4.000e-
141			10 158-175
141	BL00501	Signal peptidases I	BL00501D 16.69 9.538e-
		serine proteins.	14 113-133 BL00501C
143	BL01020	SAR1 family proteins.	9.61 8.688e-10 89-101 BL01020C 15.35 7.722e-
143	PP01050	SARI ramily proteins.	20 79-130
146	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 6.400e-
140	EDOTORO	ZINC-FINGER METAL-	25 335-374
		BINDING NU.	25 335-374
149	BL00126	3'5'-cyclic nucleotide	BL00126C 22.07 1.450e-
	2200120	phosphcdiesterases	25 509-550 BL00126E
		proteins,	35.22 3.951e-16 654-
	·		709 BL00126D 25.50
			1.360e-15 565-604
			BL00126B 15.20 8.200e-
			11 483-495 BL00126A
		· ·	27.56 8.269e-11 442-
			479
151	BL00632	Ribosomal protein S4	BL00632 23.79 5.271e-
		proteins.	20 106-149
154	BL00559	Eukaryotic molybdopterin	BL005591 13.63 5.304e-
		oxidoreductases	19 29-58 BL00559K
		proteins.	13.17 2.957e-18 172-
		[-	199 BL00559J 19.63
			8.385e-13 99-151
			BL00559L 13.60 5.814e-
			12 241-259
155	PR00449	TRANSFORMING PROTEIN P21	PR00449A 13.20 1.692e-
1.00		RAS SIGNATURE	13 13-35
157	BL00406	Actins proteins.	BL00406D 12.58 2.547e-
		İ	18 275-330 BL00406A
	*		9.95 5.776e-16 15-50
			BL00406B 5.47 7.429e-
	1		12 69-124 BL00406C
160	BL00132	7/	6.75 9.682e-12 128-183
100	· PDUUT35	Zinc carboxypeptidases,	BL00132A 26.07 7.000e-
	1	zinc-binding region 1 proteins.	14 22-63 BL00132C 21.35 3.466e-12 104-
	1	processis.	21.35 3.466e-12 104- 145
165	PR00109	TYROSINE KINASE	PR00109B 12.27 9.043e-
		CATALYTIC DOMAIN	13 139-158
		SIGNATURE	1 139-130
168	BL00362	Ribosomal protein S15	BL00362 24.67 9.700e-
-	=====	proteins.	15 129-172
169	BL00039	DEAD-box subfamily ATP-	BL00039D 21.67 1.000e-
		dependent helicases	35 640-686 BL00039A
		proteins.	18.44 1.964e-13 212
	1		251 BL00039B 19.19
			4.553e-13 378-404
		1	BL00039C 15.63 8.773e-
			12 465-489
175	PR00449	TRANSFORMING PROTEIN P21	PR00449A 13.20 3.721e-
		RAS SIGNATURE	12 14-36
178	BL01310	ATP1G1 / PLM / MAT8	BL01310 14.74 2.432e-
		family proteins.	29 133-169
179	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 9.455e-
		ZINC-FINGER METAL-	36 6-45
			

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
L	NO.	DESCRIPTION	RESULIS.
		BINDING NU.	
180	PR00007	COMPLEMENT CIQ DOMAIN	PR00007B 14.16 7.429e-
1	1	SIGNATURE	20 160-180 PR00007A
ļ			19.33 4.938e-19 133-
	1		160 PR00007C 15.60
			1.225e-15 206-228
	·		PR00007D 9.64 6.885e-
ļ	Į.		11 238-249
1.81.	BL00027	'Homeobox' domain	
	BB00027		BL00027 26.43 9.526e-
182		proteins.	24 280-323
102	BL00027	'Homeobox' domain	BL00027 26.43 9.526e-
		proteins.	24 263-306
183	BL00027	'Homeobox' domain	BL00027 26.43 9.526e-
<u></u>		proteins.	24 280-323
184	BL00027	'Homeobox' domain	BL00027 26.43 9.526e-
		proteins.	24 263-306
188	PR00929	AT-HOOK-LIKE DOMAIN	PR00929C 5.26 3.328e-
1		SIGNATURE	09 460-471
189	PR00929	AT-HOOK-LIKE DOMAIN	PR00929C 5.26 3.328e-
		SIGNATURE	,
190	BL00383		09 440-451
	2500363	Tyrosine specific	BL00383F 15.51 7.188e-
	1	protein phosphatases	17 666-682 BL00383A
		proteins.	13.34 8.714e-17 162-
		ĺ	177 BL00383E 10.35
	1		1.000e-14 333-344
	1		BL00383E 10.35 7.300e-
•	1		14 628-639 BL00383F
			15.51 1.720e-13 371-
	1		387 BL00383C 10.10
	ĺ		3.000e-13 217-228
	i		BL00383D 11.92 7.000e-
			13 295-308 BL00383B
			7.61 1.692e-11 187-196
			BL00383C 10.10 1.750e-
			09 509-520 BL00383D
			11.92 4.000e-09 589-
		i	
		1	602 BL00383B 7.61
191	PR00450	RECOVERIN FAMILY	8.000e-09 479-488
	1.00430		PR00450C 12.22 7.911e-
	1	SIGNATURE	15 83-105 PR00450C
193	DDOORE		12.22 6.286e-13 47-69
133	PF00564	Octicosapeptide repeat	PF00564B 24.74 6.164e-
		proteins.	16 227-278
194	PR00503	BROMODOMAIN SIGNATURE	PR00503D 20.81 9.156e-
	l	['	15 204-224 PR00503B
	ĺ		9.96 9.571e-13 170-187
195	BL00901	Cysteine	BL00901C 20.63 3.429e-
		synthase/cystathionine	18 67-117
		beta-synthase P-	1 3 4/-11/
		phosphate att.	1
197	BL00636		DY OAKS S
		Nt-dnaJ domain proteins.	BL00636A 8.07 6.211e-
			17 40-57 BL00636B
198	DDAGGG		15.11 2.000e-13 67-88
-70	PR00690	ADHESIN FAMILY SIGNATURE	PR00690A 10.86 9.866e-
100			09 463-482
199	BL01131	Ribosomal RNA adenine	BL01131A 26.62 2.343e-
		dimethylases proteins.	12 84-130
201	PR00910	LUTEOVIRUS ORF6 PROTEIN	PR00910A 2.51 8.352e-
		SIGNATURE	12 509-522
203	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 2.286e-
1	-		10 20 77
206	PR00261	TOM DEMOVEMENT TO THE	10 39-72
		LOW DENSITY LIPOPROTEIN	PR00261A 11.02 4.462e-
ļ		(LDL) RECEPTOR SIGNATURE	19 65-87 PR00261C
ſ			11.37 9.308e-19 65-87
ŀ			PR00261D 12.47 2.667e-
		1	18 65-87 PR00261B
ŀ		1	14.12 4.000e-18 143-
			165 PR00261A 11.02
			- 111172021 21,72

SEQ ID	NO: ACCESSION	DESCRIPTION	1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
	NO.	BESCRIPTION	RESULTS*
ĺ			4.833e-18 143-165
			PR00261D 12.47 7.500e-
i			18 143-165 PR00261B
l		•	14.12 5.065e-16 65-87
			PR00261C 11.37 8.967e-
ļ			16 143-165 PR00261F
1			11.57 4.938e-13 143-
i			165 PR00261E 11.08
İ	1		7.188e-13 65-87
l			PR00261F 11.57 7.188e-
			13 65-87 PR00261E
		1	11.08 1.643e-11 143-
209			165
209	PF00791	Domain present in ZO-1	PF00791B 28.49 6.143e-
		and Unc5-like netrin	13 118-173 PF00791C
		receptors.	20.98 7.680e-10 132-
211	770000		171
211	PR00007	COMPLEMENT CLQ DOMAIN	PR00007A 19.33 5.781e-
'		SIGNATURE	19 131-158 PR00007B
			14.16 4.115e-18 158-
			178 PR00007C 15.60
		•	1.675e-15 201-223
			PR00007D 9.64 7.231e-
212	BY 00-		11 233-244
214	BL00183	Ubiquitin-conjugating	BL00183 28.97 1.545e-
213		enzymes proteins.	30 43-91
213	BL00183	Ubiquitin-conjugating	BL00183 28.97 1.545e-
0.00		enzymes proteins.	30 43-91
215	BL00039	DEAD-box subfamily ATP-	BL00039D 21.67 1.900e-
	ļ	dependent helicases	29 568-614 BL00039A
		proteins.	18.44 1.871e-23 21-60
			BL00039C 15.63 1.720e-
			11 364-388 BL00039B
	•		19.19 4.064e-11 277-
217	117 000 00		303
211	BL00100	Chloramphenicol	BL00100D 17.22 8.484e-
		acetyltransferase	09 68-106
219	PR00213	proteins.	
	FRUUZIS	MYELIN PO PROTEIN	PR00213C 15.94 3.969e-
222	BL00678	SIGNATURE	11 199-227
~~~	PP000 /9	Trp-Asp (WD) repeat	BL00678 9.67 1.947e-09
224	PR00875	proteins proteins.	144-155
	PR008/5	MOLLUSC METALLOTHIONEIN	PR00875A 5.83 1.000e-
225	DY 00505	SIGNATURE	09 901-913
-23	BF00636	Nt-dnaJ domain proteins.	BL00636B 15.11 8.200e-
226	07.00.55		19 18-39
240	BL00636	Nt-dnaJ domain proteins.	BL00636A 8.07 1.000e-
	1	i	21 21-38 BL00636B
220	D7005		15.11 8.200e-19 45-66
229	PR00301	70 KD HEAT SHOCK PROTEIN	PR00301F 13.98 7.563e-
		SIGNATURE	13 329-346 PR00301G
			13.78 4.300e-12 361-
220		<u> </u>	382
230	BL00460	Glutathione peroxidases	BL00460A 28.67 8.773e-
	}	selenocysteine proteins.	20 35-70 BL00460B
		· ·	9.73 7.429e-16 78-96
			BL00460C 14.35 2.831e-
			12 111-134 BL00460D
			16.89 8.773e-11 140-
		1	160
231	PR00647	SENR ORPHAN RECEPTOR	PR00647B 10.19 8.522e-
		SIGNATURE	09 273-287
233	BL00292	Cyclins proteins.	BL00292B 20.31 7.429e-
	1		27 244-275 BL00292A
	· ·	1	22.87 7.750e-27 201-
		1	235
34	PR00449	TRANSFORMING PROTEIN P21	PR00449A 13.20 6.308e-
	i	RAS SIGNATURE	13 7-29 PR00449C
			, 22 ********************************

SEQ ID N	O: ACCESSION	DESCRIPTION	
	NO.	DESCRIPTION	RESULTS*
			17.27 4.462e-11 47-70 PR00449D 10.79 7.120e- 11 109-123
235	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019B 11.36 7.300e- 10 251-265 PR00019B 11.36 5.320e-09 119- 133 PR00019B 11.36 1.000e-08 229-243
236	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019B 11.36 7.300c- 10 245-259 PR00019B 11.36 5.320e-09 113- 127 PR00019B 11.36 1.000e-08 223-237
237	PD00289	PROTEIN SH3 DOMAIN REPEAT PRESYNA.	PD00289 9.97 8.448e-09
240	PR00011	TYPE III EGF-LIKE SIGNATURE	PR00011D 14.03 3.492e-
241	PR00011	TYPE III EGF-LIKE SIGNATURE	PR00011D 14.03 3.492e-
244	BL00903	Cytidine and deoxycytidylate deaminases zinc-binding region s.	BL00903 12.93 8.941e- 12 54-64
245	DM00179	w KINASE ALPHA ADHESION T-CELL.	DM00179 13.97 8.043e-
248	BL00246	Wnt-1 family proteins.	BL00246D 23.97 1.000e- 40 186-239 BL00246E 20.32 1.000e-40 305- 351 BL00246B 13.69 4.176e-36 105-140 BL00246A 15.75 2.286e- 24 70-90 BL00246C 15.56 4.857e-22 150- 175
250	PR00927	ADENINE NUCLEOTIDE TRANSLOCATOR 1 SIGNATURE	PR00927E 14.93 5.114c-
254	BL00674	AAA-protein family proteins.	BL00674B 4.46 1.000e- 09 223-245
255	PD01796	PROTEIN TRANSMEMBRANE COBALT ZINC CADMIU.	PD01796 15.01 6.045e-
256	BL50002	Src homology 3 (SH3) domain proteins profile.	BL50002B 15.18 2.800e- 10 421-435
250	PR00094	ADENYLATE KINASE SIGNATURE	PR00094C 12.94 2.200e- 18 87-104 PR00094D 12.52 2.731e-14 161- 177 PR00094A 10.31 5.500e-14 11-25 PR00094B 11.01 4.115e- 13 39-54 PR00094E 11.25 7.333e-13 178- 193
259	BL00892	HIT family proteins.	BL00892A 18.17 5.500e-
262	BL00388	Proteasome A-type subunits proteins.	BL00388A 23.14 1.000e- 40 8-54 BL00388B 31.38 3.864e-33 66-108 BL00388D 20.71 1.000e- 21 153-184 BL00388C 18.79 8.147e-16 126- 148
264	BL00903	Cytidine and deoxycytidylate deaminases zinc-binding region s.	BL00903 12.93 5.821e- 09 91-101
267	BL00107	Protein kinases ATP- binding region proteins.	BL00107B 13.31 1.529e- 09 241-257
270	BL00226	Intermediate filaments proteins.	BL00226D 19.10 1.000e- 37 362-409 BL00226B

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
	, No.		23.86 8.043e-35 196- 244 BL00226C 13.23 7.000e-20 261-292 BL00226A 12.77 6.143e-
271	PD02952	KINASE TRANSFERASE CHOLINE PROTEIN MULTIGENE FAMI.	15 96-111 PD02952C 15.76 9.731e- L6 235-265 PD02952B 15.57 5.625e-09 215- 229
272	PD02929	ADHESION GLYCOPROTEIN FRECURSOR I.	PD02929A 28.27 1.000e- 40 106-160 PD02929B 18.36 8.800e-17 179- 199
274	BL01027	Glycosyl hydrolases family 39 proteins.	BL01027B 15.34 3.486e- 09 213-250
275	PR00424	ADENOSINE RECEPTOR SIGNATURE	PR00424D 14.32 6.451e- 11 39-59
277	BL00052	Ribosomal protein S7 proteins.	BL00052A 27.85 6.000e- 13 137-184 BL00052B 15.17 5.143e-12 208- 235
279	BL00790	Receptor tyrosine kinase class V proteins.	BL00790N 13.25 5.659e- 13 267-294
280	PR00319	BETA G-PROTBIN (TRANSDUCIN) SIGNATURE	PR00319D 11.64 6.625e- 23 107-125 PR00319C 13.41 1.000e-21 89-105 PR00319A 15.27 8.364e- 21 51-68 PR00319B
281	PR00319	BETA G-PROTEIN (TRANSDUCIN) SIGNATURE	11.47 8.200e-19 70-85 PR00319D 11.64 6.625e- 23 94-112 PR00319C 13.41 1.000e-21 76-92 PR00319A 15.27 8.364e- 21 38-55 PR00319B 11.47 8.200e-19 57-72
287	PF00929	Exonuclease.	PF00929D 16.17 7.366e-
291	BL00326	Tropomyosins proteins.	BL00326A 14.01 2.360e- 09 93-127
292	BL00326	Tropomyosins proteins.	BL00326A 14.01 2.360e- 09 93-127
294	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 8.714e- 12 203-216
295	ЯL0002Я	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 5.500e- 15 322-339 BL00028 16.07 9.471e-14 433- 450 BL00028 16.07 4.600e-13 648-665 BL00028 16.07 5.500e- 13 760-777 BL00028 16.07 9.550e-13 788- 805 BL00028 16.07 3.348e-12 704-721 BL00028 16.07 6.478e- 12 461-478 BL00028 16.07 8.435e-12 844- 861 BL00028 16.07 1.692e-11 593-610 BL00028 16.07 2.038e- 11 211-228 BL00028 16.07 5.154c-11 732- 749 BL00028 16.07 5.846e-11 377-394 BL00028 16.07 6.885e- 11 816-833 BL00028 16.07 7.231e-11 676- 693 BL00028 16.07 9.654e-11 564-581

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
	NO.		· ·
	1		BL00028 16.07 4.086e-
1	1		09 517-534 BL00028
İ	1		16.07 7.429e-09 489-
296	BL00215	Mitochondrial energy	BL00215A 15.82 8.333e-
		transfer proteins.	16 111-136 BL00215A
	ĺ	İ	15.82 2.723e-11 10-35
Í			BL00215B 10.44 9.526e-
			11 152-165 BL00215B
1	ľ		10.44 7.375e-10 59-72 BL00215A 15.82 9.824e-
		ľ	10 205-230
302	PF00953	Glycosyl transferase.	PF00953C 19.70 8.773e-
1			34 236-269 PF00953A
		i	19.68 5.000e-25 102-
			129 PF00953B 6.17
304	PF00152	tRNA synthetases class	1.000e-13 182-194 PF00152D 21.30 8.364e-
		II.	28 422-461 PF00152C
	]	i	28.03 9.250e-21 220-
1	1	}	257 PF00152B 15.67
			2.658e-13 159-184
	1		PF00152A 19.68 5.714e-
305	PD01066	PROTEIN ZINC FINGER	11 44-67
		ZINC-FINGER METAL-	PD01066 19.43 8.250e- 35 37-76
		BINDING NU.	33 37-76
305	PD02784	PROTEIN NUCLEAR	PD02784B 26.46 5.840e-
307	2200121	RIBONUCLEOPROTEIN.	09 92-135
307	PR00454	ETS DOMAIN SIGNATURE	PR00454C 11.24 7.808e-
308	PR00237	RHODOPSIN-LIKE GPCR	09 1167-1186 PR00237E 13.03 5.091e-
		SUPERFAMILY SIGNATURE	13 188-212 PR00237G
			19.63 7.207e-13 268-
			295 PR00237A 11.48
	]		4.375e-11 24-49
			PR00237C 15.69 3.057e-
			10 101-124 PR00237D 8.94 4.750e-10 137-159
	1		PR00237F 13.57 5.364e-
			10 230-255 PR00237B
309	DY 00535		13.50 9.438e-10 57-79
303	BL00522	DNA polymerase family X proteins.	BL00522C 11.90 7.577e-
	ĺ	proceins.	24 315-339 BL00522F
			14.90 1.310e-15 470- 494 BL00522A 25.52
			1.265e-14 179-226
	1	į	BL00522E-19.63 8.615e-
			14 430-460 BL00522B
			27.30 9.625e-12 267-
310	BL00326	Tropomyosins proteins.	313 BL00326D 8.76 5.235e-
•		-p-my-rema processing.	10 856-897
312	BL00290	Immunoglobulins and	BL00290A 20.89 4.706e-
		major histocompatibility	14 151-174 BL00290B
		complex proteins.	13.17 9.000e-12 211-
313	BL00345	Ets-domain proteins.	229
		best domain processs.	BL00345B 21.28 1.000e- 40 34-85 BL00345A
		1	13.96 9.217e-16 1-20
315	PF00651	BTB (also known as BR-	PF00651 15.00 5.091e-
317	DY AT AD-	C/Ttk) domain proteins.	15 63-76
31/	BL01020	SAR1 family proteins.	BL01020C 15.35 3.198e-
318	BL00216	Sugar transport	17 79-130
İ		Sugar transport proteins.	BL00216B 27.64 4.696e- 11 164-214
320	PR00109	TYROSINE KINASE	PR00109B 12.27 4.814e-
		CATALYTIC DOMAIN	10 216-235
		<del></del>	

SEQ ID NO	ACCESSION NO.	DESCRIPTION	RESULTS*
		SIGNATURE	
321	BL00027	'Homeobox' domain proteins.	BL00027 26.43 5.688e- 10 329-372
322	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PR00109B 12.27 8.765e- 12 558-577
324	BL01241	Link domain proteins.	BL01241 35.81 8.313e- 30 183-236 BL01241 35.81 3.222c-13 282- 335
326	BL00412	Neuromodulin (GAP-43) proteins.	BL00412D 16.54 4.000e- 12 515-566 BL00412D 16.54 5.705e-11 516- 567 BL00412D 16.54 7.848e-10 518-569 BL00412D 16.54 1.827e- 09 514-565 BL00412D 16.54 1.918e-09 513- 564 BL00412D 16.54 2.102e-09 520-571
328	BL00232	Cadherins extracellular repeat proteins domain proteins.	BL00232B 32.79 9.557e- 20 151-199 BL00232B 32.79 2.246e-18 41-89 BL00232B 32.79 5.985e- 18 370-418 BL00232B 32.79 5.500e-16 258- 306 BL00232B 32.79 9.384e-15 475-523 BL00232C 10.65 2.537e- 12 256-274 BL00232C 10.65 4.326e-11 368- 386 BL00232C 10.65 7.261e-11 473-491 BL00232C 10.65 7.457e- 11 39-57
330	PR00454	ETS DOMAIN SIGNATURE	PR00454C 11.24 7.808e- 09 1167-1186
331	BL00598	Chromo domain proteins.	BL00598 14.45 8.393e- 18 27-49
333	BL01016	Glycoprotease family proteins.	BL01016C 22.84 3.925e- 32 70-115 BL01016E 14.88 5.286e-19 149- 177 BL01016H 13.71 7.577e-13 291-301 BL01016D 8.86 3.298e- 11 127-140 BL01016G 7.14 5.622e-10 261-271 BL01016A 5.65 7.167e- 10 4-19 BL01016F 13.34 1.563e-09 200- 212 BL01016B 8.93 8.855e-09 38-50
339	BL01115	GTP-binding nuclear protein ran proteins.	BL01115A 10.22 5.500e- 11 17-61
340	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 1.231e- 33 10-49
341	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 5.042e- 09 55-109
342	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 2.400e- 30 16-55
343	DM00031	IMMUNOGLOBULIN V REGION.	DM00031A 16.80 1.000e- 40 20-68
346	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PR00109B 12.27 4.764e- 11 135-154
347	PR00109	TYROSINE KINASE	PR00109B 12.27 4.764e-

SEQ ID NO:   ACCESSION   DESCRIPTION   RESULTS*	01187B 3 276- 12.04 9
SIGNATURE   SLO1187   Calcium-binding EGF-like   BL01187B 12.04   domain proteins pattern   13 100-l16   BL   12.04 8.435e-1   292   BL01187B   12.04 8.435e-1   292   BL01187B   12.04   10.54-70   BL01   10.54-70   BL01   12.04 5.725e-0   247   BL01187A   7.000e-09 255-   255   PD00078   REPEAT PROTEIN ANK   PD00078B   13.14   NUCLEAR ANKYR.   10 366-379   PD   13.14 4.522e-0   181   1542-553   1542-553   1542-553   1542-553   1555   PF00628   PHD-finger.   PF00628   15.84   11 116-131   116-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   166-131   1	01187B 3 276- 12.04 9
BL01187   Calcium-binding EGF-like domain proteins pattern proteins.   13 100-116 BL 12.04 8.435e-1	01187B 3 276- 12.04 9
12.04 5.725e-0 247 BL01187A 7.000e-09 255-   352   PD00078   REPEAT PROTEIN ANK NUCLEAR ANKYR.   10 366-379 PD 13.14 4.522e-0 181   1542-553   PF00628   PHD-finger.   PF00628 15.84   11 116-131   116-131	
NUCLEAR ANKYR. 10 366-379 PD 13.14 4.522e-0 181  354 BL00380 Rhodanese proteins. BL00380F 9.76 11 542-553  PF00628 PHD-finger. PF00628 15.84 11 116-131	9 231 9.98 267
355 PF00628 PHD-finger. PF00628 15.84 11 116-131	00078B
355 PF00628 PHD-finger. PF00628 15.84 11 116-131	6.694e-
	1.000e-
356 PR00587 SOMATOSTATIN RECEPTOR PR00587A 8.06	9.700e-
TYPE 1 SIGNATURE 09 17-37  359 PD00066 PROTEIN ZINC-FINGER PD00066 13.92 6 METAL-BINDI. 15 261-274 PD6 13.92 6.500e-11 246 PD00066 13	00066 3 233- 3.92
361 PF00791 Domain present in ZO-1 PF00791B 28.49 and Unc5-like netrin receptors. 28.49 1.095e-12 PF00791A 27.85 09 71-126 PF00 28.49 7.440e-05 23.9	9.604e- 0791B 2 21-76 1.432e- 0791B
362 PF00791 Domain present in ZO-1 PF00791B 28.49 and Unc5-like netrin 11 279-334 receptors.	2.273e-
363 PR00450 RECOVERIN FAMILY PR00450C 12.22 SIGNATURE 10 73-95 PR004 12.22 3.278e-09	150C
364 PF00242 DNA polymerase (viral) PF00242Q 13.51 N-terminal domain 09 22-68 proteins.	2.328e-
DNA polymerase (viral) PF00242Q 13.51 N-terminal domain 09 22-68 proteins.	2.328e-
366 BL01160 Kinesin light chain BL01160B 19.54 repeat proteins. 09 1038-1092	6.644e-
367 PRO0019 LEUCINE-RICH REPEAT PRO0019B 11.36 SIGNATURE 09 229-243 PRO 11.36 6.040e-09 PR00019A 11.19 6	0019B 91-105
PRODOLI TYPE IN EGF-LIKE PRODOLID 14.03 : 15 30-49 PRODOLID 14.06 9.830e-15 PRODOLIB 13.08 (14 30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 PRODOLID 14.30-49 P	11A 30-49 4.500e-
BL01032 Protein phosphatase 2C BL01032H 11.25 4	
372 BL00478 LIM domain proteins. BL00478B 14.79 7	7.750e-
PD01066 PROTEIN ZINC FINGER PD01066 19.43 9. ZINC-FINGER METAL- 34 26-65 BINDING NU.	.757e~
PRO0170 SODIUM CHANNEL SIGNATURE PRO0170E 6.48 2.	7396-

SEQ ID NO:	ACCESSION	DESCRIPTION ·	RESULTS*
ļ <u>.</u>	NO.		
380	BL00107	Protein kinases ATP-	10 88-118 BL00107A 18.39 1.000e-
		binding region proteins.	23 276-307 BL00107B
	İ		13.31 1.692e-12 342- 358
381	BL00455	Putative AMP-binding	BL00455 13.31 5.714e-
382	PR00624	domain proteins.	12 50-66
		HISTONE HS SIGNATURE	PR00624G 4.08 4.900e- 09 524-544
384	PD00078	REPEAT PROTEIN ANK NUCLEAR ANKYR.	PD00078B 13.14 5.950e- 10 366-379 PD00078B
		WCDDAK ANATA.	13.14 4.522e-09 168-
385	PR00511		181
		TEKTIN SIGNATURE	PR00511D 7.11 5.371e-
386	PD02870	RECEPTOR INTERLEUKIN-1 PRECURSOR.	PD02870B 18.83 6.000e- 10 97-130
388	PD00066	PROTEIN ZINC-FINGER	PD00066 13.92 5.000e-
389	BL00290	METAL-BINDI.  Immunoglobulins and	13 516-529
	2550230	major histocompatibility	BL00290A 20.89 7.657e- 09 151-174
390	DV 00015	complex proteins.	
390	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 5.200e- 15 221-246 BL00215A
			15.82 7.618e-14 20-45
			BL00215A 15.82 8.851e- 11 123-148 BL00215B
		İ	10.44 9.526e-11 69-82
			BL00215B 10.44 7.300e-
			09 272-285 BL00215B 10.44 8.500e-09 165-
			178
394	BL00674	AAA-protein family proteins.	BL00674B 4.46 2.723e- 16 299-321
397	PR00048	C2H2-TYPE ZINC FINGER	PR00048A 10.52 8.579e-
398	PR00761	SIGNATURE BINDIN PRECURSOR	11 141-155 PR00761B 9.93 6.764e-
399		SIGNATURE	09 55-74
399	BL00240	Receptor tyrosine kinase class III proteins.	BL00240B 24.70 7.907e-
401	PF00676	Dehydrogenase E1	PF00676B 24.71 8.071e-
	{	component.	18 331-369 PF00676D 14.40 3.854e-15 486-
			506 PF00676C 16.88
402	BL00514	Filmin	9.182e-14 454-478
402	PP00214	Fibrinogen beta and gamma chains C-terminal	BL00514C 17.41 4.673e- 28 4432-4469 BL00514G
		domain proteins.	15.98 6.092e-14 4555-
			4585 BL00514D 15.35 2.532e-12 4473-4486
			BL00514F 11.65 4.288e-
			10 4519-4534 BL00514H 14.95 4.955e-10 4584-
			4609
403	PF00992	Troponin.	PF00992A 16.67 5.974e- 09 105-140
404	PR00019	LEUCINE-RICH REPEAT	PR00019B 11.36 1.450e-
		SIGNATURE	10 73-87 PR00019A
		1	11.19 8.043e-10 76-90   PR00019B 11.36 1.000e-
l			09 50~64 PR00019B
405	BL00232	Cadherins extracellular	11.36 1.000e-09 96-110 BL00232B 32.79 9.557e-
j		repeat proteins domain	20 139-187 BL00232B
		proteins.	32.79 2.246e-18 29-77
j			BL00232B 32.79 5.985e- 18 358-406 BL00232B
			32.79 5.500e-16 246-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
	<del>                                     </del>		294 BL00232B 32.79
1		İ	9.384e-15 463-511
1	1	ĺ	BL00232C 10.65 2.537e-
		1	12 244-262 BL00232C
		1	10.65 4.326e-11 356-
1		1	374 BL00232C 10.65
1		1	7.261e-11 461-479
		1	BL00232C 10.65 7.457e-
1	}		11 27-45
407	PF00426	Outer Capsid protein VP4	PF00426S 15.67 5.634e-
1	1100=20	(Hemagglutinin).	09 902-940
409	BL01160	Kinesin light chain	BL01160B 19.54 9.695e-
1403	Prories	repeat proteins.	09 126-180
410	BL00741	Guanine-nucleotide	BL00741B 14.27 2.731e-
410	P700.14T	dissociation stimulators	
}			09 252-275
		CDC24 family sign.	
411	PF00646	F-box domain proteins.	PF00646A 14.37 6.344e-
			09 86-100
412	BC00603	Thymidine kinase	BL00603B 11.39 8.500e-
	L	cellular-type proteins.	09 542-557
415	BF00866	Carbamoyl-phosphate	BL00866B 36.29 3.571e-
1	1	synthase subdomain	31 245-291 BL00866C
		proteins.	23.26 9.000e-25 331-
		<u>                                     </u>	366
418	PR00239	MOLLUSCAN RHODOPSIN C-	PR00239E 1.58 6.114e-
	ł	TERMINAL TAIL SIGNATURE	09 590-602
421	PF00791	Domain present in ZO-1	PF00791B 28.49 7.955e-
l		and Unc5-like netrin	14 23-78 PF00791B
		receptors.	28.49 3.653e-12 273-
			328 PF00791B 28.49
l			4.273e-11 156-211
			PF00791B 28.49 7.818e-
ļ			11 89-144 PF00791B
1		1	28.49 1.524e-10 56-111
ĺ			PF00791C 20.98 3.559e-
<b>{</b>	,		09 37-76 PF00791C
			20.98 5.235e-09 170-
	Į.		209 PF00791C 20.98
			5.235e-09 381-420
			PF00791B 28.49 6.202e-
	1 .		09 189-244 PF00791B
	·		28.49 7.028e-09 435-
	ſ		490 PF00791B 28.49
		1	8.679e-09 367-422
424	DM00892	3 RETROVIRAL PROTEINASE.	DM00892C 23.55 7.207e-
			28 1645-1679
425	PR00109	TYROSINE KINASE	PR00109D 17.04 5.881e-
	1	CATALYTIC DOMAIN	10 228-251
	1	SIGNATURE	j
429	BL00518	Zinc finger, C3HC4 type	BL00518 12.23 4.600e-
	1	(RING finger), proteins.	11 31-40
431	BL00039	DEAD-box subfamily ATP-	BL00039D 21.67 1.844e-
	-	dependent helicases	34 490-536 BL00039A
		proteins.	18.44 5.615e-19 205-
			244 BL00039B 19.19
	1	1	8.920e-16 251-277
	ł		BL00039C 15.63 5.781e-
	1		15 333-357
432	PR00452	SH3 DOMAIN SIGNATURE	PR00452B 11.65 7.652e-
			12 169-185
433	PR00828	FORMIN SIGNATURE	PR00828B 5.23 8.218e-
			10 382-405
436	BL00415	Synapsins proteins.	BL00415N 4.29 8.643e-
		oynapatna procetna.	11 195-239 BL00415N
	Ī		4.29 3.036e-09 809~853
443	PR00834	HTRA/DEGO PROTEASE	PR00834F 10.91 6.040e-
446	PF01140	FAMILY SIGNATURE	11 221-234
	02430	Matrix protein (MA),	PF01140D 15.54 9.663e-

SEQ ID	NO: ACCESSION NO.	DESCRIPTION	RESULTS*
		p15.	10 183-218 PF01140D 15.54 3.093e-09 246- 281
449	PR00568	DOPAMINE D3 RECEPTOR SIGNATURE	PR00568G 13.95 5.551e- 09 39-53
451	PF00084	Sushi domain proteins (SCR repeat proteins.	PF00084B 9.45 3.813e-
452	BL00790	Receptor tyrosine kinase class V proteins.	BL00790I 20.01 2.821e- 09 618-649
456	PR00380	KINESIN HEAVY CHAIN SIGNATURE	PR00380A 14.18 1.000e- 25 77-99 PR00380D 9.93 1.000e-21 281-303 PR00380C 13.18 8.286e- 17 230-249 PR00380B 12.64 4.724e-16 194- 212
457	PR00253	GAMMA-AMINOBUTYRIC ACID (GABA) RECEPTOR SIGNATURE	PR00253A 9.15 9.143e- 24 246-267 PR00253B 13.47 2.000e-23 272- 294 PR00253C 13.85 7.000e-23 306-328 PR00253D 16.68 5.950e- 21 452-473
467	PR00849	GLYCOSYL HYDROLASE FAMILY 58 SIGNATURE	PR00849D 9.77 9.236e- 09 910-937
471	BL00678	Trp-Asp (WD) repeat proteins proteins	BL00678 9.67 8.200e-12
472	BL00226	Intermediate flaments proteins.	BL00226B 23.86 3.721e- 09 282-330
473	BL00344	GATA-type zinc finger domain proteins.	BL00344 17.99 7.000e- 12 814-852
474	BL00481	Thiol-activated cytolysins proteins.	BL00481E 13.07 8.909e- 09 173-199
479	PR00319	BETA G-PROTEIN (TRANSDUCIN) SIGNATURE	PR00319B 11.47 2.571e- 09 393-408
480	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 1.900e- 38 8-47
481	PR00405	HIV REV INTERACTING PROTEIN SIGNATURE	PR00405C 19.41 1.000e- 19 451-473 PR00405B 11.83 4.333e-18 430- 448 PR00405A 17.71 4.971e-18 411-431
482	PR00049	WILN'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 9.286e- 10 959-974 PR00049D 0.00 9.857e-10 958-973 PR00049D 0.00 1.305e- 09 937-952 PR00049D 0.00 8.322e-09 939-954
	PR00007	COMPLEMENT C1Q DOMAIN SIGNATURE	PR00007B 14.16 8.615e- 23 653-673 PR00007A 19.33 6.192e-22 626- 653 PR00007C 15.60 5.846e-19 698-720 PR00007D 9.64 3.647e- 13 732-743
487	PD00567	PROTEIN RNA-BINDING RNA REPEAT HYD.	PD00567B 18.23 2.853e- 09 200-214
488	PR00988	URIDINE KINASE SIGNATURE	PR00988A 6.39 4.569e- 12 3-21
189	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-	PD01066 19.43 4.882e- 27 30-69 PD01066
190	PR00049	WILM'S TUMOUR PROTEIN	19.43 3.430e-10 71-110 PR00049D 0.00 7.864e-
192	BL01128	SIGNATURE Shikimate kinase	09 663-678 BL01128A 18.84 6.464e-
197	PF00429	proteins. ENV polyprotein (coat	17 58-92 PF00429 31.08 7.171e-

SEQ ID N	O:   ACCESSION	DESCRIPTION	RESULTS*
	NO.		1
498	DY 00120	polyprotein).	15 21-71
	BL00120	Lipases, serine proteins.	BL00120B 11.37 7.923e- 09 185-200
500	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 7.353e- 11 299-318
501	BL01159	WW/rsp5/WWP domain	BL01159 13.85 8.579e-
505	BL00021	proteins.  Kringle domain proteins.	12 131-146
			BL00021B 13.33 3.739e- 17 492-510
508	PR00120	H+TRANSPORTING ATPASE (PROTON PUMP) SIGNATURE	PR00120C 9.90 5.800e- 19 705-722
509	DM01417	6 kw INDUCING XPMC2	DM01417E 20.62 2.938e-
		MUSHROOM SPAC22G7.04.	16 362-395 DM01417D
			11.08 3.800e-13 322-
510	PF00534	Glycosyl transferases	PF00534B 14.47 6.625e-
511	PF00534	group 1. Glycosyl transferases	09 346-370
	1100554	group 1.	PF005348 14.47 6.625e- 09 293-317
512	PF00534	Glycosyl transferases	PF00534B 14.47 6.625e-
513	PD01841	group 1. PHOSPHORYLASE KINASE	09 366-390
525	PD018-11	ALPHA MUSCL.	PD01841A 21.71 1.000e- 40 110-160 PD01841B
			14.35 1.000e-40 181-
	ĺ		222 PD01841D 17.87
			1.000e-40 243-295
	į.		PD01841F 13.36 1.000e- 40 333-382 PD01841G
	i		24.26 1.000e-40 386-
			440 PD01841L 18.42
			1.000e-40 968-1010
			PD01841I 23.00 4.545e- 37 762-804 PD01841E
		. ]	18.60 3.750e-36 295-
	ľ		333 PD01841J 14.94
	`		6.023e-35 851-888
		1	PD01841H 21.30 2.909e- 33 490-527 PD01841K
			14.81 7.088e-33 924-
			954 PD01841C 13.78
		}	9.386e-23 222-243
			PD01841M 10.82 8.594e- 21 1054-1073 PD01841I
			23.00 2.667e-13 549-
			591
514	PR00153	CYCLOPHILIN PEPTIDYL-	PR00153C 11.01 7.188e-
		PROLYL CIS-TRANS ISOMERASE SIGNATURE	13 95-111 PR00153E   9.10 4.150e-12 122-138
515	BL00740	MAM domain proteins.	BL00740A 13.87 7.188e-
516			12 410-423
210	DM00892	3 RETROVIRAL PROTEINASE.	DM00892C 23.55 6.087e- 12 1018-1052
517	BL00242	Integrins alpha chain	BL00242C 16.86 8.320e-
523	- BWOODE 1	proteins.	09 12-42
323	DM00031	IMMUNOGLOBULIN V REGION.	DM00031A 16.80 3.750e-
		1	39 20-68 DM00031B 15.41 1.000e-25 84-118
525	BL00319	Amyloidogenic	BL00319C 17.12 8.375e-
		glycoprotein	10 61-95
		extracellular domain proteins.	
526	PF00789	Domain present in	DV00789D 18 22 2 200
		ubiquitin-regulatory	PF00789B 19.70 3.308e- 12 322-343 PF00789C
		proteins.	20.98 5.269e-09 367-
28	P101360		392
0	BL01162	Quinone oxidoreductase /	BL01162C 22.80 1.500e-
	1	zeta-crystallin proteins.	16 120-164
		1 E-000111B.	L

SEQ ID N		DESCRIPTION	RESULTS*
529	NO. PR00910	Y YURDOY Y DAYS	
	PROUPIO	LUTEOVIRUS ORF6 PROTEIN SIGNATURE	PR00910A 2.51 3.893e- 09 60-73
532	BL00215	Mitochondrial energy	BL00215A 15.82 4.000e-
		transfer proteins.	17 11-36 BL00215A 15.82 8.660e-11 123-
			148
533	BL00215	Mitochondrial energy	BL00215A 15.82 4.000e-
		transfer proteins.	17 11-36 BL00215A 15.82 8.660e-11 97-122
534	BL00098	Thiolases acyl-enzyme	BL00098C 21.65 2.800e-
		intermediate proteins.	38 181-227 BL00098B
			32.59 5.345e-38 86-141 BL00098D 26.30 8.364e-
			35 245~288 BL00098E
			22.12 1.000e-34 314-
			352 BL00098F 10.18
			4.971e-22 365-386 BL00098A 10.60 6.455e-
			11 38-50
535	PR00370	PLAVIN-CONTAINING	PR00370E 11.96 7.429e-
		MONOOXYGENASE (FMO) SIGNATURE	22 321-340 PR00370D 16.33 6.143e-21 185-
			204 PRO0370F 17.75
			6.559e-21 376-396
			PR00370B 10.91 9.591e- 21 27-46 PR00370C
			12.72 3.500e-20 140-
			157 PR00370A 3.35
536	BL00028	Zinc finger, C2H2 type,	6.442e-17 4-20 BL00028 16.07 7.429e-
		domain proteins.	16 285-302 BL00028
		•	16.07 6.294e-14 341-
			358 BL00028 16.07 1.346e-11 369-386
		İ	BL00028 16.07 1.692e-
			11 397-414 BL00028
			16.07 4.462e-11 453- 470 BL00028 16.07
		ļ.	7.231e-11 425-442
			BL00028 16.07 4.300e-
537	BL00762	WHEP-TRS domain	10 313-330 BL00762A 23.43 9.419e-
		proteins.	15 844-881
538	BL00762	WHEP-TRS domain proteins.	BL00762A 23.43 9.419e-
539	ВЬ00762	WHEP-TRS domain	15 819-856 BL00762A 23.43 9.419e-
		proteins.	15 822-859
540	PR00985	LEUCYL-TRNA SYNTHETASE	PR00985A 12.10 9.000e-
541	PD02102	SUBUNIT E V-ATPASE	10 357-375 PD02102A 16.74 1.000e-
		VACUOLAR ATP SYNTHASE	40 3-47 PD02102B
		HYDROL.	18.28 4.375e-34 57-100
			PD02102D 21.69 1.923e- 30 179-218 PD02102C
			26.34 8.929e-26 100-
E/12	BI 00000		146
543	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 1.000e- 10 48-65 BL00028
		Dioceting.	16.07 6.400e-10 193-
			210 BL00028 16.07
			1.000e-09 343-360
			BL00028 16.07 6.914e-
545	BL00250	TGF-beta family	BL00250A 21.24 8.000e-
		proteins.	31 293-329 BL00250B
			27.37 5.286e-24 354- 390
547	PR00319	BETA G-PROTEIN	PR00319B 11.47 2.714e-

SEQ ID NO	ACCESSION NO.	DESCRIPTION	RESULTS*
	- NO.	(TRANSDUCIN) SIGNATURE	09 186-201 PR00319A
		(Induspocial) DIGNATORS	15.27 7.344e-09 210- 227
548	BL01204	NF-kappa-B/Rel/dorsal domain proteins.	RJ.01204A 17.74 1.000e- 40 8-56 BL01204D 16.42 1.000e-40 177- 221 BL01204E 13.83 7.652e-30 225-250 BL01204C 13.93 8.714e- 22 141-160 BL01204B 15.41 4.333e-16 102- 116
549	PR00326	GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE	PRO0326A 8.75 8.364e-
551	PF00632	HECT-domain (ubiquitin- transferase).	PF00632C 20.66 3.302e- 23 1569-1601 PF00632B 18.45 3.700e-21 1515- 1543
554	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290B 13.17 1.600e- 14 187-205 BL00290A 20.89 2.059e-14 130- 153
557	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 6.339e- 09 846-879
559	DM01111	4 kw PHOSPHATASE TRANSFORMING 61K PDF1.	DM01111L 11.93 3.762e- 09 7-35
562	PF00658	Poly-adenylate binding protein, unique domain proteins.	PF00658C 16.33 9.455e- 32 118-155
564	BL00141	Bukaryotic and viral aspartyl proteases proteins.	BL00141A 12.10 4.150e- 10 472-488
566	PF00855	PWWP domain proteins.	PF00855 13.75 5.667e- 15 272-289
567	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 4.977e- 13 229-268
569	BL00107	Protein kinases ATP- binding region proteins.	BL00107A 18.39 7.000e- 19 118-149 BL00107B 13.31 5.500e-15 183- 199
570	BL00107	Protein kinases ATP- binding region proteins.	BL00107A 18.39 7.000e- 19 118-149 BL00107B 13.31 5.500e-15 183-
572	PR00193	MYOSIN HEAVY CHAIN SIGNATURE	PR00193D 14.36 1.857e- 34 454-483 PR00193C 12.60 2.636e-31 223- 251 PR00193B 11.69 7.750e-29 171-197 PR00193A 15.41 2.588e- 22 115-135 PR00193E 19.47 6.559e-19 508- 537
573	PR00193	MYOSIN HEAVY CHAIN SIGNATURE	PR00193D 14.36 1.857e- 34 470-499 PR00193C 12.60 2.636e-31 239- 267 PR00193B 11.69 7.750e-29 171-197 PR00193A 15.41 2.588e- 22 115-135 PR00193E 19.47 6.559e-19 524- 553
575	BL00752	XPA protein.	BL00752B 19.17 9.703e- 10 885-929
576 577	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 7.000e- 09 276-295
3//	BL00116	DNA polymerase family B	BL00116A 12.81 5.737e-

SEQ ID NO	D: ACCESSION NO.	DESCRIPTION	RESULTS*
		proteins.	13 864-877 BL00116B
			11.82 1.529e-12 952- 965
578	BL00195	Glutaredoxin proteins.	BL00195B 15.31 7.158e- 09 121-141
579	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019B 11.36 9.000e- 11 217-231 PR00019B 11.36 1.350e-09 386- 400 PR00019A 11.19 3.333e-09 389-403 PR00019B 11.36 8.920e- 09 363-377
580	PR00253	GAMMA-AMINOBUTYRIC ACID (GABA) RECEPTOR SIGNATURE	PR00253A 9.15 2.125e- 25 275-296 PR00253B 13.47 7.923e-24 301- 323 PR00253D 16.68 5.846e-23 444-465 PR00253C 13.85 2.241e- 20 335-357
583	PR00343	SELECTIN SUPERFAMILY COMPLEMENT-BINDING REPEAT SIGNATURE	PR00343C 16.85 2.286e- 11 1233-1252 PR00343C 16.85 5.500e-11 333- 352 PR00343C 16.85 5.500e-11 783-802 PR00343C 16.85 4.246e- 10 1491-1510 PR00343C 16.85 8.230e-10 1686- 1705
584	DM01537	kw SKI2W SKI2 NUCLEOLAR HELICASE.	DM01537B 21.63 1.878e- 37 79-126 DM01537B 21.63 9.491e-30 916- 963 DM01537A 15.14 3.186e-11 784-804
586	PFC0013	KH domain proteins family of RNA binding proteins.	PF00013 5.78 1.450e-09 124-136
587	DM00892	3 RETROVIRAL PROTEINASE.	DM00892C 23.55 4.409e-
589	BL00478	LIM domain proteins.	BL00478B 14.79 1.643e- 13 261-276 BL00478B 14.79 7.709e-09 321- 336
590	PF00855	PWWP domain proteins.	PF00855 13.75 8.000e- 15 931-948
591	PF00855	PWWP domain proteins.	PF00855 13.75 8.000e-
593	PF00628	PHD-finger.	PF00628 15.84 3.455e- 12 424-439
594	PR00205	CADHERIN SIGNATURE	PR00205B 11.39 2.241e- 16 558-576 PR00205A 14.73 9.300e-13 542- 558 PR00205C 13.65 5.304e-12 594-609 PR00205B 11.39 4.273e- 10 336-354
596	BL00107	Protein kinases ATP- binding region proteins.	BL00107A 18.39 4.789e- 18 307-338
598	PD01675	GLYCOPROTEIN MAJOR ENVELOPE PROBABLE U3.	PD01675C 19.89 2.330e- 10 55-89
600	BL00242	Integrins alpha chain proteins.	BL00242E 9.03 9.591e- 27 985-1014 BL00242C 16.86 4.115e-26 286- 316 BL00242D 13.57 4.150e-25 357-382 BL00242B 8.13 7.353e- 12 189-199 BL00242D 13.57 3.455e-11 421- 446 BL00242A 13.80

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
<del></del>	- <del> </del>	<del></del>	5.000e-11 61-73
			BL00242D 13.57 4.986e-
601	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320A 16.74 5.610e- 09 198-213
602	PR00278	PANCREATIC HORMONE SIGNATURE	PR00278A 12.43 4.569e- 10 331-348
603	BL00479	Phorbol esters / diacylglycerol binding domain proteins.	BL00479C 12.01 3.250e- 12 170-183
604	BL00315	Dehydrins proteins.	BL00315A 9.35 1.672e- 09 424-452
605	BL00415	Synapsins proteins.	BL00415N 4.29 9.794e- 10 295-339
606	PR00926	MITOCHONDRIAL CARRIER PROTEIN SIGNATURE	PR00926F 17.75 1.000e-
608	PF00855	PWWP domain proteins.	PF00855 13.75 5.167e- 15 265-282
609	PF00855	PWWP domain proteins.	PF00855 13.75 5.167e-
612	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.	
615	PD02699	PROTEIN DNA-BINDING BINDING DNA.	PD02699A 8.91 2.023e- 28 129-158 PD02699C 24.84 1.000e-27 317- 364 PD02699B 18.28 1.000e-17 158-182
616	PR00380	KINESIN HEAVY CHAIN SIGNATURE	PR00380A 14.18 4.086e- 22 288-310 PR00380D 9.93 3.721e-17 486-508 PR00380B 12.64 2.241e- 16 410-428 PR00380C 13.18 2.976e-13 436- 455'
617	PR00380	KINESIN HEAVY CHAIN SIGNATURE	PR00380A 14.18 4.086e- 22 288-310 PR00380D 9.93 3.721e-17 486-508 PR00380B 12.64 2.241e- 16 410-428 PR00380C 13.18 2.976e-13 436- 455
618	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.	DM01206B 10.69 5.143e- 12 531-551 DM01206B 10.69 2.603e-10 535- 555
621	PR00700	PROTEIN TYROSINE PHOSPHATASE SIGNATURE	PR00700B 16.80 3.160e- 21 561-582
622	BL00239	Receptor tyrosine kinase class II proteins.	BL00239F 28.15 3.222e- 10 647-692 BL00239C 18.75 8.304e-10 543- 566
623	PR00407	EUKARYOTIC MOLYBDOPTERIN DOMAIN SIGNATURE	PR00407K 9.94 8.448e- 09 326-339
624	BL00641	Respiratory-chain NADH dehydrogenase 75 Kd	BL00641C 21.10 1.000e- 40 157-202 BL00641E

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
	NO.		
		subunit proteins.	24.37 1.000e-40 255- 308 BL00641F 33.12 1.000e-40 571-623 BL00641A 17.15 1.818e-
			37 48-80 BL00641B 12.62 5.846e-34 113- 139 BL00641D 13.23 9.308e-29 216-240
627	PR00103	CAMP-DEPENDENT PROTEIN KINASE SIGNATURE	PR00103E 17.80 2.500e- 18 367-380 PR00103B 13.39 2.080e-14 297- 312 PR00103A 9.59 2.957e-14 282-297 PR00103D 10.83 3.077e- 12 346-358 PR00103C 15.68 1.000e-11 334- 344 PR00103B 13.39 1.450e-11 175-190 PR00103A 9.59 1.720e- 10 160-175
630	PR00081	GLUCOSE/RIBITOL DEHYDROGENASE FAMILY SIGNATURE	PR00081A 10.53 6.211e- 16 4-22
631	PF00651	BTB (also known as BR-C/Ttk) domain proteins.	PF00651 15.00 8.500e- 14 37-50
632	DM01206	PROTEIN.	DM01206B 10.69 2.233e- 10 1324-1344 DM01206B 10.69 4.822e-10 1276- 1296 DM01206B 10.69 7.658e-10 1328-1348 DM01206B 10.69 8.274e- 10 1280-1300 DM01206B 10.69 4.532e-09 1320- 1340 DM01206B 10.69 7.266e-09 1326-1346
635	3L00107	Protein kinascs ATP- binding region proteins.	BL00107A 18.39 7.600e- 23 145-176 BL00107B 13.31 2.636e-13 211- 227
636	BL00657	Fork head domain proteins.	BL00657A 19.39 1.545e- 30 101-143 BL00657B 22.27 7.750e-26 149- 192
637	BL00107	Protein kinases ATP- binding region proteins.	BL00107B 13.31 1.000e- 10 607-623
643	BL00018	EF-hand calcium-binding domain proteins.	BL00018 7.41 4.913e-09 199-212
	PF00628	PHD-finger.	PF00628 15.84 2.350e- 13 385-400 PF00628 15.84 3.455e-12 464- 479
648	BL01129	Hypothetical yab0/yceC/sfhB family proteins.	BL01129E 13.25 4.000e- 25 332-357 BL01129C 25.56 8.200e-23 236- 279 BL01129B 12.51 6.118e-13 191-212
649	BL01228	Hypothetical cof family proteins.	BL01228D 17.44 3.908e- 10 455-480
650	BL00027	'Homeobox' domain proteins.	BL00027 26.43 6.684e- 13 771-814
651	BL50002	Src homology 3 (SH3) domain proteins profile.	BL50002A 14.19 1.750e- 12 1026-1045
653	PR00253	GAMMA-AMINOBUTYRIC ACID (GABA) RECEPTOR SIGNATURE	PR00253A 9.15 4.000e- 24 253-274 PR00253C 13.85 8.800e-24 313- 335 PR00253B 13.47 3.143e-22 279-301 PR00253D 16.68 7.652e-

SEQ ID NO	: ACCESSION	DESCRIPTION	RESULTS+
· <del></del> · ·	1.0.		20 422-443
654	PD01719	PRECURSOR GLYCOPROTEIN SIGNAL RE.	PD01719A 12.89 4.452e- 11 969-997 PD01719A 12.89 3.961e-10 128- 156 PD01719A 12.89 7.395e-10 1276-1304 PD01719A 12.89 1.222e- 09 1220-1248
657	BL00354	HMG-I and HMG-Y DNA- binding domain proteins (Ahook).	BL00354C 6.61 8.397e- 09 563-578
658	BL00354	HMG-I and HMG-Y DNA- binding domain proteins (Ahook).	BL00354C 6.61 8.397e- 09 580-595
659	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 2.174e- 13 539-572 DM00215 19.43 4.750e-12 549- 582 DM00215 19.43 9.824e-11 551-584 DM00215 19.43 2.929e- 10 548-581 DM00215 19.43 4.054e-1C 550- 583 DM00215 19.43 5.339e-10 552-585 DM00215 19.43 7.107e- 10 544-577
660	PR00688	XYLOSE ISOMERASE SIGNATURE	PR00688I 13.78 9.518e- 09 224-236
661	ВЬ00027	'Homeobox' domain proteins.	BL00027 26.43 5.950e- 23 249-292
662	PR00360	C2 DOMAIN SIGNATURE	PR00360B 13.61 7.158e- 10 596-610
663	PR00360	C2 DOMAIN SIGNATURE	PR00360B 13.61 7.158e- 10 596-610
664	PR00360	C2 DOMAIN SIGNATURE	PR00360B 13.61 7.158e- 10 596-610
666	PR00819	CPXX/CFQX SUPERFAMILY SIGNATURE	PR00819B 10.83 8.988e- 10 704-720
667	BL50040	Elongation factor 1 gamma chain profile.	BL50040C 22.62 2.143e- 16 135-178
668	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019B 11.36 1.360e- 09 139-153 PR00019A 11.19 1.667e-09 94-108 PR00019B 11.36 4.600e- 09 163-177
670	BL00018	EF-hand calcium-binding domain proteins.	BL00018 7.41 3.250e-10 681-694 BL00018 7.41 6.400e-10 717-730
672	PD00131	ATF-BINDING TRANSPORT TRANSMEMBR.	PD00131B 34.97 1.000e- 34 356-410 PD00131C 19.59 1.346e-26 504- 542
673	PR00667	RETINAL PIGMENT EPITHELIUM-RETINAL GPCR SIGNATURE	PRC0667G 15.33 7.557e- 10 106-123
674	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320A 16.74 4.857e- 13 593-608 PR00320B 12.19 4.115e-12 635- 650 PR00320C 13.01 8.435e-11 717-732 PR00320C 13.01 2.800e- 10 635-650 PR00320C 13.01 6.400e-10 593- 608 PR00320B 12.19 3.250e-09 593-608
675	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320A 16.74 4.857e- 13 572-587 PR00320B 12.19 4.115e-12 614-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			629 PR00320C 13.01 8.435e-11 696-711 PR00320C 13.01 2.800e- 10 614-629 PR00320C 13.01 6.400e-10 572- 587 PR00320B 12.19
676	PR00019	LEUCINE-RICH REPEAT	3.250e-09 572-587 PR00019A 11.19 9.667e- 09 249-263
679	PF00642	Zinc finger C-x8-C-x5-C-x3-H type (and similar).	PF00642 11.59 3.700e- 16 225-236 PF00642 11.59 7.900e-12 187-
680	PR00308	TYPE I ANTIFREEZE PROTEIN SIGNATURE	PR00308C 3.83 8.754e- 10 286-296
681	BL00019	Actinin-type actin- binding domain proteins.	BL00019D 15.33 4.200e- 19 227-257
682	PR00700	PROTEIN TYROSINE PHOSPHATASE SIGNATURE	PR00700D 12.47 4.000e- 09 99-118
687	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 8.500e-
689	BL01024	Protein phosphatase 2A regulatory subunit PR55 proteins.	BL01024A 10.26 1.000e- 40 22-69 BL01024B 8.91 1.000e-40 86-127 BL01024C 7.80 1.000e- 40 146-185 BL01024D 13.22 1.000e-40 185- 222 BL01024E 11.96 1.000e-40 222-266 BL01024F 9.42 1.000e- 40 266-317 BL01024G 11.09 1.000e-40 317- 349 BL01024H 13.88 1.000e-40 389-442
691	BL00027	'Homeobox' domain proteins.	BL00027 26.43 8.071e- 31 152-195
692	BL00211	ABC transporters family proteins.	BL00211A 12.23 5.050c- 09 45-57
693	BL00211	ABC transporters family proteins.	BL00211A 12.23 5.050e- 09 45-57
694	BL00211	ABC transporters family proteins.	BL00211A 12.23 5.050e- 09 58-70
696	BL00680	Methionine aminopeptidase subfamily 1 proteins.	BL00680 14.37 5.304e- 17 173-195
697	BL00741	Guanine-nucleotide dissociation stimulators CDC24 family sign.	BL00741B 14.27 3.418e- 11 242-265
698	DM01930	2 kw FINGER SMCX SMCY YDR096W.	DM01930E 15.41 1.367e- 37 170-215 DM01930F 14.16 B.232e-28 267- 303 DM01930B 19.86
700	PR00869	DNA-POLYMERASE FAMILY X SIGNATURE	9.163e-10 37-71 PR00869A 12.80 1.281e-
	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	16 245-263 PR00048A 10.52 2.174e- 10 77-91 PR00048A 10.52 6.870e-10 133- 147 PR00048A 10.52 8.826e-10 105-119 PR00048A 10.52 5.320e-
702	BL00523	Sulfatases proteins.	09 161-175 BL00523E 19.27 2.565e- 25 326-356 BL00523A 13.36 5.050e-16 38-55 BL00523B 8.64 5.909e- 15 86-98 BL00523C 12.64 5.500e-13 137-

SEQ ID NO	D: ACCESSION	L DEGCD YOMYOV	
020 10 110	NO.	DESCRIPTION	RESULTS*
			148 BL00523D 9.89
		İ	1.844e-11 290-302 BL00523G 9.46 5.500e-
	İ		10 513-523 BL00523F
ļ			10.85 6.351e-09 413-
703	PR00048	COUR THE STAG TENGEN	424
.03	2100040	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 8.412e- 12 376-390 PR00048B
			6.02 1.000e-10 334-344
			PR00048B 6.02 1.474e-
707	PD00787		09 364-374
707	2000787	SYNTHASE BIOSYNTHESIS TRANSPERASE.	PD00787A 14.84 8.941e-
708	PR00761	BINDIN PRECURSOR	PR00761E 14.32 8.500e-
		SIGNATURE	10 822-841
712	DM01354	kw TRANSCRIPTASE REVERSE	DM01354Y 10.69 4.977e-
		II ORF2.	38 425-465 DM01354X
			13.86 7.300e-34 376-
			415 DM01354V 12.97 4.923e-17 311-358
	Ī		DM01354W 12.64 5.596e-
444			10 356-376
713	BL00039	DEAD-box subfamily ATP-	BL00039D 21.67 7.545e-
		dependent helicases proteins.	27 450-496 BL00039A 18.44 2.537e-18 147-
		process.	186 BL00039C 15.63
			2.216e-14 280-304
	1		BL00039B 19.19 1.947e-
715	BL00383	Tyrosine specific	13 194-220
, 25	200363	protein phosphatases	BL00383E 10.35 4.981e- 10 150-161
		proteins.	10 130-101
717	PF00777	Sialyltransferase	PF00777C 18.60 4.035e-
718	DM00031	family.  IMMUNOGLOBULIN V REGION.	21 106-161 DM00031A 16.80 3.750e-
			39 20-68 DM00031B
			15.41 2.688e-28 84-118
			DM00031C 12.79 1.300e-
719	BL00243	Integrins beta chain	12 131-142 BL00243B 17.54 1.000e-
		cysteine-rich domain	40 131-172 BL00243C
		proteins.	16.42 1.000e-40 172-
	Į.		208 BL00243D 24.07
			1.000e-40 222-274 BL00243F 22.63 1.000e-
			40 314-358 BL00243I
		1	31.77 6.571e-39 607-
			650 BL00243E 16.70
	· }		3.077e-35 274-304 BL00243G 21.38 3.625e-
			34 358-400 BL00243H
			17.53 5.235e-29 567-
	1		593 BL00243A 17.61
			3.250e-21 63-84
		J	BL00243H 17.53 7.167e-
		1	17.53 2.304e-11 524-
			550 BL00243H 17.53
			5.304e-11 606-632
		1	BL00243I 31.77 1.380e-
720	PR00217	43 KD POSTSYNAPTIC	09 610-653 PR00217C 10.91 8.022e-
		PROTEIN SIGNATURE	09 20-36
722	PR00704	CALPAIN CYSTEINE	PR00704D 11.05 5.909e-
	1	PROTEASE (C2) FAMILY	34 135-161 PR00704P
	-	SIGNATURE	13.61 7.000e-26 190-
_			218 PR00704E 12.55 8.071e-26 165-189
			0.0/16-20 103-183

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
	NO.		
			PR00704B 17.94 2.241e-
			23 75-98 PR00704A 14.68 4.094e-19 30-54
			PR00704C 11.88 1.871e-
L		ĺ	18 99-116
725	PR00194	TROPOMYOSIN SIGNATURE	PR00194A 7.86 7.652e-
			09 169-187
726	PR00194	TROPOMYOSIN SIGNATURE	PR00194A 7.86 7.652e-
727	PR00320	G-PROTEIN BETA WD-40	09 169-187
'2'	PR00320	REPEAT SIGNATURE	PR00320C 13.01 2.125e- 13 277-292 PR00320A
i		REFERENCE DEGINATORS	16.74 1.310e-11 277-
1		1	292 PR00320C 13.01
j		•	4.522e-11 323-338
Ì	-		PR00320A 16.74 6.586e-
	1		11 323-338 PR00320B
			12.19 4.343e-10 323- 338 PR00320B 12.19
j			6.914e-10 277-292
731	PR00195	DYNAMIN SIGNATURE	PR00195A 11.94 8.627e-
			16 288-307 PR00195E
733	PF00642	Ting fires a constant	9.82 3.912e-11 457-474
	2500042	Zinc finger C-x8-C-x5-C- x3-H type (and similar).	PF00642 11.59 9.082e- 10 787-798
738	BL00039	DEAD-box subfamily ATP-	BL00039A 18.44 2.565e-
		dependent helicases	28 26-65 BL00039D
		proteins.	21.67 2.105e-20 338-
	i ·		384 BL00039C 15.63
			9.100e-13 160-184
			BL00039B 19.19 9.617e-
739	BL01289	TSC-22 / dip / bun	BL01289A 12.18 8.909e-
		family proteins.	31 326-353 BL01289B
	ļ	•	10.45 9.571e-17 353-
742	BL01019	ADP-ribosylation factors	383
		family proteins.	BL01019A 13.20 7.078e- 12 41-81
743	BL00965	Phosphomannose isomerase	BL00965C 23.78 1.000e-
		type I proteins.	40 256-305 BL00965B
	[	1	17.77 1.600e-25 126-
			153 BL00965A 10.57 6.400e-19 94-113
747	BL00021	Kringle domain proteins.	BL00021D 24.56 4.563e-
	ľ		25 231-273 BL00021B
		<u> </u>	13.33 5.345e-21 60-78
748	BL00612	Osteonectin domain	BL00612B 11.35 2.034e-
749	PR00450	proteins. RECOVERIN FAMILY	11 93-126
	-100430	SIGNATURE	PR00450C 12.22 6.880e- 10 135-157
752	BL00795	Involucrin proteins.	BL00795C 17.06 6.000e-
			11 384-429 BL00795C
		1	17.06 9.444e-11 370-
754	DT OOGE 1		415
.73	BL00051	Ribosomal protein L39e	BL00051 20.92 1.935e-
755	DM01970	proteins. 0 kw ZK632.12 YDR313C	16 4-50 DM01970B 8.60 7.723e-
	<del>-</del>	ENDOSOMAL III.	09 171-184
760	BL01020	SAR1 family proteins.	BL01020C 15.35 9.020e-
755		<u> </u>	12 99-150
762	BL00046	Histone H2A proteins.	BL00046 12.95 1.000e-
763	PD02411	DDOTETY MEANCED FORTON	40 33-88
	- 0054TT	PROTEIN TRANSCRIPTION REGULATION NUCLEAR.	PD02411 21.89 9.137e-
764	BL00027	'Homeobox' domain	10 206-240 BL00027 26.43 8.800e-
	•	proteins.	29 417-460
767	BL01208	VWFC domain proteins.	BL01208B 15.83 6.063e-
ł			10 309-324 BL01208B
		<u></u>	15.83 8.031e-10 165-

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
	NO.		
			180 BL01208B 15.83 4.162e-09 85-100
770	BL00031	Nuclear hormones	BL00031A 19.55 9.571e-
		receptors DNA-binding	32 -208-241 BL00031B
		region proteins.	22.25 5.500e-27 242-
772	PR00449	TRANSFORMING PROTEIN P21	274 PR00449A 13.20 1.450e-
		RAS SIGNATURE	18 4-26 PR00449E
			13.50 3.520e-14 142-
			165 PR00449C 17.27 3.032e-13 44-67
		·	PR00449D 10.79 8.579e-
	1		13 107-121 PR00449B
773	BL00523	Sulfatases proteins.	14.34 3.455e-11 27-44
•		Darracases processis.	BL00523E 19.27 9.333e- 23 299-329 BL00523A
		l	13.36 2.200e-13 47-64
	1	i	BL00523B 8.64 2.607e-
			13 91-103 BI.00523D 9.89 7.923e-12 224-236
			BLC0523C 12.64 4.512e-
	1		10 141-152 BL00523F
			10.85 5.821e-10 373-
775	BL00028	Zinc finger, C2H2 type,	BL00028 16.07 7.686e-
776	BL00028	domain proteins.	09 568-585
	BE00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 7.686e-
777	BL00028	Zinc finger, C2H2 type.	09 621-638 BL00028 16.07 7.686e-
778	PT 00000	domain proteins.	09 595-612
,,,	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 8.412e-
	.]	region RNP-1 proceins.	11 322-341 BL00030A 14.39 7.000e-10 220-
779			239
, , ,	PR00079	GLUCOSE-6-PHCSPHATE DEHYDROGENASE SIGNATURE	PR00079B 12.9B 2.929e-
	i	DESTIDATORE SIGNATURE	26 193-222 PR00079E 16.65 4.150e-23 348-
	J		375 PR00079C 8.68
			6.351e-16 246-264
			PR00079D 13.51 7.070e- 16 264-281 PR00079A
			16.12 6.769e-13 169-
781	BL00215	Mitochondrial energy	183
	-200220	transfer proteins.	BL00215A 15.82 9.250e- 17 10-35 BL00215A
			15.82 6.000e-16 221-
•	1		246 BL00215A 15.82
.			7.857e-12 108-133
0.2			BL00215B 10.44 9.526e- 11 168-181
83	PD00289	PROTEIN SH3 DOMAIN	PD00289 9.97 6.276e-09
85	BL00690	REPEAT PRESYNA.  DEAH-box subfamily ATP-	159-173
	·	dependent helicases	BL00690B 13.38 1.000e- 12 147-165 BL00690A
		proteins.	6.87 5.320e-10 114-124
1		1	BL00690C 7.51 3.189e-
86	PR00449	TRANSFORMING PROTEIN P21	09 218-228 PR00449C 17.27 8.500e-
İ		RAS SIGNATURE	16 50-73 PR00449A
			13.20 5.235e-14 8-30
			PR00449E 13.50 2.853e-
		1	
			11 150-173 PR00449D 10.79 1.545e-09 111-
18	DM01305		10.79 1.545e-09 111-
38	DM01206	CORONAVIRUS NUCLEOCAPSID	10.79 1.545e-09 111- 125 DM01206B 10.69 8.767e-
	DM01206 BL00915	CORONAVIRUS NUCLEOCAPSID PROTEIN. Phosphatidylinositol 3-	10.79 1.545e-09 111- 125

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
	NO.		
1	ĺ		22.78 5.050e-33 633-
1		ľ	671 BL00915D 27.02
	ł		1.529e-21 795-831 BL00915A 10.09 1.000e-
1	ļ	<b>1</b>	13 395-407
791	PR00208	GLIADIN AND LMW GLUTENIN	
	- }	SUPERFAMILY SIGNATURE	10 120-138 PR00208A
	Ì		12.59 6.294e-10 121-
İ		ĺ	139 PR00208A 12.59
		}	6.294e-10 122-140
	i		PR00208A 12.59 6.294e-
			10 123-141 PR00208A
	ĺ		12.59 6.294e-10 124-
			142 PR00208A 12.59
			6.294e-10 125-143
}			PR00208A 12.59 6.294e-
			10 126-144 PR00208A
			12.59 6.294e-10 127-
			145 PR00208A 12.59
j	}		6.294e-10 128-146
		1 .	PR00208A 12.59 6.294e- 10 129-147 PR00208A
	1		12.59 7.411e-09 130-
	· · · · · ·		148 PR00208A 12.59
•			7.658e-09 131-149
			PR00208A 12.59 7.904e-
			09 132-150 PR00208A
			12.59 8.274e-09 118-
	ļ		136 PR00208A 12.59
		<u>,                                     </u>	8.274e-09 119-137
795	PR00205	CADHERIN SIGNATURE	PR00205B 11.39 5.034e-
			16 302-320 PR00205A
	į.		14.73 1.257e-11 284-
	1.		300 PR00205C 13.65
796	BL00412	Neuromodulin (GAP-43)	1.333e-11 337-352
		proteins.	BL00412D 16.54 4.000c- 12 196-247 BL00412D
	İ	F	16.54 5.705e-11 197-
	l l		
	i	,	248 BI-00412D 16 54
		,	248 BL00412D 16.54 7.848e-10 199-250
•		,	7.848e-10 199-250
			7.848e-10 199-250 BL00412D 16.54 1.827e-
			7.848e-10 199-250 BL00412D 16.54 1.827e- 09 195-246 BL00412D
707			7.848e-10 199-250 BL00412D 16.54 1.827e- 09 195-246 BL00412D 16.54 1.918e-09 194- 245 BL00412D 16.54 2.102e-09 201-252
797	BF00051	Kringle domain proteins.	7.848e-10 199-250 BL00412D 16.54 1.827e- 09 195-246 BL00412D 16.54 1.918e-09 194- 245 BL00412D 16.54 2.102e-09 201-252 BL00021B 13.33 6.339e-
		†	7.848e-10 199-250 BL00412D 16.54 1.827e- 09 195-246 BL00412D 16.54 1.918e-09 194- 245 BL00412D 16.54 2.102e-09 201-252 BL00021B 13.33 6.339e- 13 40-58
797	BL00021	Calponin family repeat	7.848e-10 199-250 BL00412D 16.54 1.827e- 09 195-246 BL00412D 16.54 1.918e-09 194- 245 BL00412D 16.54 2.102e-09 201-252 BL00021B 13.33 6.339e- 13 40-58 BL01052C 18.51 1.000e-
		†	7.848e-10 199-250 BL00412D 16.54 1.827e- 09 195-246 BL00412D 16.54 1.918e-09 194- 245 BL00412D 16.54 2.102e-09 201-252 BL00021B 13.33 6.339e- 13 40-58 BL01052C 18.51 1.000e- 40 87-127 BL01052A
		Calponin family repeat	7.848e-10 199-250 BL00412D 16.54 1.827e- 09 195-246 BL00412D 16.54 1.918e-09 194- 245 BL00412D 16.54 2.102e-09 201-252 BL00021B 13.33 6.339e- 13 40-58 BL01052C 18.51 1.000e- 40 87-127 BL01052A 16.12 1.529e-32 3-35
		Calponin family repeat	7.848e-10 199-250 BL00412D 16.54 1.827e- 09 195-246 BL00412D 16.54 1.918e-09 194- 245 BL00412D 16.54 2.102e-09 201-252 BL00021B 13.33 6.339e- 13 40-58 BL01052C 18.51 1.000e- 40 87-127 BL01052A 16.12 1.529e-32 3-35 BL01052B 15.31 1.257e-
		Calponin family repeat	7.848e-10 199-250 BL00412D 16.54 1.827e- 09 195-246 BL00412D 16.54 1.918e-09 194- 245 BL00412D 16.54 2.102e-09 201-252 BL00021B 13.33 6.339e- 13 40-58 BL01052C 18.51 1.000e- 40 87-127 BL01052A 16.12 1.529e-32 3-35 BL01052B 15.31 1.257e- 25 52-78 BL01052D
799		Calponin family repeat	7.848e-10 199-250 BL00412D 16.54 1.827e- 09 195-246 BL00412D 16.54 1.918e-09 194- 245 BL00412D 16.54 2.102e-09 201-252  BL00021B 13.33 6.339e- 13 40-58 BL01052C 18.51 1.000e- 40 87-127 BL01052A 16.12 1.529e-32 3-35 BL01052B 15.31 1.257e- 25 52-78 BL01052D 10.26 5.737e-25 174-
		Calponin family repeat proteins.	7.848e-10 199-250 BL00412D 16.54 1.827e- 09 195-246 BL00412D 16.54 1.918e-09 194- 245 BL00412D 16.54 2.102e-09 201-252 BL00021B 13.33 6.339e- 13 40-58 BL01052C 18.51 1.000e- 40 87-127 BL01052A 16.12 1.529e-32 3-35 BL01052B 15.31 1.257e- 25 52-78 BL01052D 10.26 5.737e-25 174- 194
799	BL01052	Calponin family repeat proteins.  p53 tumor antigen proteins.	7.848e-10 199-250 BL00412D 16.54 1.827e- 09 195-246 BL00412D 16.54 1.918e-09 194- 245 BL00412D 16.54 2.102e-09 201-252  BL00021B 13.33 6.339e- 13 40-58 BL01052C 18.51 1.000e- 40 87-127 BL01052A 16.12 1.529e-32 3-35 BL01052B 15.31 1.257e- 25 52-78 BL01052D 10.26 5.737e-25 174-
799	BL01052	Calponin family repeat proteins.  p53 tumor antigen proteins.  Vertebrate galactoside-	7.848e-10 199-250 BL00412D 16.54 1.827e- 09 195-246 BL00412D 16.54 1.918e-09 194- 245 BL00412D 16.54 2.102e-09 201-252 BL00021B 13.33 6.339e- 13 40-58 BL01052C 18.51 1.000e- 40 87-127 BL01052A 16.12 1.529e-32 3-35 BL01052B 15.31 1.257e- 25 52-78 BL01052D 10.26 5.737e-25 174- 194 BL00348F 23.19 3.714e- 09 197-240
799 800	BL00348 BL00309	Calponin family repeat proteins.  p53 tumor antigen proteins.  Vertebrate galactoside-binding lectin proteins.	7.848e-10 199-250 BL00412D 16.54 1.827e- 09 195-246 BL00412D 16.54 1.918e-09 194- 245 BL00412D 16.54 2.102e-09 201-252 BL00021B 13.33 6.339e- 13 40-58 BL01052C 18.51 1.000e- 40 87-127 BL01052A 16.12 1.529e-32 3-35 BL01052B 15.31 1.257e- 25 52-78 BL01052D 10.26 5.737e-25 174- 194 BL00348F 23.19 3.714e-
799	BL01052	Calponin family repeat proteins.  p53 tumor antigen proteins.  Vertebrate galactoside-binding lectin proteins.  OLFACTORY RECEPTOR	7.848e-10 199-250 BL00412D 16.54 1.827e- 09 195-246 BL00412D 16.54 1.918e-09 194- 245 BL00412D 16.54 2.102e-09 201-252 BL00021B 13.33 6.339e- 13 40-58 BL01052C 18.51 1.000e- 40 87-127 BL01052A 16.12 1.529e-32 3-35 BL01052B 15.31 1.257e- 25 52-78 BL01052D 10.26 5.737e-25 174- 194 BL00348F 23.19 3.714e- 09 197-240 BL00309C 18.65 1.621e- 09 62-87
799 800 801 802	BL01052  BL00348  DL00309  PR00245	Calponin family repeat proteins.  p53 tumor antigen proteins.  Vertebrate galactoside-binding lectin proteins.  OLFACTORY RECEPTOR SIGNATURE	7.848e-10 199-250 BL00412D 16.54 1.827e- 09 195-246 BL00412D 16.54 1.918e-09 194- 245 BL00412D 16.54 2.102e-09 201-252 BL00021B 13.33 6.339e- 13 40-58 BL01052C 18.51 1.000e- 40 87-127 BL01052A 16.12 1.529e-32 3-35 BL01052B 15.31 1.257e- 25 52-78 BL01052D 10.26 5.737e-25 174- 194 BL00348F 23.19 3.714e- 09 197-240 BL00309C 18.65 1.621e-
799 800	BL00348 BL00309	Calponin family repeat proteins.  p53 tumor antigen proteins.  Vertebrate galactosidebinding lectin proteins.  OLFACTORY RECEPTOR SIGNATURE Dihydropyridine	7.848e-10 199-250 BL00412D 16.54 1.827e- 09 195-246 BL00412D 16.54 1.918e-09 194- 245 BL00412D 16.54 2.102e-09 201-252 BL00021B 13.33 6.339e- 13 40-58 BL01052C 18.51 1.000e- 40 87-127 BL01052A 16.12 1.529e-32 3-35 BL01052B 15.31 1.257e- 25 52-78 BL01052D 10.26 5.737e-25 174- 194 BL00348F 23.19 3.714e- 09 197-240 BL00309C 18.65 1.621e- 09 62-87 PR00245D 10.47 5.224e-
799 800 801 802	BL01052  BL00348  DL00309  PR00245	Calponin family repeat proteins.  p53 tumor antigen proteins.  Vertebrate galactoside-binding lectin proteins.  OLFACTORY RECEPTOR SIGNATURE Dihydropyridine sensitive L-type calcium	7.848e-10 199-250 BL00412D 16.54 1.827e- 09 195-246 BL00412D 16.54 1.918e-09 194- 245 BL00412D 16.54 2.102e-09 201-252  BL00021B 13.33 6.339e- 13 40-58 BL01052C 18.51 1.000e- 40 87-127 BL01052A 16.12 1.529e-32 3-35 BL01052B 15.31 1.257e- 25 52-78 BL01052D 10.26 5.737e-25 174- 194 BL00348F 23.19 3.714e- 09 197-240 BL00309C 18.65 1.621e- 09 62-87 PR00245D 10.47 5.224e- 09 187-199
800 801 802	BL00348 BL00309 PR00245 PF00774	Calponin family repeat proteins.  p53 tumor antigen proteins.  Vertebrate galactoside-binding lectin proteins.  OLFACTORY RECEPTOR SIGNATURE Dihydropyridine sensitive L-type calcium channel (Beta subuni.	7.848e-10 199-250 BL00412D 16.54 1.827e- 09 195-246 BL00412D 16.54 1.918e-09 194- 245 BL00412D 16.54 2.102e-09 201-252  BL00021B 13.33 6.339e- 13 40-58 BL01052C 18.51 1.000e- 40 87-127 BL01052A 16.12 1.529e-32 3-35 BL01052B 15.31 1.257e- 25 52-78 BL01052D 10.26 5.737e-25 174- 194 BL00348F 23.19 3.714e- 09 197-240 BL00309C 18.65 1.621e- 09 62-87 PR00245D 10.47 5.224e- 09 187-199 PF00774A 16.47 8.457e-
799 800 801 802	BL01052  BL00348  DL00309  PR00245	Calponin family repeat proteins.  p53 tumor antigen proteins.  Vertebrate galactoside-binding lectin proteins.  OLFACTORY RECEPTOR SIGNATURE  Dihydropyridine sensitive L-type calcium channel (Beta subuni.  RETINAL PIGMENT	7.848e-10 199-250 BL00412D 16.54 1.827e- 09 195-246 BL00412D 16.54 1.918e-09 194- 245 BL00412D 16.54 2.102e-09 201-252 BL00021B 13.33 6.339e- 13 40-58 BL01052C 18.51 1.000e- 40 87-127 BL01052A 16.12 1.529e-32 3.35 BL01052B 15.31 1.257e- 25 52-78 BL01052D 10.26 5.737e-25 174- 194 BL00348F 23.19 3.714e- 09 197-240 BL00309C 18.65 1.621e- 09 62-87 PR00245D 10.47 5.224e- 09 187-199 PF00774A 16.47 8.457e- 10 110-156
800 801 802	BL00348 BL00309 PR00245 PF00774	Calponin family repeat proteins.  p53 tumor antigen proteins.  Vertebrate galactosidebinding lectin proteins.  OLFACTORY RECEPTOR SIGNATURE  Dihydropyridine sensitive L-type calcium channel (Beta subuni.  RETINAL PIGMENT EPITHELIUM-RETINAL GPCR	7.848e-10 199-250 BL00412D 16.54 1.827e- 09 195-246 BL00412D 16.54 1.918e-09 194- 245 BL00412D 16.54 2.102e-09 201-252 BL00021B 13.33 6.339e- 13 40-58 BL01052C 18.51 1.000e- 40 87-127 BL01052A 16.12 1.529e-32 3-35 BL01052B 15.31 1.257e- 25 52-78 BL01052D 10.26 5.737e-25 174- 194 BL00348F 23.19 3.714e- 09 197-240 BL00309C 18.65 1.621e- 09 62-87 PR0245D 10.47 5.224e- 09 187-199 PF00774A 16.47 8.457e- 10 110-156
800 801 802 804	BL01052  BL00348  DL00309  PR00245  PF00774  PR00667	Calponin family repeat proteins.  p53 tumor antigen proteins.  Vertebrate galactoside-binding lectin proteins.  OLFACTORY RECEPTOR SIGNATURE  Dihydropyridine sensitive L-type calcium channel (Beta subuni.  RETINAL PIGMENT EPITHELIUM-RETINAL GPCR SIGNATURE	7.848e-10 199-250 BL00412D 16.54 1.827e- 09 195-246 BL00412D 16.54 1.918e-09 194- 245 BL00412D 16.54 2.102e-09 201-252 BL00021B 13.33 6.339e- 13 40-58 BL01052C 18.51 1.000e- 40 87-127 BL01052A 16.12 1.529e-32 3-35 BL01052B 15.31 1.257e- 25 52-78 BL01052D 10.26 5.737e-25 174- 194 BL00348F 23.19 3.714e- 09 197-240 BL00309C 18.65 1.621e- 09 62-87 PR00245D 10.47 5.224e- 09 187-199 PF00774A 16.47 8.457e- 10 110-156  PR00667C 11.71 9.875e- 09 12-28
800 801 802	BL00348 BL00309 PR00245 PF00774	Calponin family repeat proteins.  p53 tumor antigen proteins.  Vertebrate galactosidebinding lectin proteins.  OLFACTORY RECEPTOR SIGNATURE  Dihydropyridine sensitive L-type calcium channel (Beta subuni.  RETINAL PIGMENT EPITHELIUM-RETINAL GPCR	7.848e-10 199-250 BL00412D 16.54 1.827e- 09 195-246 BL00412D 16.54 1.918e-09 194- 245 BL00412D 16.54 2.102e-09 201-252 BL00021B 13.33 6.339e- 13 40-58 BL01052C 18.51 1.000e- 40 87-127 BL01052A 16.12 1.529e-32 3.35 BL01052B 15.31 1.257e- 25 52-78 BL01052D 10.26 5.737e-25 174- 194 BL00348F 23.19 3.714e- 09 197-240 BL00309C 18.65 1.621e- 09 62-87 PR00245D 10.47 5.224e- 09 187-199 PF00774A 16.47 8.457e- 10 110-156

SEQ ID N	O:   ACCESSION	DESCRIPTION	RESULTS*
	NO.		1000010
		PHOTOSYNTHESIS.	
811	BL00685	CBF-A/NF-YB subunit	BL00685B 14.41 6.779e-
		proteins.	14 54-95 BL00685A
812	PR00080	ALCOHOL DEHYDROGENASE	11.22 4.798e-13 5-54
012	PROODSO	SUPERFAMILY SIGNATURE	PR00080A 9.32 9.419e-
813	BL00357	Histone H2B proteins.	BL00357 7.74 1.988e-17
		miscome aza proceins.	22-65
815	PD00066	PROTEIN ZINC-FINGER	PD00066 13.92 7.923e-
		METAL-BINDI.	15 158-171 PD00066
			13.92 5.200e-14 46-59
			PD00066 13.92 7.000e- -14 18-31 PD00066
			13.92 7.000e-13 130-
			143 PD00066 13.92
			7.500e-13 214-227
	1		PD00066 13.92 9.000e-
			13 102-115 PD00066
			13.92 4.429e-12 186-
			199 PD00066 13.92
816	BL01195	Dont i deal Laws Laws	1.783e-11 74-87
310	BP01132	Peptidyl-tRNA hydrolase proteins.	BL01195C 20.12 3.348e-
820	BLC0520	Interleukin-10 family	20 100-139 BL00520A 6.21 6.471e-
		proteins.	09 1-14
822	BL00972	Ubiquitin carboxyl-	BL00972A 11.93 8.113e-
		terminal hydrolases	09 224-242
		family 2 proteins.	
825	PR00876	NEMATODE METALLOTHIONEIN	PR00876B 7.66 2.268e-
000		SIGNATURE	10 101-115
829	PD02855	FLAVOPROTEIN PROTEIN	PD02855A 18.37 4.732c-
	i	DNA/PANTOTHEN.	28 88-124 PD02855B 8.36 6.478e-09 132-142
830	PRO0405	HIV REV INTERACTING	PR00405B 11.83 7.000e-
	1	PROTEIN SIGNATURE	21 44-62 PR00405C
			19.41 1.000e-13 65-87
			PR00405A 17.71 7.283e-
			13 25-45
831	2R00019	LEUCINE-RICH REPEAT	PR00019A 11.19 1.000e-
		SIGNATURE	09 47-61 PR00019B
		1	11.36 1.720e-09 136- 150 PR00019B 11.36
		Ì	3.880e-09 44-58
832	PR00011	TYPE III EGF-LIKE	PR00011B 13.08 3.438e-
	ŀ	SIGNATURE	16 164-183 PR00011D
			14.03 6.850e-16 164-
	1		183 PRO0011A 14.06
		1	8.364e-14 164-183
	1		PR00011C 24.25 5.415e-
		1	12 231-260 PR00011D 14.03 9.852e-11 212-
	1		231
834	PD00306	PROTEIN GLYCOPROTEIN	PD00306A 10.26 7.000e-
		PRECURSOR RE.	12 232-246
835	PD00306	PROTEIN GLYCOPROTEIN	PD00306A 10.26 4.000e-
016	100000	PRECURSOR RE.	10 290-304
836	PD00306	PROTEIN GLYCOPROTEIN	PD00306A 10.26 7.000e-
837	DM00215	PRECURSOR RE.	12 216-230
· · ·	DN00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 3.898e-
839	PD02784	PROTEIN NUCLEAR	09 78-111
-		RIBONUCLEOPROTEIN.	PD02784B 26.46 8.302e- 09 73-116
840	PR00700	PROTEIN TYROSINE	PR00700B 16.80 5.091e-
		PHOSPHATASE SIGNATURE	22 369-390 PR00700D
			12.47 5.765e-21 491-
			510 PR00700C 13.17
			4.750e-14 449-467
			PR00700F 11.18 8.500e-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			11 538-549 PR00700E 17.57 3.100e-10 522- 538
841 .	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PR00109B 12.27 5.404e- 13 134-153
844	PD02785	PROTEIN RIBOSOMAL 60S L22 RNA-BINDING HEP	PD02785B 14.43 1.000e- 40 58-112 PD02785A 15.23 1.915e-28 8-57
845	BLC0826	MARCKS family proteins.	BL00826C 7.63 6.738e- 09 203-230
846	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 4.429e- 10 15-24
849	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 1.000e- 08 340-349
850	PR00308	TYPE I ANTIFREEZE PROTEIN SIGNATURE	PR00308A 5.90 6.506e-
851	PD02411	PROTEIN TRANSCRIPTION	PD02411 21.89 7.000e-
852	BL00420	REGULATION NUCLEAR.  Speract receptor repeat proteins domain proteins.	16 246-280  BL00420B 22.67 1.000e- 40 723-778 BL00420B 22.67 1.321e-38 933- 988 BL00420B 22.67 8.457e-28 482-537 BL00420B 22.67 4.500e- 27 587-642 BL00420B 22.67 9.625e-27 270- 325 BL00420B 22.67 4.205e-26 163-218 BL00420B 22.67 5.731e- 23 55-110 BL00420B 22.67 6.464e-20 377- 432 BL00420B 22.67 2.800e-15 830-885 BL00420C 11.90 1.900e- 13 355-366 BL00420C 11.90 1.900e-12 808- 819 BL00420C 11.90 3.550e-12 248-259 BL00420C 11.90 2.831e- 11 141-152 BL00420C 11.90 5.119e-11 1018- 1029 BL00420C 11.90 7.955e-10 567-578
	BL00420	Speract receptor repeat proteins domain proteins.	### BL00420B 22.67 1.000e- 40 756-811 BL00420B 22.67 1.321e-38 966- 1021 BL00420B 22.67 8.457e-28 482-537 BL00420B 22.67 4.500e- 27 620-675 BL00420B 22.67 9.625e-27 270- 325 BL00420B 22.67 4.205e-26 163-218 BL00420B 22.67 5.731e- 23 55-110 BL00420B 22.67 6.464e-20 377- 432 BL00420B 22.67 2.800e-15 863-918 BL00420C 11.90 1.900e- 13 355-366 BL00420C 11.90 1.900e-12 841- 852 BL00420C 11.90 3.550e-12 248-259 BL00420C 11.90 2.831e- 11 141-152 BL00420C 11.90 5.119e-11 1051- 1062 BL00420C 11.90

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
<del></del>	NO.	<del></del>	7.955e-10 567-578
857	PR00388	3',5'-CYCLIC NUCLEOTIDE	PR00388A 10.45 2.778e-
		CLASS II PHOSPHODIESTERASE SIGNATURE	09 64-83
859	BL00030	Eukaryotic RNA-binding	BL00030A 14.39 2.929e-
		region RNP-1 proteins.	13 37-56 BL00030B
	}		7.03 1.900e-11 167-177
		•	BL00030A 14.39 2.000e- 10 128-147
861	PR00988	URIDINE KINASE SIGNATURE	PR00988A 6.39 4.250e-
ļ			17 23-41 PR00988C
ĺ			13.64 8.714e-16 107- 123 PR00988F 12.23
	İ		7.828e-15 198-212
			PR00988E 8.27 9.769e-
			12 176-188 PR00988D
			5.95 8.250e-11 163-174
			PR00988B 11.60 4.512e-
863	BL00215	Mitochondrial energy	BL00215B 10.44 8.071e-
864	22000	transfer proteins.	12 41-54
864	PR00775	90 KD HEAT SHOCK PROTEIN SIGNATURE	PR00775E 8.06 1.000e-
		S_GNATURE	24 198-221 PR00775B 3.52 1.837e-23 107-130
		į	PR00775D 8.91 4.484e-
			17 171-189 PR00775A
	4	1	9.90 8.342e-17 86-107
		:	PR00775C 10.68 9.379e- 17 153-171 PR00775G
	•	1	10.64 6.850e-15 267-
			286 PR00775F 12.76
866	DM01688	2 POLY-IG RECEPTOR	6.769e-14 249-267
		2 POLITIG RECEPTOR.	DM01688G 16.45 9.460e- 09 89-121
867	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 5.596e-
		ZINC-FINGER METAL- BINDING NU.	29 14-53
868	BL01287	RNA 3'-terminal	BL01287A 17.95 2.688e-
		phosphate cyclase	26 16-48
869	DM00215	PROLINE-RICH PROTEIN 3.	
	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 6.464e- 10 304-337
872	BL00046	Histone H2A proteins.	BL00046 12.95 1.000e-
0.7			40 30-85
874	BL00188	Biotin-requiring enzymes attachment site	BL00188 30.29 9.036e-
1		proteins.	32 665-711
876	BL00028	Zinc finger, C2H2 type,	BL00028 16.07 7.686e-
977		domain proteins.	09 298-315
877	PD02102	SUBUNIT E V-ATPASE	PD02102A 16.74 4.176e-
		VACUOLAR ATP SYNTHASE HYDROL.	10 97-141
879	BL01189	Ribosomal protein S12e	BL01189A 14.27 1.000e-
		proteins.	40 35-71 BL01189B
882	BL00284		13.49 1.000e-40 71-125
	DUUU294	Serpins proteins.	BL00284C 28.56 6.400e-
_			25 62-104 BL00284B 17.99 6.182e-12 35-56
889	BL00216	Sugar transport	BL00216B 27.64 4.375e-
995	770000	proteins.	21 35-85
896	PR00391	PHOSPHATIDYLINOSITOL	PR00391E 12.50 7.785e-
1		TRANSFER PROTEIN SIGNATURE	15 211-231 PR00391B 8.39 1.000e-13 83-104
1	}		PR00391D 12.21 9.328e-
-			13 191-207 PR00391A
897	PR00327	V. C. C. C. C. C. C. C. C. C. C. C. C. C.	7.83 5.390e-11 16-36
	EKUU321	ICE NUCLEATION PROTEIN	PR00327C 6.37 5.247e-

SEQ ID NO	ACCESSION	DESCRIPTION	RESULTS*
	NO.		
898	- DV 00077	SIGNATURE	09 313-328
090	BL00039	DEAD-box subfamily ATP- dependent helicases proteins.	BL00039D 21.67 7.800e- 26 386-432 BL00039A 18.44 6.674e-16 113- 152 BL00039B 19.19 1.947e-13 153-179 BL00039C 15.63 9.460e- 11 236-260
901	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 8.200e- 16 254-267 PD00066 13.92 8.200e-16 282- 295 PD00066 13.92 8.200e-16 310-323 PD00066 13.92 8.200e- 16 366-379 PD00066 13.92 8.200e-16 394- 407 PD00066 13.92
902	BL01115	GTP-binding nuclear	8.200e-14 338-351 BL01115A 10.22 9.321e-
903	PR00806	protein ran proteins. VINCULIN SIGNATURE	11 6-50
			PR00806B 4.28 9.160e- 09 97-111
904	PR00381	KINESIN LIGHT CHAIN SIGNATURE	PR00381E 8.75 6.586e- 25 335-356 PR00381B 18.17 2.667e-24 204- 224 PR00381A 9.55 2.800e-24 107-125 PR00381C 12.48 4.522e- 24 226-245 PR00381D 13.94 1.084e-22 291- 309 PR00381F 9.13 3.288e-22 370-392 PR00381F 9.13 7.181e- 13 286-308 PR00381E 8.75 4.066e-11 251-272 PR00381E 8.75 7.033e- 11 293-314 PR00381E 8.75 8.364e-10 377-398 PR00381D 13.94 5.230e- 09 333-351 PR00381C 12.48 7.120e-09 310- 329
906	PR00345	STATHMIN FAMILY SIGNATURE	PR00345C 4.54 8.557e- 09 525-549
907	PR00345	STATHMIN FAMILY	PR00345C 4.54 8.557e-
908	BL00678	SIGNATURE Trp-Asp (WD) repeat	09 513-537 BL00678 9.67 9.308e-11
910	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-	144-155 PD01066 19.43 2.800e- 30 48-87
912	BL01104	BINDING NU. Ribosomal protein 113e	BL01104C 15.14 6.000e-
922	3L00678	proteins. Trp-Asp (WD) repeat	09 364-392 BL00678 9.67 3.842e-09
022		proteins proteins.	500-511
923	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320C 13.01 2.500e- 09 323-338 PR00320C 13.01 5.500e-09 187- 202
924	PD02181	PROTOCHLOROPHYLLIDE	PD02181D 12.85 8.609e-
926	BL00019	REDUCTASE PHOTOSYNT.  Actinin-type actin- binding domain proteins.	09 36-54 BL00019C 14.66 7.453e- 25 108-144 BL00019B 13.34 6.510c-11 61-84 BL00019D 15.33 9.338e- 11 205-235 BL00019A
928	BL00678	Trp-Asp (WD) repeat	12.56 2.373e-10 34-45 BL00678 9.67 9.308e-11
	<del></del>	15 -us (un) Tehear	220000 9.07 9.308E-11

SEQ ID I	NO: ACCESSION	DESCRIPTION	RESULTS*
	NO.	<b>_</b>	
		proteins proteins.	273-284 BL00678 9.67 1.600e-10 314-325
	}		BL00678 9.67 7.600e-10
			360-371 BL00678 9.67
929	77.005.0		8.579e-09 206-217
929	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 1.857e-
930	BL01085	Ribulose-phosphate 3-	10 137-146 BL01085D 16.55 4.600e-
		epimerase family	24 134-165 BL01085B
		proteins.	10.15 5.680e-22 30-52
			BL01085E 18.87 8.676e-
			20 172-202 BL01085C 21.81 2.038e-14 66-97
931	BL01085	Ribulose-phosphate 3-	BLC1085D 16.55 4.600e-
		epimerase family	24 152-183 BL01085B
		proteins.	10.15 5.680e-22 30-52
			BL01085E 18.87 8.676e-
		İ	20 190-220 BL01085C 21.81 2.038e-14 66-97
933	PD00301	PROTEIN REPEAT MUSCLE	PD00301A 10.24 6.400e-
03.5		CALCIUM-BI.	09 160-171
936	PF00168	C2 domain proteins.	PF00168C 27.49 4.000e-
937	BL00415	Synapsins proteins.	12 336-362 BL00415N 4.29 9.519e-
		-1pozno proterna.	10 5-49
940	PR00862	PROLYL OLIGOPEPTIDASE	PR00862D 16.17 4.086e-
		SERINE PROTEASE (S9A)	09 63-84
945	BL01230	RNA methyltransferase	BL01230B 11.62 2.373e-
	5202250	trmA family proteins.	09 407-420
948	BL00479	Phorbol esters /	BL00479B 12.57 7.429e-
		diacylglycerol binding	18 52-68 BL00479A
949	BL00678	domain proteins. Trp-Asp (WD) repeat	19.86 2.200e-13 26-49
	3200078	proteins proteins.	BL00678 9.67 1.474e-09
954	PD01311	PROTEIN OXIDOREDUCTASE	PD01311A 30.23 5.909e-
		NAD INTERGENIC RE.	10 66-111
955	PF00651	BTB (also known as BR-	PF00651 15.00 3.250e-
956	PF00651	C/Ttk) domain proteins.  BTB (also known as BR-	12 47-60 PF00651 15.00 3.250e-
		C/Ttk) domain proteins.	12 47-60
957	BL00379	CDP-alcohol	BL00379 24.64 1.610e-
		phosphatidyltransferases proteins.	15 111-148
959	BL01115	GTP-binding nuclear	BL01115A 10.22 1.884e-
		protein ran proteins.	10 31-75
960	BL01115	GTP-binding nuclear	BL01115A 10.22 3.438e-
962	BL00061	protein ran proteins. Short-chain	14 110-154
	PP00091	Short-chain dehydrogenases/reductase	BL00061B 25.79 6.586e- 13 198-236
		s family proteins.	13 130-230
963	PR00502	MUTT DOMAIN SIGNATURE	PR00502A 15.06 8.200e-
966	PRO0300		11 210-225
	PR00308	TYPE I ANTIFREEZE PROTEIN SIGNATURE	PR00308A 5.90 7.035e-
967	DM01206	CORONAVIRUS NUCLEOCAPSID	09 55-70 DM01206B 10.69 1.286e-
	1	PROTEIN.	12 104-124 DM01206B
			10.69 5.299e-11 23-43
			DM01206B 10.69 8.274e-
			10 73-93 DM01206B 10.69 3.962e-09 108-
			128 DM01206B 10.69
			5.671e-09 38-58
969	PF01008	Initiation factor 2	PF01008B 25.59 4.724e-
	1	subunit.	31 417-460 PF01008C
		· {	12.25 5.333e-18 506- 526 PF01008A 20.14
			5.875e-15 369-390

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
970	NO. BL01277		
370	BL01277	Ribonuclease PH proteins.	BL01277C 10.18 7.648e- 10 112-143 BL01277A
		proteins.	17.39 9.805e-10 40-78
975	BL01159	WW/rsp5/wwp domain	BL01159 13.85 3.605e-
]		proteins.	12 130-145 BL01159
1			13.85 4.122e-10 171-
688			186
977	PF00791	Domain present in ZO-1	PF00791C 20.98 2.235e-
		and Unc5-like netrin receptors.	09 55-94
978	BL01167	Ribosomal protein L17	BL01167B 20.66 8.258e-
		proteins.	19 88-127
979	BL00478	LIM domain proteins.	BL00478B 14.79 9.357e-
			13 33-48 BL00478B
980	77000110		14.79 7.250e-12 98-113
360	PR00312	CALSEQUESTRIN SIGNATURE	PR00312E 8.32 3.423e-
			36 169-199 PR00312I 15.78 5.286e-35 332-
	}		361 PR00312F 15.06
			5.865e-35 199-229
•			PR00312H 13.31 8.313e-
	]		35 263-291 PR00312J
	İ		13.73 5.688e-34 363-
			392 PR00312D 9.43 2.636e-33 128-158
			PR00312C 15.14 8.839e-
			33 92-122 PR00312B
			15.08 8.941e-33 62-92
			PR00312G 11.11 6.657e-
			32 230-258 PR00312A
981	PF00992	Troponin.	11.70 6.914e-27 35-59 PF00992A 16.67 8.816e-
			09 414-449
982	PR00299	ALPHA CRYSTALLIN	PR00299F 13.20 2.367e-
000		SIGNATURE	09 127-149
983	BL01150	Respiratory-chain NADH	BL01150B 17.16 1.000e-
		dehydrogenase 20 Kd subunit proteins.	40 156-202 BL01150A 14.10 8.200e-39 100-
•	i	basanze protectis.	138
986	BL00795	Involucrin proteins.	BL00795C 17.06 7.211e-
			14 4-49 BL00795C
	ł		17.06 1.778e-11 1-46
		}	BL00795C 17.06 3.407e-
•		1	17.06 7.802e-10 2-47
			BL00795C 17.06 8.640e-
			10 19-64 BL00795C
			17.06 7.400e-09 11-56
			BL00795C 17.06 7.800e-
987	3L00939	Ribosomal protein Lie	09 3-48
		proteins.	BL00939F 17.27 5.393e- 09 810-840
988	PR00452	SH3 DOMAIN SIGNATURE	PR00452B 11.65 6.538e-
000			11 525-541
989	PR00452	SH3 DOMAIN SIGNATURE	PR00452B 11.65 6.538e-
994	BL00027	- Home-V	11 497-513
	200027	'Homeobox' domain proteins.	BL00027 26.43 2.500e- 25 146-189
997	BL01304	ubiH/COQ6 monooxygenase	BL01304A 8.05 3.893e-
	<u> </u>	family proteins.	11 65-79
998	DM01767	5 TRANSMITTER DOMAIN.	DM01767B 10.07 7.868e-
1000			09 22-39
1000	PR00926	MITOCHONDRIAL CARRIER	PR00926C 16.07 1.750e-
		PROTEIN SIGNATURE	24 73-94 PR00926D
ł		1	10.53 3.250e-23 126-
1		1	145 PR00926F 17.75 6.211e-23 217-240
1			PR00926E 11.70 6.625e-
		······	

SEQ ID NO:	ACCESSION	DESCRIPTION	I BERRY BOL
	NO.	DESCRIPTION	RESULTS*
			20 174-193 PR00926B
ļ			16.07 2.125e-18 24-39
	Ì		PR00926A 10.41 1.000e-
			15 11-25 PR00926F
<b>{</b>	İ		17.75 5.565e-09 120-
1000			143
1005	BL00406	Actins proteins.	BL00406B 5.47 1.000e-
			40 88-143 BL00406C
			6.75 1.000e-40 147-202
			BL00406D 12.58 3.700e-
			40 270-325 BL00406E
	ļ		8.44 7.375e-38 327-377
			BL00406A 9.95 3.348e-
			29 11-46
1006	BL00406	Actins proteins.	BL00406B 5.47 1.000e-
		_	40 88-143 BL00406C
			6.75 1.000e-40 147-202
		ľ	BL00406E 8.44 1.000e-
			35 248-298 BL00406A
			9.95 3.348e-29 11-46
1007	PR00304	TAILLESS COMPLEX	PR00304D 11.04 8.714e-
	1	POLYPEPTIDE 1	22 384-407 PR00304C
	1	(CHAPERONE) SIGNATURE	8.69 4.667e-20 98-118
			PR00304B 11.60 7.577e-
			19 68-87 PROC304A
			9.20 3.382e-16 46-63
			PR00304E 7.79 6.870e-
			13 418-431
1009	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 2.929e-
		ZINC-FINGER METAL	32 9-48
	1	BINDING NU.	32 3-40
1011	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 2.929e-
		ZINC-FINGER METAL-	32 68-107
		BINDING NU.	32 08-107
1012	BL00518	Zinc finger, C3HC4 type	BL00518 12.23 6.143e-
		(RING finger), proteins.	10 64-73
1016	PD01168	SYNTHETASE LIGASE	PD01168H 12.08 1.000e-
		PROTEIN ALANYL.	11 174-194
1018	PD00930	PROTEIN GTPASE DOMAIN	PD00930B 33.72 1.391e-
		ACTIVATION.	32 261-302 PD00930A
			25.62 9.550e-22 157-
	1		183
1022	BL00175	Phosphoglycerate mutase	BL00175A 15.42 5.179e-
		family phosphohistidine	12 6-26 BL00175C
		proteins.	23.75 8.062e-10 79-111
1025	PR00305	14-3-3 PROTEIN ZETA	
		SIGNATURE	PR00305D 16.34 1.439e- 10 158-185
1026	BL00353	HMG1/2 proteins.	
		or/2 processs.	BL00353B 11.47 2.436e-
			18 238-288 BL00353C
			14.83 8.844e-11 288-
1028	BL00183	Ubiquitin-conjugating	335
	2200103		BL00183 28.97 1.310e-
1033	2F00580	enzymes proteins.	33 43-91
	1100300	UvrD/REP helicase.	PF00580A 13.37 4.720e-
1034	PR00413	UNIONGER	09 111-133
	1.00413	HALOACID	PR00413E 15.78 3.429e-
		DEHALOGENASE/EPOXIDE	09 154-171
	1	HYDROLASE FAMILY	j
1037	DD01036	SIGNATURE	
-431	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 9.657e-
		ZINC-FINGER METAL-	09 5-44
1020	-	BINDING NU.	
1038	PD01796	PROTEIN TRANSMEMBRANE	PD01796 15.01 4.259e-
1030	 	COBALT ZINC CADMIU.	11 55-82
1039	BL00299	Ubiquitin domain	BL00299 28.84 9.036e-
1040		proteins.	09 17-69
1040	PR00970	ARGININE ADP-	PR00970A 17.73 6.143e-
		RIBOSYLTRANSFERASE	20 56-78 PR00970D
	·		00-70 EKOU3/UD

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		SIGNATURE	9.96 2.154e-18 154-171 PR00970F 12.30 1.000e-
}			16 224-241 PR00970G
		1	9.97 9.229e-15 242-258 PR00970B 16.37 1.290e-
			13 86-105 PR00970C
			11.05 1.643e-11 115-
j			130 PR00970E 11.23 9.820e-11 202-218
1042	BL00678	Trp-Asp (WD) repeat	BL00678 9.67 2.200e-10
1043	777	proteins proteins.	243-254
1043	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 6.786e- 13 114-128 PR00048A
			10.52 1.000e-09 172-
			186
1045	BL00615	C-type lectin domain proteins.	BL00615A 16.68 1.720e- 11 218-236 BL00615B
		proceins.	12.25 1.857e-10 317-
			331
1046	BL01092	Adenylate cyclases	BL01092N 13.54 B.924e-
1047	BL01216	class-I proteins. ATP-citrate lyase /	10 3-40 BL01216D 21.75 4.316e-
		succinyl-CoA ligases	28 314-344 BL01216A
1049	DM00031	family proteins.	13.91 1.000e-10 97-112
1049	DWOOGST	IMMUNOGLOBULIN V REGION.	DM00031B 15.41 7.618e-
1050	BL01073	Ribosomal protein L24e	BL01073 24.30 1.000e-
1054	BL00571	proteins.	40 12-62
1034	B700217	Amidases proteins.	BL00571 25.69 5.875e- 31 160-212
1055	BL00030	Eukaryotic RNA-binding	BL00030A 14.39 5.235e-
•		region RNP-1 proteins.	11 98-117 BL00030B
1058	BL00223	Annexins repeat proteins	7.03 4.316e-09 137-147 BL00223C 24.79 8.754e-
		domain proteins.	23 262-317 BL00223A
			15.59 9.478e-14 46-80
			BL00223A 15.59 5.557e-
1060	BL00027	'Homeobox' domain	BL00027 26.43 3.455e-
1064	BL00455	proteins.	35 158-201
1004	BLOOTS	Putative AMP-binding domain proteins.	8L00455 13.31 6.211e- 13 280-296
1065	PR00019 .	LEUCINE-RICH REPEAT	PR00019A 11.19 2.000e-
	1	SIGNATURE	09 115-129 PR00019B
1066	PR00326	GTP1/OBG GTP-BINDING	11.36 3.880e-09 87-101 PR00326A 8.75 4.600e-
		PROTEIN FAMILY SIGNATURE	16 151-172 PR00326C
			9.79 1.290e-14 200-216
			PR00326B 16.74 8.548e-
			19.09 1.257e-13 217-
1071	2002070	DEGERMON VIII	236
10/1	PD02870	RECEPTOR INTERLEUKIN-1 PRECURSOR	PD02870B 18.83 8.518e- 11 164-197
1072	PF00856	SET domain proteins.	PF00856A 26.14 5.976e-
1075	BI 01000	7	09 350-387
10/5	BL01009	Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7	BL01009D 14.19 4.300e- 20 127-148 BL01009A
		proteins.	13.75 6.586e-13 57-75
			BL01009E 13.50 1.439e-
1077	PR00724	CAPBOVVDPDTIDACE	11 159-175
		CARBOXYPEPTIDASE C SERINE PROTEASE (S10)	PR00724A 10.91 1.000e- 08 366-379
1000		FAMILY SIGNATURE	
1078	BL00215	Mitochondrial energy	BL00215A 15.82 1.000e-
		transfer proteins.	12 170-195 BL00215A 15.82 7.529e-10 79-104
1079	BL00678	Trp-Asp (WD) repeat	BL00678 9.67 4.316e-09

SEQ ID N	O: ACCESSION NO.	DESCRIPTION	RESULTS*
		proteins proteins.	298-309
1081 .	BL00326	Tropomyosins proteins.	BL00326A 14.01 7.398e- 10 23-57
1094	BJ.00460	Glutathione peroxidases selenocysteine proteins.	BL00460A 28.67 3.204e- 18 57-92 BL00460B 9.73 6.400e-13 100-118 BL00460D 16.89 9.143e- 12 162-182 BL00460C 14.35 5.500e-09 133- 156
1095	PD02811	PROTEIN PEPTIDE REDUCTASE MG448 PILB FIMBRIA TRAN.	PD02811A 20.67 3.017e- 22 67-105 PD02811B 17.07 2.263e-21 118- 151 PD02811C 13.25 5.696e-13 154-167
1096	PD02811	PROTEIN PEPTIDE REDUCTASE MG448 PILB FIMBRIA TRAN.	PD02811A 20.67 3.017e- 22 60-98 PD02811B 17.07 2.263e-21 111- 144 PD02811C 13.25 5.696e-13 147-160
1097	BL00479	Phorbol esters / diacylglycerol binding domain proteins.	BL00479B 12.57 6.143e- 09 200-216
1105	PF00881	Nitroreductase family.	PF00881A 27.15 9.229e-
1109	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PRO0449A 13.20 3.077e- 10 15-37 PRO0449E 13.50 1.857e-09 185- 208 PR00449D 10.79 8.364e-09 131-145
1115	PR00405	HIV REV INTERACTING PROTEIN SIGNATURE	PR00405B 11.83 5.737e- 20 42-60 PR00405A 17.71 2.703e-17 23-43 PR00405C 19.41 6.902e- 10 63-85
1116	BL00355	HMG14 and HMG17 proteins.	BL00355 5.97 2.528e-25 20-51
1117	BL00355	HMG14 and HMG17 proteins.	BL00355 5.97 2.528e-25 20-51
1120	BL00107	Protein kinases ATP- binding region proteins.	BL00107B 13.31 4.857e-
1123	PR00412	BPOXIDE HYDROLASE SIGNATURE	PR00412F 18.76 9.526e-
1125	PR00186	HEMERYTHRIN SIGNATURE	PR00186A 13.62 2.800e- 09 87-101
1129	BL00170	Cyclophilin-type peptidyl-prolyl cis- trans isomerase signatur.	BL00170C 18.49 3.077e- 33 84-129 BL00170B 20.97 6.838e-25 37-77 BL00170A 17.08 3.455e- 15 10-37
1131	BL00636	Nt-dnaJ domain proteins.	BL00636A 8.07 5.304e- 15 29-46 BL00636B
1132	BL00678	Trp-Asp (WD) repeat proteins proteins.	15.11 1.360e-14 59-80 BL00678 9.67 6.211e-09 29-40
1133	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 6.211e-09
1136	BL00990	Clathrin adaptor complexes medium chain proteins.	29-40 BL00990C 18.78 4.176e- 38 235-269 BL00990A 21.44 4.316e-36 94-132 BL00990B 20.15 2.125e- 27 157-187 BL00990D 16.13 5.320e-18 403- 422
1137	PR00314	CLATHRIN COAT ASSEMBLY PROTEIN SIGNATURE	PR00314B 15.68 8.000e- 34 100-128 PR00314D 9.66 3.531e-33 233-261 PR00314C 16.05 8.909e-

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
	NO.		
			32 159-188 PR00314A
1139	BL01115	GTP-binding nuclear	14.53 1.281e-22 13-34 BL01115A 10.22 6.364e-
		protein ran proteins.	13 13-57
1141	BL00107	Protein kinases ATP-	BL00107A 18.39 4.00Ce-
		binding region proteins.	19 451-482 BL00107B
		ļ ·	13.31 3.077e-12 519-
1148	PR00685	TRANSCRIPTION INITIATION	PR00685A 13.62 4.676e-
		FACTOR IIB SIGNATURE	09 21-42
1155	PD01652	RECEPTOR CELL NK	PD01652B 8.50 9.396e-
		GLYCOPROTEIN IMMUNOGLOB.	10 522-574 PD01652B
1157	PD02894		8.50 9.463e-10 740-792
1137	PD02894	HYDROLASE N4- PRECURSOR PROTEIN SIGNAL BE.	PD02894A 21.96 7.873e-
	1	PROTEIN SIGNAL BE.	28 81-127 PD02894B 13.93 1.188e-27 178-
			211
1159	BL00623	GMC oxidoreductases	BL00623E 15.00 3.531e-
		proteins.	20 391-414 BL00623C
			10.86 4.240e-20 155-
1161	PD01937	777	176
	FD01937	DNA PROTEIN POLYMERASE ENDONUCLEASE DNA	PD01937A 6.68 3.475e-
1162	PD01937	DNA PROTEIN POLYMERASE	09 330-341 PD01937A 6.68 3.475e-
		ENDONUCLEASE DNA	09 221-232
1163	PR00624	HISTONE H5 SIGNATURE	PR00624D 11.94 7.455e-
	1		10 214-239 PR00624D
			11.94 1.961e-09 312-
1167	BL00226	Intermediate filaments	337
	2200220	proteins.	BL00226B 23.86 7.384e- 09 302-350
1177	BL01032	Protein phosphatase 2C	BL01032G 8.33 1.422e-
		proteins.	10 34-48
1178	PR00320	G-PROTEIN BETA WD-40	PR00320A 16.74 1.794e-
	1	REPEAT SIGNATURE	10 205-220 PR00320C
		į.	13.01 7.840e-10 205-
	l		220 PR00320B 12.19 . 8.457e-10 35-50
			PR00320A 16.74 7.146e-
			09 35-50 PR00320B
1180	PR00454		12.19 9.100e-09 79-94
1100	PROUTST	ETS DOMAIN SIGNATURE	PR00454D 10.89 4.150e-
1181	BL00291	Prion protein.	19 765-784 BL00291A 4.49 8.962e-
	1	. Jacob passoum	11 152-187
1184	BL00720	Guanine-nucleotide	BL00720B 16.57 4.103e-
		dissociation stimulators	18 1089-1113
1185	BL00215	CDC25 family sign. Mitochondrial energy	
	BD00213	transfer proteins.	BL00215A 15.82 4.553e-
	1	processa.	13 204-229 BL00215A 15.82 1.429e-12 11-36
			BL00215A 15.82 9.809e-
1.05			11 104-129
1187	BL00983	Ly-6 / u-PAR domain	BL00983C 12.69 2.761e-
1188	BL00878	proteins. Orn/DAP/Arg	10 77-93
		decarboxylases family 2	BL00878B 10.95 6.000e-
		pyridoxal-P attachment	16 189-204 BL00878C 17.74 8.435e-15 225-
		si.	245 BL00878F 19.67
[			3.625e-13 379-402
		ŀ	BL00878D 16.56 1.621e-
.191	PD02939	DROWN OF THE	09 270-289
	. 204333	PROTBIN GLUTATHIONE SYNTHETASE SY.	PD02939B 10.10 2.723e-
			12 203-220 PD02939C 20.01 1.000e-11 224-
	•		252 1.000e-11 224-
193	PR00345	STATHMIN FAMILY	PR00345B 7.12 2.800e-
		SIGNATURE	28 72-101 PR00345B

1000 VX 32	T T T T T T T T T T T T T T T T T T T		
SEQ ID NO	NO.	DESCRIPTION	RESULTS +
			8.54 7.652e-28 149-174 PR00345C 4.54 9.100e- 28 101-125 PR00345D 10.97 1.964e-24 125- 149 PR00345A 13.46 5.645e-16 43-62
1194	PR00345	STATHMIN FAMILY SIGNATURE	PR00345B 7.12 2.800e- 28 108-137 PR00345E 8.54 7.652e-28 185-210 PR00345C 4.54 9.100e- 28 137-161 PR00345D 10.97 1.964e-24 161- 185 PR00345A 13.46 5.645e-16 79-98
1195	PP00995	Sec1 family.	PF00995B 17.37 1.120e-
1196	BL00982	Bacterial-type phytoene dehydrogenase proteins.	BL00982A 18.41 6.738e- 11 15-47
1197	BL01298	Dihydrodipicolinate reductase proteins.	BL01298A 13.90 5.959c- 09 51-73
1203	BL00061	Short-chain dehydrogenases/reductase s family proteins.	BL00061B 25.79 1.000e- 14 152-190
1204	PR00118	BETA-LACTAMASE CLASS A SIGNATURE	PR00118F 16.42 9.386e- 09 213-229
1206	BL01183	ubiE/COQ5 methyltransferase family proteins.	BL01183B 21.31 1.429e- 37 184-229 BL01183D 27.71 8.535e-27 264- 307 BL01183A 13.25 3.250e-23 51-73 BL01183C 10.77 5.295e- 09 246-258
1208	BL00979	G-protein coupled receptors family 3 proteins.	BL00979L 20.63 2.485e- 09 105-146
1209	PFC0023	Ank repeat proteins.	PF00023A 16.03 4.857e- 11 49-65 PF00023B 14.20 1.818e-09 45-55
1212	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 7.750e- 14 227-241 PR00048A 10.52 4.316e-11 199- 213
1213	PR00450	RECOVERIN FAMILY SIGNATURE	PR00450C 12.22 1.720e- 10 20-42 PR00450C 12.22 3.506e-09 56-78 PR00450D 16.58 6.769e- 09 44-64
1216	BL00412	Neuromodulin (GAP-43) proteins. RIBOSOMAL PROTEIN P2	BL00412D 16.54 5.598e- 10 179-230 PR00456E 3.06 5.348e-
1222	PD00066	SIGNATURE PROTEIN ZINC-FINGER	11 249-264
		METAL-BINDI.	PD00066 13.92 7.231e- 15 295-308 PD00066 13.92 7.231e-15 406- 419 PD00066 13.92 2.286e-12 378-391 PD00066 13.92 7.857e- 12 434-447 PD00066 13.92 3.348e-11 350- 363
1223	BL50058	G-protein gamma subunit profile.	BL50058 27.23 1.000e- 40 13-61
1223	BL50058		BL50058 27.23 1.000e- 40 13-61 BL00412D 16.54 8.439e- 09 279-330

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
	NO.	DESCRIPTION	RESULIS*
	<del></del>		1.000e-40 190-239
			BL00437D 25.72 1.000e-
		1	40 248-301 BL00437E
			23.95 1.000e-40 327-
			379
1230	BL01160	Kinesin light chain	BL01160B 19.54 8.297e-
[		repeat proteins.	10 5-60
1231	PR00735	GLYCOSYL HYDROLASE	PR00735A 11.19 6.857e-
-	1	FAMILY 8 SIGNATURE	09 391-405
1232	PR00497	NEUTROPHIL CYTOSOL	PR00497A 6.92 5.553e-
	1	FACTOR P40 SIGNATURE	10 158-176
1233	PR00497	NEUTROPHIL CYTOSOL	PR00497A 6.92 5.553e-
		FACTOR P40 SIGNATURE	10 158-176
1235	BL00866	Carbamoyl-phosphate	BL00866B 36.29 2.776e-
		synthase subdomain	09 75-121
		proteins.	
1237	BL00027	'Homeobox' domain	BL00027 26.43 1.818e-
		proteins.	21 36-79
1243	PR00403	WW DOMAIN SIGNATURE	PR00403B 12.19 1.184c-
			11 10-25
1246	PD01168	SYNTHETASE LIGASE	PD01168L 9.47 2.837e-
		PROTEIN ALANYL.	10 31-46 PD01168L
			9.47 4.490e-10 174-189
		[	PD01168L 9.47 7.612e-
1249	BL00018	EF-hand calcium-binding	10 183-198
1243	PE00019	domain proteins.	BL00018 7.41 2.800e-10
1254	BL00183	Ubiquitin-conjugating	183-196 BL00183 28.97 2.440e-
		enzymes proteins.	36 96-144
1255	BL01115	GTP-binding nuclear	BL01115A 10.22 5.670s-
	]	protein ran proteins.	11 8-52
1256	BL00373	Phosphoribosylglycinamid	BL00373C 10.35 3.348e-
	1	e formyltransferase	12 143-156
		proteins.	· ·
1258	PR00011	TYPE III EGF-LIKE	PR00011B 13.08 3.217e-
1259	D7 40 # 2	SIGNATURE	10 174-193
1259	BL00518	Zinc finger, C3HC4 type	BL00518 12.23 8.286e-
1261	PR00070	(RING finger), proteins. DIHYDROFOLATE REDUCTASE	10 31-40
	1200070	SIGNATURE	PR00070D 11.63 1.000e- 15 112-127 PR00070C
		O TOMATOKE	13.09 9.500e-15 51-63
	}		PR00070A 12.92 5.500e-
			12 16-27
1262	BL00462	Gamma-	BL00462A 20.89 6.438e-
		glutamyltranspeptidase	24 140-183 BL00462B
		proteins.	17.88 5.500e-20 230-
			267 BL00462C 27.41
			2.023e-11 292-347
1263	BT00038	Myc-typc, helix-loop-	BL00038B 16.97 9.455e-
		helix' dimerization	11 62-83
1264	Promis	domain proteins.	
-603	BL01115	GTP-binding nuclear	BL01115A 10.22 5.670e-
1266	PR00837	protein ran proteins.  ALLERGEN V5/TPX-1 FAMILY	11 17-61
		SIGNATURE	PR00837C 17.21 2.714e- 18 165-182 PR00837A
			16 165-182 PR00837A   14.77 4.512e-12 86-105
			PR00837D 11.12 7.577e-
	<u> </u>		12 201-215
1269	PR00449	TRANSFORMING PROTEIN P21	PR00449C 17.27 9.308e-
		RAS SIGNATURE	22 40-63 PR00449E
i			13.50 1.000e-16 137-
			160 PR00449D 10.79
1270	Dr 00377		3.520e-11 102-116
1270	BL00276	Channel forming colicins	BL00276A 8.87 1.500e-
1275	PD02327	proteins.	09 17-29
	- 20236/	GLYCOPROTEIN ANTIGEN	PD02327C 15.47 9.769e-
1276	PR00412	PRECURSOR IMMUNOGLO.  EPOXIDE HYDROLASE	09 228-243
			PR00412B 12.59 7.894e-

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SEQ ID N	O: ACCESSION NO.	DESCRIPTION	RESULTS*
		SIGNATURE	12 119-135 PR00412C
			11.30 1.857e-11 165-
			179 PR00412A 13.23
1277	PF00756		3.400e-11 100-119
	PF00/56	Putative esterase.	PF00756C 14.12 9.538e- 10 127-157
1279	BL00134	Serine proteases,	BL00134A 11.96 9.325e-
		trypsin family,	13 128-145
		histidine proteins.	1
1280	BL01220	Phosphatidylethanolamine	BL01220C 14.75 9.348e-
	ł	-binding protein family	15 248-276
1285	DV AGELO	proteins.	
1203	BL00518	Zinc finger, C3HC4 type	BL00518 12.23 2.286e-
1287	PF00791	(RING finger), proteins.  Domain present in ZO-1	10 33-42
1207	1200731	and Unc5-like netrin	PF00791B 28.49 7.182e-
	Ì	receptors.	11 288-343
1292	PR00802	SERUM ALBUMIN FAMILY	PR00802B 16.51 1.610e-
		SIGNATURE	10 81-105
1297	PR00716	M-PHASE INDUCER	PR00716C 17.65 5.696e-
		PHOSPHATASE SIGNATURE	09 23-44
1298	BL00478	LIM domain proteins.	BL00478B 14.79 6.478e-
_		production	14 268-283
1301	BL00127	Pancreatic ribonuclease	BL00127C 31.49 3.571e-
		family proteins.	28 82-126 BL00127B
			26.57 8.800e-28 23-68
1302	PR00637	TYPE 3 BOMBESIN RECEPTOR	PR00637E 11.27 4.250e-
		SIGNATURE	09 290-306
1307	BL00215	Mitochondrial energy	BL00215A 15.82 5.500e-
	1.	transfer proteins.	17 13-38 BL00215A
			15.82 1.000e-16 226-
	1		251 BL00215A 15.82
1308	PR00898	WASARRESTN WA REGURDOR	2.658e-13 107-132
2300	FROODS	VASOPRESSIN V2 RECEPTOR SIGNATURE	PR00898H 11.34 4.682e-
1309	PD00301	PROTEIN REPEAT MUSCLE	09 552-572 PD00301B 5.49 2.731e-
		CALCIUM-BI.	09 390-401
1310	BL00983	Ly-6 / u-PAR domain	BL00983C 12.69 9.654e-
	j	proteins.	13 73-89 BL00983B
		1-	8.19 3.132e-09 12-22
1313	BL00194	Thioredoxin family	BL00194 12.16 1.900e-
		proteins.	11 15-28
1314	BL00594	Aromatic amino acids	BL00594A 16.75 8.969e-
		permeases proteins.	10 53-97
1316	BL00134	Serine proteases,	BL00134A 11.96 9.325e-
	1	trypsin family,	13 128-145
1320	BL00783	histidine proteins.	
	BU00/83	Ribosomal protein L13	BL00783C 22.43 6.559e-
		proteins.	24 87-117 BL00783A
*			14.55 1.600e-19 8-33
		1	BL00783B 12.76 3.500e-
1327	PF00514	Armadillo/beta-catenin-	12 74-86
		like repeat proteins.	PF00514A 31.30 7.268e- 11 82-120
1329	BL00030	Eukaryotic RNA-binding	BL00030A 14.39 6.294e-
		region RNP-1 proteins.	11 129-148 BL00030B
			7.03 4.789e-09 168-178
1331	PR00497	NEUTROPHIL CYTOSOL	PR00497A 6.92 7.239e-
		FACTOR P40 SIGNATURE	09 25-43
1332	PR00161	NICKEL-DEPENDENT	PR00161C 9.51 4.930e-
	1	HYDROGENASE/B-TYPE	09 317-337
		CYTOCHROME SIGNATURE	
1333	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 6.769e-
		ZINC-FINGER METAL-	33 10-49
	77000	BINDING NU.	' I
1336	PR00700	PROTEIN TYROSINE	PR00700D 12.47 2.200e-
337	PR00700	PHOSPHATASE SIGNATURE	09 262-281
	1200700	PROTEIN TYROSINE	PR00700D 12.47 2.200e-

SEQ ID NO:	ACCESSION	DESCRIPTION	
	NO.		RESULTS*
1340	PRADOCA	PHOSPHATASE SIGNATURE	09 211-230
	PR00860	VERTEBRATE METALLOTHIONEIN SIGNATURE	PR00860A 5.46 5.034e- 13 5-18
1341	BL00893	mutT domain proteins.	BL00893 18.99 6.750e-
1343	BL01282	BIR repeat proteins.	BL01282B 30.49 5.974e- 21 383-422
1344	DM00099	4 kw A55R REDUCTASE TERMINAL DIHYDROPTERIDINE.	DM00099B 14.73 8.313e- 09 417-427
1345	BL00923	Aspartate and glutamate racemases proteins.	BL00923B 11.41 5.935e-
1348	PF00651	BTB (also known as BR-C/Ttk) domain proteins.	10 135-146 PF00651 15.00 7.231e- 13 44-57
1350	PR00193	MYOSIN HEAVY CHAIN SIGNATURE	PR00193D 14.36 3.571e- 32 416-445 PR00193C 12.60 6.318e-31 179- 207 PR00193B 11.69 3.571e-24 133-159 PR00193E 19.47 9.069e- 22 470-499 PR00193A
1352	PR00447	NATURAL RESISTANCE- ASSOCIATED, MACROPHAGE PROTEIN SIGNATURE	15.41 1.783e-20 77-97 PR00447E 9.73 1.554e- 15 299-319 PR00447D 13.54 3.408e-15 200- 224 PR00447A 12.73 6.357e-11 97-124 PR00447G 6.69 9.877e-
1353 -	BL00303	S-100/ICaBP type calcium binding protein.	10 353-373 BL00303A 21.77 6.667e- 26 45-82 BL00303B
1355	BL00039	DEAD-box subfamily ATP-dependent helicases proteins.	26.15 1.000e-24 93-130 BL00039D 21.67 5.950e- 29 375-421 BL00039A 18.44 7.136e-29 99-138 BL00039C 15.63 4.000e- 18 225-249 BL00039B 19:19 3.182e-14 141- 167
1357	PF00615	Regulator of G protein signalling domain proteins.	PF00615B 16.25 2.216e- 12 84-101 PF00615C 10.06 8.412e-12 162-
1360	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 9.234n- 29 10-49
1361	PR00925	NONHISTONE CHROMOSOMAL PROTEIN HMG17 FAMILY SIGNATURE	PR00925A 5.47 5.091e- 18 14-29 PR00925B 3.73 6.143e-14 29-42 PR00925C 5.57 4.789e- 12 53-64 PR00925D 6.56 1.857e-10 76-87
	BL01272	Glucokinase regulatory protein family proteins.	BL01272B 19.61 6.870e- 30 136-171 BL01272C 11.68 3.314e-25 249- 274 BL01272A 6.49 1.231e-18 99-117
	BL01272	Glucokinase regulatory protein family proteins.	BL01272B 19.61 6.870e- 30 113-148 BL01272C 11.68 3.314e-25 226- 251 BL01272A 6.49 1.231e-18 76-94
	DM00179	w KINASE ALPHA ADHESION T-CELL.	DM00179 13.97 5.304e- 09 167-177
344	2000260		UP 401-111
368	PR00169	POTASSIUM CHANNEL SIGNATURE	PR00169A 16.77 1.592e- 09 76-96

SEQ ID N	O: ACCESSION NO.	DESCRIPTION	RESULTS*
1371	BL00242	Type a surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the surface of the	10 1-19
		Integrins alpha chain proteins.	BL00242B 8.13 8.615e- 09 469-479
1372	PR00625	DNAJ PROTEIN FAMILY SIGNATURE	PR00625B 13.48 7.353e- 19 46-67 PR00625A 12.84 1.391e-16 14-34
1373	BL00434	HSF-type DNA-binding domain proteins.	BL00434C 23.85 3.778e-
1374	PR00962	LETHAL (2) GIANT LARVAE	09 90-130 PR00952C 8.00 6.337e-
1375	PD02475	PROTEIN SIGNATURE MUCIN EPITHELIAL TUMOR-	09 505-526 PD02475A 23.1B B.552e-
1376	PD01066	ASSOCIATE. PROTEIN ZINC FINGER	10 1111-1150 PD01066 19.43 9.571e-
1380		ZINC-FINGER METAL- BINDING NU.	32 24-63
	BL00194	Thioredoxin family proteins.	BLC0194 12.16 8.333e- 12 48-61
1381	DM01970	0 kw ZK632.12 YDR313C ENDOSOMAL III.	DM019708 8.60 1.458e- 15 1123-1136
1383	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 7.600e-10 243-254
1384	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 7.600e-10
1385	BL00303	S-100/ICaBP type calcium binding protein.	BL00303B 26.15 6.203e- 10 95-132
1386	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 5.042e-
1387	BL00518	Zinc finger, C3HC4 type	09 1574-1628 BL00518 12.23 1.000e-
1389	PD01066	(RING finger), proteins. PROTEIN ZINC FINGER	PD01066 19.43 3.600e-
1390		ZINC-FINGER METAL- BINDING NU.	30 10-49
1390	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 3.512e- 31 32-71
1392	PR00308	TYPE I ANTIFREEZE PROTEIN SIGNATURE	PR00308C 3.83 9.723e- 10 127-137
1393	PR00380	KINESIN HEAVY CHAIN SIGNATURE	PR00380A 14.18 9.625e- 25 88-110 PR00380D 9.93 2.406e-20 304-326 PR00380B 12.64 4.414e- 16 208-226 PR00380C 13:18 6.538e-16 243- 262
1394	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 3.400e- 14 462-475 PD00066 13.92 8.800e-14 348- 361 PD00066 13.92 9.571e-12 405-418 PD00066 13.92 6.087e- 11 490-503 PD00066 13.92 8.043e-11 320- 333
1398	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 6.786c- 32 10-49
1400	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.	DM01206B 10.69 7.038e- 09 270-290
1406	PD00930	PROTEIN GTPASE DOMAIN ACTIVATION.	PD00930A 25.62 7.324e- 15 363-389
1407	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 7.500e-
1408	PR00019	LEUCINE-RICH REPEAT SIGNATURE	10 457-476 PRO0019A 11.19 9.550e- 11 179-193 PR00019A 11.19 8.826e-10 228- 242 PR00019B 11.36 1.360e-09 199-213 PR00019B 11.36 4.960e-

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
	NO.		
1409	PR00510	NEBULIN SIGNATURE	09 176-190
1	1	MEDOSIN SIGNATURE	PR00510A 9.09 4.150e-
	1		12 182-202 PR00510B
			12.96 8.767e-12 210-
		}	230 PR00510F 9.88
			8.172e-10 58-75
	ļ	}	PR00510D 9.21 2.367e-
1410	PD00078	REPEAT PROTEIN ANK	
	}	NUCLEAR ANKYR.	PD00078B 13.14 5.696e- 09 31-44
1412	BL00358	Ribosomal protein L5	BL00358B 22.76 1.00Ce-
		proteins.	40 57-103 BL00358C
		•	13.75 6.087e-14 122-
			136 BL00358D 14.26
	i		5.500e-13 143-158
	ŀ	ŀ	BL00358A 13.06 1.931e-
		1	11 33-44
1414	BL00282	Kazal serine protease	BL00282 16.88 7.338e-
		inhibitors family	10 511-534
		proteins.	
1415	BL00023	Type II fibronectin	BL00023 24.31 4.300e-
ľ	1	collagen-binding domain	29 40-77
		proteins.	
1417	PR00681	RIBOSOMAL PROTEIN S1	PR00681G 12.54 2.149e-
		SIGNATURE	09 38-60
1418	DMO0973	3 kw RESISTANCE BENOMYL	DM00973A 21.17 1.462e-
	· ————————————————————————————————————	YLL028W CYCLOHEXIMIDE.	09 171-208
1419	PR00319	BETA G-PROTEIN	PR00319B 11.47 1.571e-
		(TRANSDUCIN) SIGNATURE	09 428-443
1420	PD01941	TRANSMEMBRANE	PD01941A 14.81 1.000e-
		COTRANSPORTER SYMP.	40 142-196 PD01941B
ŀ			15.02 7.049e-30 400-
			447 PD01941B 15.92
			2.475e-20 817-864
		1	PD01941C 19.96 3.118e~
			19 488-543 PD01941D
i		•	27.18 9.614e-18 641-
ľ			690 PD01941F 28.52
1422	PR00205	CARVITATION	5.382e-15 1038-1093
	1200203	CADHERIN SIGNATURE	PR00205B 11.39 8.043e-
1423	PR00209	ALDUA (DIME)	12 199-217
1	1800209	ALPHA/BETA GLIADIN FAMILY SIGNATURE	PR00209B 4.88 6.318e-
1424	BL50002	Src homology 3 (SH3)	11 1009-1028
	-03000	orc nomorogy 3 (SM3)	
		domain proportion access	BL50002A 14.19 8.200e-
		domain proteins profile.	14 367-386 BL50002A
		domain proteins profile.	14 367-386 BL50002A 14.19 9.250e-12 298-
		domain proteins profile.	14 367-386 BL50002A 14.19 9.250e-12 298- 317 BL50002A 14.19
		domain proteins profile.	14 367-386 BL50002A 14.19 9.250e-12 298- 317 BL50002A 14.19 4.462e-11 208-227
		domain proteins profile.	14 367-386 BL50002A 14.19 9.250e-12 298- 317 BL50002A 14.19 4.462e-11 208-227 BL50002B 15.18 1.000e-
1425	PF00628	domain proteins profile.	14 367-386 BL50002A 14.19 9.250e-12 298- 317 BL50002A 14.19 4.462e-11 208-227 BL50002B 15.18 1.000e- 09 244-258
.425	PF00628	domain proteins profile.	14 367-386 BL50002A 14.19 9.250e-12 298- 317 BL50002A 14.19 4.462e-11 208-227 BL50002B 15.18 1.000e- 09 244-258 PF00628 15.84 3.045e-
	PF00628	domain proteins profile.	14 367-386 BL50002A 14.19 9.250e-12 298- 317 BL50002A 14.19 4.462e-11 208-227 BL50002B 15.18 1.000e- 09 244-258 PF00628 15.84 3.045e- 12 330-345
		domain proteins profile.	14 367-386 BL50002A 14.19 9.250e-12 298- 317 BL50002A 14.19 4.462e-11 208-227 BL50002B 15.18 1.000e- 09 244-258 PF00628 15.84 3.045e- 12 330-345 PF00628 15.84 3.045e-
.426		domain proteins profile.  PHD-finger.  PHD-finger.	14 367-386 BL50002A 14.19 9.250e-12 298- 317 BL50002A 14.19 4.462e-11 208-227 BL50002B 15.18 1.000e- 09 244-258 PF00628 15.84 3.045e- 12 330-345 PF00628 15.84 3.045e- 12 377-392
.426	PF00628	PHD-finger.  PHD-finger.  HIV REV INTERACTING	14 367-386 BL50002A 14.19 9.250e-12 298- 317 BL50002A 14.19 4.462e-11 208-227 BL50002B 15.18 1.000e- 09 244-258 PF00628 15.84 3.045e- 12 330-345 PF00628 15.84 3.045e- 12 377-392 PR00405B 11.83 5.114e-
.426	PF00628	domain proteins profile.  PHD-finger.  PHD-finger.	14 367-386 BL50002A 14.19 9.250e-12 298- 317 BL50002A 14.19 4.462e-11 208-227 BL50002B 15.18 1.000e- 09 244-258 PF00628 15.84 3.045e- 12 330-345 PF0062B 15.84 3.045e- 12 377-392 PR00405B 11.83 5.114e- 16 281-299 PR00405A
426	PF00628	PHD-finger.  PHD-finger.  HIV REV INTERACTING	14 367-386 BL50002A 14.19 9.250e-12 298- 317 BL50002A 14.19 4.462e-11 208-227 BL50002B 15.18 1.000e- 09 244-258 PF00628 15.84 3.045e- 12 330-345 PF00628 15.84 3.045e- 12 377-392 PR00405B 11.83 5.114e- 16 281-299 PR00405A 17.71 4.306e-14 262-
426	PF00628	PHD-finger.  PHD-finger.  PHD-finger.  HIV REV INTERACTING PROTEIN SIGNATURE	14 367-386 BL50002A 14.19 9.250e-12 298- 317 BL50002A 14.19 4.462e-11 208-227 BL50002B 15.18 1.000e- 09 244-258 PF00628 15.84 3.045e- 12 330-345 PF00628 15.84 3.045e- 12 377-392 PR00405B 11.83 5.114e- 16 281-299 PR00405A 17.71 4.306e-14 262- 282
426	PF00628 PR00405	PHD-finger.  PHD-finger.  PHD-finger.  HIV REV INTERACTING PROTEIN SIGNATURE  DEAD-box subfamily ATP-	14 367-386 BL50002A 14.19 9.250e-12 298- 317 BL50002A 14.19 4.462e-11 208-227 BL50002B 15.18 1.000e- 09 244-258  PF00628 15.84 3.045e- 12 330-345  PF00628 15.84 3.045e- 12 377-392  PR00405B 11.83 5.114e- 16 281-299 PR00405A 17.71 4.306e-14 262- 282  BL00039D 21.67 5.219e-
426 I	PF00628 PR00405	PHD-finger.  PHD-finger.  PHD-finger.  HIV REV INTERACTING PROTEIN SIGNATURE	14 367-386 BL50002A 14.19 9.250e-12 298- 317 BL50002A 14.19 4.462e-11 208-227 BL50002B 15.18 1.000e- 09 244-258 PF00628 15.84 3.045e- 12 330-345 PF00628 15.84 3.045e- 12 377-392 PR00405B 11.83 5.114e- 16 281-299 PR00405A 17.71 4.306e-14 262- 282
426 I	PF00628 PR00405	PHD-finger.  PHD-finger.  HIV REV INTERACTING PROTEIN SIGNATURE  DEAD-box subfamily ATP-dependent helicases proteins.	14 367-386 BL50002A 14.19 9.250e-12 298- 317 BL50002A 14.19 4.462e-11 208-227 BL50002B 15.18 1.000e- 09 244-258 PF00628 15.84 3.045e- 12 330-345 PF00628 15.84 3.045e- 12 377-392 PR00405B 11.83 5.114e- 16 281-299 PR00405A 17.71 4.306e-14 262- 282 BL00039D 21.67 5.219e- 34 147-193
426 I	PR00405	PHD-finger.  PHD-finger.  HIV REV INTERACTING PROTEIN SIGNATURE  DEAD-box subfamily ATP-dependent helicases proteins.  G-PROTEIN BETA WD-40	14 367-386 BL50002A 14.19 9.250e-12 298- 317 BL50002A 14.19 4.462e-11 208-227 BL50002B 15.18 1.000e- 09 244-258 PF00628 15.84 3.045e- 12 330-345 PF00628 15.84 3.045e- 12 377-392 PR00405B 11.83 5.114e- 16 281-299 PR00405A 17.71 4.306e-14 262- 282 BL00039D 21.67 5.219e- 34 147-193 PR00320C 13.01 8.920e-
426 1 427 1 428 E	PR00405	PHD-finger.  PHD-finger.  HIV REV INTERACTING PROTEIN SIGNATURE  DEAD-box subfamily ATP-dependent helicases proteins.  G-PROTEIN BETA WD-40 REPEAT SIGNATURE	14 367-386 BL50002A 14.19 9.250e-12 298- 317 BL50002A 14.19 4.462e-11 208-227 BL50002B 15.18 1.000e- 09 244-258 PF00628 15.84 3.045e- 12 330-345 PF00628 15.84 3.045e- 12 377-392 PR00405B 11.83 5.114e- 16 281-299 PR00405A 17.71 4.306e-14 262- 282 BL00039D 21.67 5.219e- 34 147-193  PR00320C 13.01 8.920e- 10 577-592
426 I	PR00405 3L00039 PR00320	PHD-finger.  PHD-finger.  PHD-finger.  HIV REV INTERACTING PROTEIN SIGNATURE  DEAD-box subfamily ATP-dependent helicases proteins.  G-PROTEIN BETA WD-40 REPEAT SIGNATURE  INOSITOL PHOSPHATASE	14 367-386 BL50002A 14.19 9.250e-12 298- 317 BL50002A 14.19 4.462e-11 208-227 BL50002B 15.18 1.000e- 09 244-258  PF00628 15.84 3.045e- 12 330-345  PF00628 15.84 3.045e- 12 377-392  PR00405B 11.83 5.114e- 16 281-299 PR00405A 17.71 4.306e-14 262- 282  BL00039D 21.67 5.219e- 34 147-193  PR00320C 13.01 8.920e- 10 577-592  PR00378D 16.86 7.563e-
426 I	PR00405 3L00039 PR00320	PHD-finger.  PHD-finger.  HIV REV INTERACTING PROTEIN SIGNATURE  DEAD-box subfamily ATP-dependent helicases proteins.  G-PROTEIN BETA WD-40 REPEAT SIGNATURE	14 367-386 BL50002A 14.19 9.250e-12 298- 317 BL50002A 14.19 4.462e-11 208-227 BL50002B 15.18 1.000e- 09 244-258  PF00628 15.84 3.045e- 12 330-345  PF00628 15.84 3.045e- 12 377-392  PR00405B 11.83 5.114e- 16 281-299 PR00405A 17.71 4.306e-14 262- 282  BL00039D 21.67 5.219e- 34 147-193  PR00320C 13.01 8.920e- 10 577-592  PR00378D 16.86 7.563e- 12 295-314 PR00378B
426 I	PR00405 3L00039 PR00320	PHD-finger.  PHD-finger.  PHD-finger.  HIV REV INTERACTING PROTEIN SIGNATURE  DEAD-box subfamily ATP-dependent helicases proteins.  G-PROTEIN BETA WD-40 REPEAT SIGNATURE  INOSITOL PHOSPHATASE	14 367-386 BL50002A 14.19 9.250e-12 298- 317 BL50002A 14.19 4.462e-11 208-227 BL50002B 15.18 1.000e- 09 244-258  PF00628 15.84 3.045e- 12 330-345  PF00628 15.84 3.045e- 12 377-392  PR00405B 11.83 5.114e- 16 281-299 PR00405A 17.71 4.306e-14 262- 282  BL00039D 21.67 5.219e- 34 147-193  PR00320C 13.01 8.920e- 10 577-592  PR00378D 16.86 7.563e-

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
	NO.		1
		PROTEIN SIGNATURE	10 103-124
1433	BL01113	Clq domain proteins.	BL01113B 18.26 7.049e- 15 14-50 BL01113C 13.18 7.000e-12 82-102
1434	PR00319	BETA G-PROTEIN (TRANSDUCIN) SIGNATURE	PR00319B 11.47 7.983e- 10 135-150
1436	BL00030	Eukaryotic RNA-binding	BL00030A 14.39 1.000e-
1438	BL00290	region RNP-1 proteins. Immunoglobulins and	12 84-103 BL00290B 13.17 2.500e-
		major histocompatibility	09 250-268 BL00290A
		complex proteins.	20.89 4.000e-09 188- 211
1440	PR00806	VINCULIN SIGNATURE	PR00806B 4.28 4.960e-
1441	PR00806	VINCULIN SIGNATURE	PR00806B 4.28 4.960e-
1444	BL00422	Granins proteins.	BL00422D 19.48 1.000e-
1445	PD01841	PHOSPHORYLASE KINASE	08 114-138
1113	101041	ALPHA MUSCL.	PD01841A 21.71 1.000e- 40 73-123 PD01841B
			14.35 1.000e-40 144-
			185 PD01841D 17.87
			1.000e-40 206-258
			PD01841F 13.36 1.000e- 40 296-345 PD01841G
			24.26 1.000e-40 349-
			403 PD01841I 23.00
			1.000e-40 494-536
			PD01841J 14.94 1.000e- 40 895-932 PD01841L
		Ì	18.42 1.000e-40 1083-
			1125 PD01841E 18.60
			9.719e-38 258-296
			PD01841K 14.81 1.000e- 35 1041-1071 PD01841H
		!	21.30 3.189e-31 435-
		1	472 PD01841C 13.78
		İ	1.000e-25 185-206 PD01841M 10.82 1.250e-
			20 1175-1194
1446	PF00816	H-NS histone family.	PF00816B 13.84 8.875e- 09 190-220
1447	PR00048	C2H2-TYPE ZINC FINGER	PR00048A 10.52 2.080e-
1448	50.000	SIGNATURE	09 402-416
1448	DM00315	072 RIBONUCLEASE INHIBITOR.	DM00315D 18.40 7.393e-
1451	BL00030	Eukaryotic RNA-binding	09 23-67 BL00030B 7.03 2.800e-
		region RNP-1 proteins.	10 94-104
1454	DM01688	2 POLY-IG RECEPTOR.	DM01688D 13.44 7.146e-
1455	PF00777	Sialyltransferase	09 382-405
_		family.	PF00777C 18.60 2.929e- 22 4-59
1457	BL00927	Trehalase proteins.	BL00927C 10.83 8.085e-
1460	BL00545	Aldose 1-epimerase	09 42-53 BL00545C 11.28 7.353e-
		proteins.	17 169-182 BL00545A
			10.20 2.071e-15 73-89
			BL00545B 13.10 3.942e-
1466	PR00097	ANTHRANILATE SYNTHASE	PR00097C 9.42 9.069e-
1472	BL01129	COMPONENT II SIGNATURE Hypothetical	09 233-245
		yabO/yceC/sfhB family	BL01129E 13.25 5.250e- 22 170-195 BL01129C
		proteins.	25.56 9.526e-18 63-106
1473	BL00790	Receptor tyrosine kinase	BL007901 20.01 2.821e-
1475	PF00686	Class V proteins. Starch binding domain	09 2114-2145
		proteins.	PF00686A 13.45 9.100e- 09 267-277
			UJ 201-211

SEQ ID N	O:   ACCESSION	DESCRIPTION	L DDGVV max
	NO.		RESULTS*
1477	PF00566	Probable rabGAP domain proteins.	PF00566A 12.64 7.333e- 10 466-476
1478	BL00030	Eukaryotic RNA-binding	BL00030B 7.03 9.400e-
1479	DM00406	region RNP-1 proteins.	10 43-53 DM00406 7.73 8.541e-10
1480	BL00290	Immunoglobulins and	292-305
	15500250	major histocompatibility	BL00290B 13.17 2.385e- 15 69-87 BL00290A
1481	PR00150	complex proteins. PHOSPHOENOLPYRUVATE	20.89 5.091e-11 12-35
		CARBOXYLASE SIGNATURE	PR00150F 10.45 9.039e- 09 21-51
1482	PF00780	Domain found in NIK1- like kinases, mouse	PF00780I 14.69 4.825e-
		citron and yeast ROM.	09 107-137
1483	BL01160	Kinesin light chain	BL01160B 19.54 1.153e-
1485	PD01066	repeat proteins. PROTEIN ZINC FINGER	09 108-162 PD01066 19.43 5.909e-
		ZINC-FINGER METAL- BINDING NU.	25 17-56
1486	BL00107	Protein kinases ATP-	BL00107B 13.31 1.529e-
1488	BL00039	binding region proteins.	09 34-50
	5000033	DEAD-box subfamily ATP- dependent helicases	BL00039D 21.67 9.586e- 10 116-162
1490	BL00166	proteins. Enoyl-CoA	
1150	8200166	hydratase/isomerase	BL00166D 22.87 2.607e- 24 190-226 BL00166C
	ł	proteins.	18.93 5.500e-14 140-
	İ		167 BL00166B 16.92 9.357e-11 93-115
1491	BL00452	Guanylate cyclases	BL00452D 28.59 3.700e-
		proteins.	31 63-106 BL00452E 11.92 3.045e-13 115-
			131
1492	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 3.667e- 09 532-546
1497	BL00107	Protein kinases ATP-	BL00107B 13.31 1.000e-
		binding region proteins.	11 384-400 BL00107A 18.39 5.345e-11 322-
			353
1500	PF00876	Ogre family.	PF00876E 7.99 1.947e-
1502	BL00027	'Homeobox' domain	BL00027 26.43 4.789e-
1503	BL00027	'Homeobox' domain	24 112-155 BL00027 26.43 4.789e-
		proteins.	24 112-155
1505	BL01177	Anaphylatoxin domain proteins.	BL01177B 20.64 5.800e- 24 448-475 BL01177C
		prosection.	17.39 5.333e-19 402-
			421 BL01177B 13.61
			7.840e-16 155-171 BL01177D 17.50 1.900e-
1506	BL00972	Ubiquitin carboxyl-	15 427-445
	12200372	terminal hydrolases	BL00972D 22.55 5.500e- 14 311-336 BL00972A
		family 2 proteins.	11.93 7.429e-14 48-66
			BL00972B 20.72 8.759e- 10 341-363
1512	BL00523	Sulfatases proteins.	BL00523E 19.27 4.536e-
			22 76-106 BL00523D 9.89 1.563e-11 40-52
			BL00523F 10.85 4.162e-
			09 159-170 BL00523G 9.46 5.333e-09 256-266
1516	BL00914	Syntaxin / epimorphin	BL00914 24.91 7.045e-
1518	BL00600	family proteins. Aminotransferases class-	14 168-218
		III pyridoxal-phosphate	BL00600A 17.98 6.143e- 19 98-122 BL00600E
		attachment si.	16.43 1.771e-17 302-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			331 BL006C0G 12.43 9.625e-17 377-396 BL00600B 19.60 5.091e- 15 160-186 BL00600C 16.18 6.04Ce-12 190- 206 BL006C0F 8.77 1.000e-11 343-356 BL00600D 8.71 1.000e- 10 281-295
1523	PD00930	PROTEIN GTPASE DOMAIN ACTIVATION.	PD00930B 33.72 9.600e- 18 41-82
1528	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PRO0320B 12.19 4.774e- 11 192-207 PR00320B 12.19 8.839e-11 272- 287 PR00320B 12.19 9.743e-10 106-121 PR00320A 16.74 1.878e- 09 192-207 PR00320A 16.74 2.317e-09 106- 121 PR00320A 16.74 8.683e-09 272-287 PR00320C 13.01 8.800e- 09 106-121
1538	DM01970	0 kw ZK632.12 YDR313C ENDOSOMAL III.	DM01970B 8.60 4.508e- 15 171-184
1539	PF00781	Diacylglycerol kinase catalytic domain proteins (presumed).	PF00781D 11.11 7.593e- 10 103-127
1540	PR00965	OCULAR ALBINISM TYPE 1 PROTEIN SIGNATURE	PR00965H 10.73 1.231e- 29 312-334 PR00965E 12.93 5.846e-29 172- 195 PR00965F 5.98 1.123e-28 209-231 PR00965C 15.04 1.000e- 27 131-151 PR00965D 5.84 1.000e-27 150-170 PR00965G 8.52 2.440e- 27 258-279 PR00965B 4.80 8.650e-26 88-109 PR00965A 12.52 1.000e- 25 35-55 PR00965I 3.91 6.442e-25 385-406
1541	BL01013	Oxysterol-binding protein family proteins.	BL01013D 26.81 9.719e- 17 163-207
1543	PD02699	PROTEIN DNA-BINDING BINDING DNA.	PD02699C 24.84 1.000e- 40 599-646 PD02699A 8.91 2.286e-34 219-248 PD02699B 18.28 6.143e- 21 485-509
1544	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 7.857e- 10 182-197 PR00049D 0.00 7.102e-09 67-82
1547	BL00951	ER lumen protein retaining receptor proteins.	BL00951C 19.35 1.000e- 40 93-142 BL00951D 13.94 8.714e-40 142- 177 BL00951A 15.10 1.000e-38 2-38 . BL00951B 14.23 6.250e- 33 38-69
1548	BL00536	Ubiquitin-activating enzyme proteins.	BL00536F 13.65 8.920e- 30 279-318 BL00536D 22.91 5.737e-24 21-65 BL00536E 16.94 4.696e- 18 248-279
1549	PR00139	ASPARAGINASE/GLUTAMINASE FAMILY SIGNATURE	PR00139C 11.72 9.679e- 09 550-569
1553	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 5.119e- 09 58-73

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
	NO.		RESULIS.
1556	BL00061	Short-chain	BL00061B 25.79 6.276c-
		dehydrogenases/reductase s family proteins.	13 67-105
1557	BL01228	Hypothetical cof family	BL01228D 17.44 8.105e-
		proteins.	12 107-132
1558	BL01228	Hypothetical cof family	BL01228D 17.44 8.105e-
		proteins.	12 107-132
1559	BL01228	Hypothetical cof family	BL01228D 17.44 8.105e-
1562	BL00522	DNA polymerase family X	12 107-132
1	2200322	proteins.	BL00522C 11.90 6.600e- 18 412-436 BL00522B
			27.30 1.738e-16 364-
	1	·	410 BL00522A 25.52
	1		6.000e-16 279-326
·		1	BL00522E 19.63 6.123e-
			14 502-532 BL00522F 14.90 2.385e-13 551-
İ			575
1563	PF00651	BTB (also known as BR-	PF00651 15.00 1.947c-
L.		C/Ttk) domain proteins.	11 46-59
1564	BL00299	Ubiquitin domain	BL00299 28.84 2.823e-
1566	BL01013	proteins. Oxysterol-binding	10 324-376
1	2202023	protein family proteins.	BL01013D 26.81 8.594e- 17 184-228 BL01013C
L	1	z rumity proceins.	9.97 4.906e-12 14-24
1567	BL00678	Trp-Asp (WD) repeat	BL00678 9.67 3.400e-10
	1	proteins proteins.	378-389 BL00678 9.67
İ			5.800e-10 418-429
		j	BL00678 9.67 8.800e-10
1570	BL00479	Phorbol esters /	295-306 BL00479B 12.57 5.235e-
		diacylglycerol binding	17 297-313 BL00479A
	1	domain proteins.	19.86 6.625e-15 271-
		i	294 BL00479A 19.86
			2.667e-14 147-170 BL00479B 12.57 6.294e-
			12 173-189
1576	PR00665	OXYTOCIN RECEPTOR	PR00665G 12.36 4.673e-
		SIGNATURE	24 364-384 PR00665D
			9.93 1.200e-22 138-155
			PR00665F 11.73 4.000e- 22 337-354 PR00665C
		1	5.89 1.000e-20 65-80
			PR00665B 5.29 4.337e-
			19 24-39 PR00665E
		!	5.60 2.929e-15 246-260 PR00665A 5.99 5.622e-
		1	15 11-25
1577	DM00099	4 kw A55R REDUCTASE	DM00099B 14.73 9.308e-
		TERMINAL	10 127-137
1579	BL00524	DIHYDROPTERIDINE.	DY 005043
· · · -		Somatomedin B domain proteins.	BL00524A 9.65 6.776e-
1580	PD02894 ·	HYDROLASE N4- PRECURSOR	14 52-73 PD02894B 13.93 6.959e-
Į	•	PROTEIN SIGNAL BE.	16 182-215 PD02894A
1501	HV NH		21.96 2.125e-10 57-103
1581	BL00411	Kinesin motor domain	BL00411C 15.04 5.292e-
		proteins.	12 32-54 BL00411H
į			15.66 4.441e-11 245- 276
1582	PR00604	CLASS IA AND IB	PR00604A 11.13 2.440e-
1504		CYTOCHROME C SIGNATURE	09 79-87
1584	PF00651	BTB (also known as BR-	PF00651 15.00 1.000c-
1585	DM01551	C/Ttk) domain proteins.	10 225-238
		kw OSTEOINDUCTIVE YOPM MEMBRANE OUTER.	DM01551C 14.62 9.455e- 11 125-145
1586	DM01354	kw TRANSCRIPTASE REVERSE	DM01354S 11.61 7.750e-
		II ORF2.	09 474-495
		·	

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
1587	PR00072	MALIC ENZYME SIGNATURE	PR00072B 13.77 7.955c- 33 180-210 PR00072A 12.75 6.040e-25 120- 145 PR00072C 11.42 2.286e-24 216-239 PR00072D 10.77 3.400e- 22 276-295 PR00072E 10.54 1.360e-19 301- 318 PR00072G 10.45 5.304e-19 433-450 PR00072F 8.87 5.935e- 15 332-349
1589	BL00191	Cytochrome b5 family, heme-binding domain proteins.	BL00191H 15.64 1.537e- 22 61-113 BL00191K 17.38 9.027e-12 398- 442
1590	DM01970	0 kw ZK632.12 YDR313C ENDOSOMAL III.	DM01970B 8.60 7.716e- 13 211-224 DM01970B 8.60 2.157e-12 94-107
1591	DM00517	5 kw NUCLEAR 60.7 NUP1 CHROMOSOME.	DM00517B 10.96 6.625e- 16 1175-1193 DM00517A 8.21 1.000e-11 1015- 1026
1592	BL00037	Myb DNA-binding domain proteins repeat proteins proteins.	BL00037B 15.92 3.250e- 27 116-142 BL00037A 16.68 2.500e-24 83-107 BL00037A 16.68 3.250e- 12 31-55 BL00037B 15.92 3.526e-11 64-90 BL00037C 16.86 9.654e- 10 146-164
1595	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 1.514e- 09 110-127
1598	PF00628	PHD-finger.	PF00628 15.84 3.250e- 11 1667-1682
1599	PR00014	FIBRONECTIN TYPE III REPEAT SIGNATURE	PR00014D 12.04 5.500e- 09 980-995
1600	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 6.571e- 10 30-39
1602	BL00412	Neuromodulin (GAP-43) proteins.	BL00412D 16.54 5.402e- 10 136-187
1605	PF00651	BTB (also known as BR- C/Ttk) domain proteins.	PF00651 15.00 3.571e- 10 44-57
1607	BL00252	Interferon alpha, beta and delta family proteins.	BL00252A 18.49 6.657e- 23 20-57 BL00252B 19.78 9.125e-16 58-109
1610	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 1.000e- 08 61-94
1611	BL00904	Protein prenyltransferases alpha subunit repeat proteins proteins.	BL00904C 8.98 7.353e- 10 91-125 BL00904D 1.47 6.018e-09 127-168
1612	PF00168	C2 domain proteins.	PF00168C 27.49 3.250e- 09 365-391
1613 .	BL00412	Neuromodulin (GAP-43) proteins.	BL00412D 16.54 6.051e- 09 932-983 BL00412D 16.54 7.153e-09 933- 984
1614	BL00559	Eukaryotic molybdopterin oxidoreductases proteins.	BL00559I 13.63 3.53le- 25 54-83 BL00559K 13.17 2.957e-18 197- 224 BL00559J 19.63 6.870e-16 124-176 BL00559L 13.60 9.000e- 16 266-284
1615	PD01427	TRANSFERASE METHYLTRANSFERASE BI.	PD01427B 22.45 3.025e- 22 500-541 PD01427A 19.94 8.773e-18 439-

SEQ ID NO	: ACCESSION	DESCRIPTION	RESULTS*
	NO.		472
1616	BL00115	Eukaryotic RNA	
1010	DBOOTES	polymerase II	BL00115Z 3.12 7.485e-
		heptapeptide repeat	09 152-201 BL00115Z
l		proteins.	3.12 9.603e-09 145-194
1617	BL00303	S-100/ICaBP type calcium	PY 00303P 06 16 2 28
2017	2200303	binding protein.	BL00303B 26.15 7.750e-
1		binding procein.	32 51-88 BL00303A
1618	BL01254	Patrice Coulds	21.77 1.947e-31 4-41
1010	PDUIESA	Fetuin family proteins.	BL01254F 10.02 8.754e-
1619	PD01888	DOMEST REPROPER	09 137-147
1013	2001080	PEPTIDE REDUCTASE	PD01888B 25.10 1.000e-
		PROTEIN METHI.	40 47-97 PD01888C
			21.56 7.000e-30 125-
			155 PD01888A 12.84
1621	PR00239	MOLVINGONY BUODADAYY A	8.800e-15 7-23
1021	FROUZSS	MOLLUSCAN RHODOPSIN C-	PR00239E 1.58 3.455e-
	i	TERMINAL TAIL SIGNATURE	09 692-704 PR00239E
	- 1	1.	1.58 4.580e-09 697-709
		1	PR00239E 1.58 1.580e-
			09 702-714 PR00239E
1622	PR00860	VERTEBRATE	1.58 5.193e-09 703-715
	***************************************	METALLOTHIONEIN	PR00860B 7.04 1.900e-
		SIGNATURE	18 27-41 PR00860C
		SIGNATURE	9.61 1.474e-14 41-51
		į	PR00860A 5.46 1.720e-
1624	PR00784	MITOCHONDRIAL BROWN FAT	14 5-18
	1100707	UNCOUPLING PROTEIN	PR00784D 15.86 8.027e-
		SIGNATURE	11 77-95
1626	BL00325	Actin-depolymerizing	DY AGREE OF CO.
	2200323	proteins.	BL00325B 21.66 1.000e-
		process.	40 93-139 BL00325A
1631	BL00064	L-lactate dehydrogenase	24.83 6.786e-23 61-93 BL00064B 23.57 1.000e-
		proteins.	40 82-130 BL00064C
		proterns.	17.28 1.000e-40 137-
	1		182 BL00064E 27.20
			1.000e-40 223-275
			BL00064F 25.14 7.882e-
	1		36 286-331 BL00064A
•			21.16 1.000e-33 22-60
	1		BL00064D 14.19 6.500e-
			31 182-212
1632	PR00063	RIBOSOMAL PROTEIN L27	PR00063B 15.24 9.700e-
	·	SIGNATURE	11 59-84 PR00063A
			11.71 1.614e-09 34-59
1634	PR00239	MOLLUSCAN RHODOPSIN C-	PR00239D 0.00 1.105e-
		TERMINAL TAIL SIGNATURE	11 36-49 PR00239C
			3.51 2.538e-09 37-45
1636	BL01210	Caveolins proteins.	BL01210B 13.92 9.531e-
1275			10 133-183
1637	BL00982	Bacterial-type phytoene	BL00982A 18.41 5.388e-
1.520	<u> </u>	dehydrogenase proteins.	11 11-43
1639	BL01183	ubiE/COQ5	BL01183B 21.31 8.144e-
	1	methyltransferase family	12 132-177
1640	77744	proteins.	
1640	PR00015	GRAM-POSITIVE COCCUS	PR00015B 9.84 8.468e-
	1	SURFACE PROTEIN ANCHOR	10 128-149
	7700000	SIGNATURE	
	PR00320	G-PROTEIN BETA WD-40	PR00320B 12.19 5.935e-
1641	l.		3. 24. 22. 22. 22.
1041		REPBAT SIGNATURE	11 364-379 PR00320A
1041		REPEAT SIGNATURE	16.74 7.828e-11 364-
1041		REPBAT SIGNATURE	16.74 7.828e-11 364- 379 PR00320C 13.01
1041		REPBAT SIGNATURE	16.74 7.828e-11 364- 379 PR00320C 13.01 2.800e-10 279-294
1041		REPBAT SIGNATURE	16.74 7.828e-11 364- 379 PR00320C 13.01 2.800e-10 279-294 PR00320C 13.01 2.800e-
1041		REPBAT SIGNATURE	16.74 7.828e-11 364- 379 PR00320C 13.01 2.800e-10 279-294 PR00320C 13.01 2.800e- 10 364-379 PR00320B
1041		REPBAT SIGNATURE	16.74 7.828e-11 364- 379 PR00320C 13.01 2.800e-10 279-294 PR00320C 13.01 2.800e- 10 364-379 PR00320B 12.19 5.114e-10 279-
1041		REPBAT SIGNATURE	16.74 7.828e-11 364- 379 PR00320C 13.01 2.800e-10 279-294 PR00320C 13.01 2.800e- 10 364-379 PR00320B

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
	NO.	DOCKIFIION .	
	1		PRO0320A 16.74 2.098e- 09 229-244
1642	PP00023	Ank repeat proteins.	PF00023A 16.03 6.464e- 09 114-130
1643	PR00169	POTASSIUM CHANNEL SIGNATURE	PR00169A 16.77 1.806e-
1644	BL00678	Trp-Asp (WD) repeat	BL00678 9.67 2.200e-10
		proteins proteins.	109-120 BL00678 9.67 5.737e-09 528-539
1645	BL01108	Ribosomal protein L24 proteins.	BL01108A 20.33 7.366e- 17 56-89
1646	PR00380	KINESIN HEAVY CHAIN	PR00380A 14.18 9.270e-
Ĭ	Ĭ	SIGNATURE	21 103-125 PR00380D
			9.93 6.308e-18 386-408 PR00380C 13.18 7.923e-
(			16 332-351 PR00380B
			12.64 6.657e-15 292-
1647	DM01242	3 MINOROVENIA MANAGE	310
1204/	DN01242	3 THREONINETRNA LIGASE.	DM01242C 17.15 9.791e- 37 340-381 DM01242E
ļ.			23.00 5.071e-31 463-
]			505 DM01242D 23.29
i			3.925e-30 420-463 DM01242B 23.57 8.054e-
			18 265-314 DM01242F
		-	10.61 7.618e-14 526-
1649	PD00126	PROTEIN REPEAT DOMAIN	540
	1500120	TPR NUCLEA.	PD00126A 22.53 5.500e- 10 13-34
1651	BL01150	Kinesin light chain	BL01160B 19.54 6.720e-
1652	BL00933	repeat proteins. FGGY family of	11 431-485
2002	BH00333	carbohydrate kinases	BL00933A 17.50 4.673e- 12 11-35 BL00933E
	1	proteins.	13.80 9.217e-09 456-
1653	BL00795	Involucrin proteins.	472
	2200133	involuciin proceins.	BL00795C 17.06 2.988e- 10 70-115
1654	BL00982	Bacterial-type phytoene	BL00982A 18.41 7.750e-
1655	BL00982	dehydrogenase proteins.  Bacterial-type phytoene	17 302-334
	1 2200302	dehydrogenase proteins.	BL00982A 18.41 7.750e- 17 282-314
1656	BL00741	Guanine-nucleotide	BL00741B 14.27 1.391e-
		dissociation stimulators	16 607-630
1657	PR00449	CDC24 family sign. TRANSFORMING PROTEIN P21	PR00449A 13.20 7.938e-
		RAS SIGNATURE	11 114-136
1658	PR00910	LUTEOVIRUS ORF6 PROTEIN	PR00910A 2.51 8.889e-
1659	BL00972	SIGNATURE   Ubiquitin carboxyl-	10 442-455 BL00972D 22.55 4.140e-
		terminal hydrolases	12 376-401 BL00972E
		family 2 proteins.	20.72 5.629e-09 446-
1660	BL00406	Actins proteins.	81.024.05D 12 58 8 7570
		proteins.	BL00406D 12.58 8.767e- 15 188-243
1661	PR00105	CYTOSINE-SPECIFIC DNA	PR00105A 10.36 4.900e-
i		METHYLTRANSFERASE SIGNATURE	13 1140-1157 PR00105B
		J-SMATORS	12.32 2.800e-12 1259- 1274 PR00105C 10.86
1.681			1.000e-10 1305-1319
1662	BL00280	Pancreatic trypsin	BL00280 24.61 3.172e-
		inhibitor (Kunitz) family proteins.	33 3119-3163
1663	PR00319	BETA G-PROTEIN	PR00319D 11.64 6.625e-
		(TRANSDUCIN) SIGNATURE	23 107-125 PR00319C
ļ			13.41 5.714e-20 89-105
ļ			PR00319A 15.27 5.286e- 19 51-68 PR00319B
			11.47 8.200e-19 70-85

CEO TO	7A		
SEQ ID N	NO: ACCESSION NO.	DESCRIPTION	RESULTS*
1664	BL00018	EF-hand calcium-binding	BL00018 7.41 5.050e-10
1667	PD01066	domain proteins.	489-502
100/	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-	PD01066 19.43 8.500e-
		BINDING NU.	38 7-46
1669	BL01153	NOL1/NOP2/sun family	BL01153D 19.69 1.188e-
ł		proteins.	17 115-141 BL01153C
		1.	13.67 8.977e-15 66-80
			BL01153B 20.52 1.885e-
		<u> </u>	10 13-37
1671	PR00678	PI3 KINASE P85	PR00678H 9.13 3.100e-
		REGULATORY SUBUNIT	10 1146-1169
1672	BL00598	SIGNATURE	
1072	PF00238	Chromo domain proteins.	BL00598 14.45 8.500e-
1673	PR00326	GTP1/OBG GTP-BINDING	20 27-49
2072	1,00320	PROTEIN FAMILY SIGNATURE	PR00326A 8.75 8.329e-
1674	PR00049	WILM'S TUMOUR PROTEIN	09 686-707 PR00049D 0.00 7.580e-
		SIGNATURE	11 343-358 PR30049D
-			0.00 1.286e-10 342-357
1676	PR00747	GLYCOSYL HYDROLASE	PR00747H 12.76 8.636e-
		FAMILY 47 SIGNATURE	19 427-448 PR00747G
			14.50 2.286e-18 368-
			393 PR00747C 12.06
			7.500e-18 112-131
			PR00747A 14.05 4.600e-
	İ	ľ	17 42-63 PR00747D
	ſ	,	15.23 8.759e-17 163-
		1	183 PR00747E 15.13 8.244e-15 254-272
		]	PR00747B 7.65 5.355e-
			13 75-90 PR00747F
	j		13.56 8.714e-10 311-
		<u></u>	328
1677	PR00747	GLYCOSYL HYDROLASE	PR00747H 12.76 8.636e-
	]	FAMILY 47 SIGNATURE	19 309-330 PR00747G
			14.50 2.286e-18 250-
		ŀ	275 PR00747C 12.06 7.500e-18 112-131
			PR00747A 14.05 4.600e-
			17 42-63 PR00747B
			7.65 5.355e-13 75-90
			PR00747F 13.56 8.714e-
1680	NY OAK TO		10 193-210
1900	BL00678	Trp-Asp (WD) repeat	BL00678 9.67 4.600e-10
		proteins proteins.	406-417 BL00678 9.67
1681	BL00678	Trp-Asp (WD) repeat	6.684e-09 320-331
		proteins proteins.	BL00678 9.67 4.600e-10 329-340 BL00678 9.67
		Francisco Programs.	6.684e-09 243-254
1683	PR00326	GTP1/OBG GTP-BINDING	PR00326A 8.75 1.346e-
		PROTEIN FAMILY SIGNATURE	13 389-410
1685	PR00646	RDC1 ORPHAN RECEPTOR	PR00646H 6.32 4.188e-
1600		SIGNATURE	09 755-771
1690	BL01160	Kinesin light chain	BL01160B 19.54 6.644e-
1691	DROOM 5.5	repeat proteins.	09 75-129
* V J T	PR00456	RIBOSOMAL PROTEIN PZ	PR00456E 3.06 7.281e-
		SIGNATURE	10 418-433 PR00456E
	J		3.06 7.281e-10 419-434
		1	PR00456E 3.06 8.125e-
1692	PR00456	RIBOSOMAL PROTEIN P2	10 420-435
		SIGNATURE	PR00456E 3.06 7.281e- 10 487-502 PR00456E
			3.06 7.281e-10 488-503
	•	1	PR00456E 3.06 8.125e-
			10 489-504
1693	BL00674	AAA-protein family	BL00674C 22.60 8.043e-
<del></del>		proteins.	24 274-317 BL00674B

SEQ ID N	O: ACCESSION NO.	DESCRIPTION	RESULTS*
			4.46 4.000e-23 241-263 BL00674D 23.41 8.560e- 18 338-385 BL00674E 15.24 1.720e-15 414- 434
1697	PR00409	PHTHALATE DIOXYGENASE REDUCTASE FAMILY SIGNATURE	PR00409F 12.70 4.388e- 10 427-447
1698	PR00466	CYTOCHROME B-245 HEAVY CHAIN SIGNATURE	PR00466C 10.17 3.443e- 13 187-208 PR00466B 5.03 5.500e-11 162-186 PR00466F 9.16 6.159e- 09 498-517
1699	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 9.217e- 12 283-300 BL00028 16.07 3.769e-11 255- 272 BL00028 16.07 5.154e-11 171-188 BL00028 16.07 5.500e- 11 227-244 BL00028 16.07 1.600e-10 199- 216
1700	BL01019	ADP-ribosylation factors family proteins.	BL01019A 13.20 3.348e- 15 62-102 BL01019B 19.49 4.000e-15 107- 162
1703	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 2.484e- 12 200-239
1707	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PR00109B 12.27 4.558e- 14 134-153
1710	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PRO0019A 11.19 2.565e- 10 116-130 PR00019B 11.36 4.600e-09 113- 127 PR00019B 11.36 7.120e-09 204-218
1711	BL01159	WW/rsp5/WWP domain proteins.	BL01159 13.85 6.523e- 11 232-247 BL01159 13.85 5.408e-10 613- 628
1712	PF00023	Ank repeat proteins.	PF00023A 16.03 7.000e- 10 187-203
1713	PF00642	Zinc finger C-x8-C-x5-C-x3-H type (and similar).	PF00642 11.59 9.550e- 11 230-241
1714	PF00642	Zinc finger C-x8-C-x5-C- x3-H type (and similar). GTP-binding nuclear	PF00642 11.59 9.550e- 11 230-241
1718	BL00353	protein ran proteins.  HMG1/2 proteins.	BL01115A 10.22 7.129e- 09 7-51 BL00353C 14.83 6.018e-
		,	10 136-183 BL00353B 11.47 8.866e-09 86-136
1719	BL00412	Neuromodulin (GAP-43) proteins.	BL00412D 16.54 5.408e- 09 432-483
1721	BL00038	Myc-type, 'helix-loop- helix' dimerization domain proteins.	BL00038B 16.97 8.448e- 12 79-100 BL00038A 13.61 4.000e-11 52-68
1723	PD00567	PROTBIN RNA-BINDING RNA REPEAT HYD.	PD00567C 9.17 8.500e-
1724	BL01279	Protein-L- isoaspartate(D- aspartate) O- methyltransferase signa.	BL01279A 24.27 5.663c- 12 233-281
1728	BL00018	EF-hand calcium-binding domain proteins.	BL00018 7.41 2.059e-11 73-86 BL00018 7.41 4.176e-11 157-170
1730	BL00594	Aromatic amino acids permeases proteins.	BL00594A 16.75 1.089e- 09 17-61

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
177	NO.		
1731	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 9.676e- 10 296-350
1732	BL01160	Kinesin light chain	BL01160B 19.54 9.676e-
		repeat proteins.	10 316-370
1733	PF00850	Histone deacetylase	PF00850F 15.70 4.349e-
	1	family.	22 246-279 PF00850D
			14.76 6.850e-20 177-
	j	]	201 PF00850E 8.88 8.691e-18 209-235
			PF00850G 22.75 4.098e-
			14 281-323
1734	BL00354	HMG-I and HMG-Y DNA-	BL00354C 6.61 5.932e-
	ì	binding domain proteins (Ahook)	09 292-307
1735	DM00179	w KINASE ALPHA ADHESION	DM00179 13.97 5.263e-
		T-CELL.	10 492-502
1743	PR00449	TRANSFORMING PROTEIN P21	PR00449A 13.20 1.188e-
		RAS SIGNATURE	11 5-27 PR00449D
		Í	10.79 2.241e-10 109- 123 PR00449E 13.50
			9.289e-10 144-167
1744	PR00449	TRANSFORMING PROTEIN P21	PR00449A 13.20 1.188e-
		RAS SIGNATURE	11 5-27 PR00449D
			10.79 2.241e-10 109-
			123 PR00449E 13.50 9.289e-10 144-167
1745	BL00720	Guanine-nucleotide	BL00720B 16.57 8.297e-
		dissociation stimulators	15 136-160
1746	PR00081	CDC25 family sign.	
1/40	PK00081	GLUCOSE/RIBITOL DEHYDROGENASE FAMILY	PR00081B 10.38 6.727e- 11 45-57 PR00081E
		SIGNATURE	17.54 3.935e-10 150-
			168
1747	BL00439	Acyltransferases	BL00439H 18.24 8.435e-
		ChoActase / COT / CPT family proteins.	14 65-91 BL00439G 13.40 2.895e-12 3-14
1749	PR00819	CBXX/CFQX SUPERFAMILY	PR00819B 10.83 7.158e-
		SIGNATURB	11 4-20
1751	PD00066	PROTEIN ZINC-FINGER	PD00066 13.92 3.400e-
	ļ	METAL-BINDI.	14 33-46 PD00066 13.92 1.000e-13 89-102
			PD00066 13.92 7.000e-
			13 61-74 PD00066
			13.92 6.571e-12 117-
1753	BL01013	Oxysterol-binding	130
	2101013	protein family proteins.	BL01013D 25.81 6.516e- 18 33-77
1754	BL00790	Receptor tyrosine kinase	BL00790I 20.01 2.393e-
		class V proteins.	09 490-521 BL00790I
			20.01 2.821e-09 60-91
			BL00790I 20.01 6.357e- 09 287-318
1756	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 9.750e-
		ZINC-FINGER METAL-	35 10-49
1750	DMOCAGE	BINDING NU.	
1758	DM00406	GLIADIN.	DM00406 7.73 7.600e-09
1762	PD02929	ADHESION GLYCOPROTEIN	653-666 PD02929A 28.27 4.529e-
	-	PRECURSOR I.	09 224-278
1765	PR00326	GTP1/OBG GTP-BINDING	PR00326A 8.75 5.950e-
1775	BEOGGS	PROTEIN FAMILY SIGNATURE	11 146-167
11.12	PF00023	Ank repeat proteins.	PF00023A 16.03 3.077e-
1776	BL00942	glpT family of	14 523-539 BL00942F 15.07 4.343e-
	· <del>-</del>	transporters proteins.	10 371-389 BL00942B
			20.36 8.040e-09 94-137
1777	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 2.373e-
		<u> </u>	09 279-312

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS+
1778	BL00084	Copper type II, ascorbate-dependent monooxygenases proteins.	BL00084D 25.11 3.700e- 20 169-224 BL00084B 24.26 8.134e-16 10-58 BL00084C 27.71 8.412e- 11 107-158
1779	BL01013	Oxysterol-binding protein family proteins.	BL01013D 26.81 3.758e- 18 611-655 BL01013A 25.14 2.881e-15 344- 380 BL01013C 9.97 6.308e-13 435-445 BL01013B 11.33 3.717e- 12 409-420
1783	BL00741	Guanine-nucleotide dissociation stimulators CDC24 family sign.	BL00741B 14.27 8.138e- 13 492-515
1784	BL00741	Guanine-nucleotide dissociation stimulators CDC24 family sign.	BL00741B 14.27 8.138e- 13 492-515

^{*} results include in order: accession number subtype; raw score; p-value; postion of signature in amino acid sequence.
TRADOCS:1416223.I(%CRJ0!!.DOC)

TABLE 4

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM
2	ig	Immunoglobulin domain	2.1e-32	SCORE
3	pkinase	Eukaryotic protein kinase	1.3e-29	109.5
		domain	1.3e-29	110.7
4	zf-C2H2	Zinc finger, C2H2 type	1.6e-21	84.9
5	fn3	Fibronectin type III domain	0	1097.1
6	fn3	Fibronectin type III domain	To	1035.0
7	fn3	Fibronectin type III domain	<del>-  </del>	1090.4
8	fn3	Fibronectin type III domain	0	1097.1
9	TBC	TBC domain	4e-40	146.7
10	p450	Cytochrome P450	9.5e-17	62.0
12	ank	Ank repeat	6e-20	79.7
14	ig	Immunoglobulin domain	1.7e-05	22.7
15	zf-MYND	MYND finger	1.3e-06	35.4
16	zf-MYND	MYND finger	1.3e-06	35.4
17	zf-C2H2	Zinc finger, C2H2 type	1.7e-99	343.9
18	CAP_GLY	CAP-Gly domain	1.2e-25	98.7
20	IMPDH_C	IMP dehydrogenase / GMP	1.6e-119	410.5
	_	reductase C terminus	1 2	120.5
21	IMPDH_C	IMP dehydrogenase / GMP	4.3e-102	352.6
		reductase C terminus		
22	pkinase	Eukaryotic protein kinase	2.4e-79	277.0
	<u> </u>	domain		1
23	pkinase	Eukaryotic protein kinase	8.4e-74	258.6
		domain	1	1
25	RNA_pol_A	RNA polymerase alpha subunit	0	1077.7
26	Clq	Clq domain	1.9e-10	44.4
27	Ribosomal_L2	Ribosomal protein L23	7.8e-32	111.2
	3		1	
28	Ribosomal_L2	Ribosomal protein L23	le-29	104.2
	3	1		1
30	zf-A20	A20-like zinc finger	1.5e-10	48.5
31	zf-A20	A20-like zinc finger	1.5e-10	48.5
32	FMN_dh	FMN-dependent dehydrogenase	5.4e-179	608.1
34	PID	Phosphotyrosine interaction	3.8e-59	209.9
		domain (PTB/PID)	1	1
35	ig	Immunoglobulin domain	1.4e-13	48.8
36	ig	Immunoglobulin domain	1.4e-13	48.8
40	kinesin	Kinesin motor domain	6.7e-76	265.6
44	Ets	Ets-domain	1.4e-56	182.1
45	Ets	Ets-domain	1.4e-56	182.1
46	LRR	Leucine Rich Repeat	1.7e-13	58.3
48	zf-CZH2	Zinc finger, C2H2 type	2.3e-162	552.8
49	ITAM	Immunoreceptor tyrosine-based	1.4e-05	31.9
		activation mot	ĺ	1
50	UCH-2	Ubiquitin carboxyl-terminal	1.1e-26	102.0
51	77077	hydrolase family	1	
21	UCH-5	Ubiquitin carboxyl-terminal	1.1e-26	102.0
52		hydrolase family		1
53	ras	Ras family	8.5e-45	162.3
54	PRK	Phosphoribulokinase	2.1e-65	230.7
	myb_DNA-	Myb-like DNA-binding domain	0.096	15.2
55	binding		1	i
56	voltage_CLC	Voltage gated chloride channels	3.3e-186	631.9
57	Sugar_tr TBC	Sugar (and other) transporter	0.00015	-64.3
58		TBC domain	2.2e-37	137.6
59	ank	Ank repeat	5.9e-25	96.3
	ank	Ank repeat	5.9e-25	96.3
57	PMP22_Claudi	PMP-22/EMP/MP20/Claudin family	7.9e-49	175.6
	n		L	
58	C2	C2 domain	7.9e-54	192.2
	C2	C2 domain	2.3e-54	194.0
70	Kelch	Kelch motif	9.4e-99	341.5
72	ig	Immunoglobulin domain	8.2e-28	94.7
3	pkinase	Eukaryotic protein kinase		

SEQ I	D PFAM NAME	DESCRIPTION	p-value	PFAM
NO:			p-varue	SCORE
74		domain		
1	pkinase	Eukaryotic protein kinase domain	2.8e-3B	140.6
76	zf- C4_Topoisom	Topoisomerase DNA binding C4 zinc fing	5.4e-54	192.8
83	Peptidase_S9		4.3e-10	36.8
84	fn3	Fibronectin type III domain	4.1e-51	183.2
86	SH2	Src homology domain 2	3.1e-22	67.7
88	ig	Immunoglobulin domain	0.0091	14.0
89	WD40	WD domain, G-beta repeat	2.1e-21	84.6
92	laminin_G	Laminin G domain	6.1e-27	98.5
93 95	AMP-binding	AMP-binding enzyme	2.4e-13	-37.2
	pkinase	Eukaryotic protein kinase domain	1.4e-59	211.4
96	pkinase	Eukaryotic protein kinase domain	2.6e-51	183.9
97	adh_short	short chain dehydrogenase	2e-61	217.5
98	kinesin	Kinesin motor domain	2.2e-86	300.4
101	IRS	PTB domain (IRS-1 type)	5.40-36	133.0
102	AAA	ATPases associated with various	6.8e-05	-5.2
104	pkinase	cellular act Eukaryotic protein kinase	2.7e-73	
106	ras	domain		256.9
107	FYVE	Ras family	8.3e-24	92.5
108	Cyt reductas	FYVE zinc finger FAD/NAD-binding Cytochrome	5.4e-27	100.7
109	e	reductase	7.7e-61	215.5
113	zf-C2H2	Zinc finger, C2H2 type	2.3e-122	420.0
	pkinase	Eukaryotic protein kinase domain	4e-88	306.2
116	PH	PH domain	3.1e-11	45.2
117	lipocalin	Lipocalin / cytosolic fatty- acid binding pr	2.4e-14	53.5
118	pkinase	Eukaryotic protein kinase domain	4.5e-20	76.3
120	WD40	WD domain, G-beta repeat	2.4e-14	61.1
121	WD40	WD domain, G-beta repeat	2.4e-14	61.1
123	IF5_eIF4_eIF	eIF4-gamma/eIF5/eIF2-epsilon	1e-32	122.2
124	ig	Immunoglobulin domain	6.5e-08	30.6
127	mito_carr	Mitochondrial carrier proteins	3e-16	58.6
128	PP2C	Protein phosphatase 2C	2.2e-71	250.6
129	ATP1G1_PLM_M AT8	ATP1G1/PLM/MAT8 family	3.1e-20	80.6
130	pfkB	pfkB family carbohydrate kinase	4.5e-42	137.1
133	ACBP	Acyl CoA binding protein	4.6e-22	86.7
134	rrm	RNA recognition motif	1.2e-31	118.5
135 136	IQ	IQ calmodulin-binding motif	2.6e-08	41.0
	ATPIG1_PLM_M AT8	ATPIGI/PLM/MAT8 family	9.3e-22	85.7
139	WH2	Wiskott Aldrich syndrome homology region 2	0.0067	23.1
140	zf-C2H2	Zinc finger, C2H2 type	1.7e-82	+207
141	Peptidase_S2	Signal peptidase I	5.7e-10	287.5 35.7
143	arf	ADP-ribosylation factor family	1.2e-39	1-4E-5
146	KRAB	KRAB box	7.3e-30	145.2
148	DUF6	Integral membrane protein DUF6	0.096	112.6
149	PDEase	3'5'-cyclic nucleotide phosphodiesterase	3.8e-80	231.1
151	S4	S4 domain	11.	<del> </del>
.53	tRNA-synt_1d	tRNA synthetases class I (R)	1.1e-08	42.3
.54	Cyt_reductas e	FAD/NAD-binding Cytochrome	3.8e-103 7.8e-60	356.1
55	ras	reductase Ras family		[
57	actin	Actin	3.6e-28	107.0
		-100211	3.8e-26	87.1

SEQ ID		DESCRIPTION	p-value	PFAM SCORE
158	Jacalin	Jacalin-like lectin domain	0.09	-24.9
160	Zn_carbOpept	Zinc carboxypeptidase	5e-138	471.9
165	pkinase	Eukaryotic protein kinase	5.1e-67	236.1
		domain	<u> </u>	
167	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	5.3e-07	27.0
168	Ribosomal_S1 5	Ribosomal protein S15	1.1e-06	29.0
169	DEAD	DEAD/DEAH box helicage	le-48	157.0
171	DUF59	Domain of unknown function	0.07	-17.4
172	pkinase	DUF59 Eukaryotic protein kinase	3.7e-15	58.6
	F.12.1000	domain	3.76-13	30.0
173	globin	Globin	4.6e-18	67.4
174	WW	WW domain	7.3e-06	32.9
175	ras	Ras family	le-31	118.8
178	ATPIG1 PLM M	ATP1G1/PLM/MAT8 family	2.5e-17	71.0
	AT8			
179	2f-C2H2	Zinc finger, C2H2 type	1.5e-99	344.2
180	Clq	Clq domain	8.8e-72	251.9
190	Y_phosphatas e	Protein-tyrosine phosphatase	4.9e-287	967.0
191	efhand	EF hand	7.5e-16	66.1
193	pkinase	Eukaryotic protein kinase	6.5e-82	285.6
		domain	j	1
194	bromodomain	Bromodomain	5.8e-31	111.4
195	PALP	Pyridoxal-phosphate dependent enzyme	2.5e-64	227.1
197	DnaJ	DnaJ domain	1.6e-38	141.4
199	RrnaAD	Ribosomal RNA adenine	0.00018	16.9
200	acid_phospha	dimethylases Histidine acid phosphatase	12.5-10	1
	t		2.5e-10	37.2
201	WH2	Wiskott Aldrich syndrome homology region 2	0.00048	26.9
204	VATP-	ATP synthase (C/AC39) subunit	1.3e-159	543.7
	synt_AC39	mi bynemade (cynedd) dabanie	1.36-137	343.7
205	vATP- synt AC39	ATP synthase (C/AC39) subunit	1.6e-139	476.9
206	ldl_recept_a	Low-density lipoprotein	2.4e-25	97.6
209		receptor domain		
	ank	Ank repeat	1.4e-19	78.4
210	Rhomboid	Rhomboid family	0.0035	1.2
211	Clq	Clq domain	1.6e-70	247.7
212	UQ_con	Ubiquitin-conjugating enzyme	7.4e-74	258.8
215	UQ_con	Ubiquitin-conjugating enzyme	le-53	191.9
	DEAD	DEAD/DEAH box helicase	1.8e-43	140.4
216	PMP22_Claudi n	PMP-22/EMP/MP20/Claudin family	4.5e-21	83.4
218	Glycos_trans f_2	Glycosyl transferases	4e-21	83.6
219	ig	Immunoglobulin domain	0.092	10.7
222	WD40	WD domain, G-beta repeat	7.4e-23	89.4
224	TPR	TPR Domain	1.2e-08	42.1
225	DnaJ_CXXCXGX	DnaJ central domain (4 repeats)	1.5e-38	141.5
226	DnaJ_CXXCXGX	DnaJ central domain (4 repeats)	1.5e-38	141.5
229	HSP70	Hsp70 protein	2.4e-54	194 0
230	GSHP×	Glutathione peroxidases		194.0
231	tsp 1	Thrombospondin type 1 domain	3.4e-47	170.2
233	cyclin	Cyclin	0.0075	17.1
234	ras	Ras family	4.6e-144	492.0
235	LRR	1	4.8e-50	179.7
236	LRR	Leucine Rich Repeat	1.2e-30	115.3
237	PDZ	Leucine Rich Repeat PDZ domain (Also known as DHR	6.7e-29	109.4
		or GLGF).	1.7e-09	45.0
			<del></del>	

COO TO	C none in the			_
SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
244	dCMP_cyt_dea	Cytidine and deoxycytidylate	2.5e-05	31.1
245	m iq	deaminase		
248	vnt	Immunoglobulin domain	6.7e-08	30.5
240	wite	wnt family of developmental signaling protei	9.1e-270	742.6
250	mito carr	Mitochondrial carrier proteins	1.3e-55	193.6
254	adenylatekin	Adenylate kinase	1.8e-14	55.7
365	ase	_		33.7
255	Cation_efflu x	Cation efflux family	2.8e-33	124.0
256	SH3	SH3 domain	3.9e-14	60.4
257	Aa_trans	Transmembrane amino acid	2.6e-52	187.2
050		transporter protein		j
258	adenylatekin ase	Adenylate kinase	2.le-110	380.2
259	HIT	HIT family	8.2e-07	25.3
260	Bacterial PQ	PQQ enzyme repeat	1.6e-15	65.0
	Q		1.06-15	1 83.0
262	proteasome	Proteasome A-type and B-type	6.5e-64	225.7
267	pkinase	Eukaryotic protein kinase	6.3e-27	101.0
270	filament	Intermediate filament proteins	3.2e-150	512.5
271	Choline kina	Choline/ethanolamine kinase	2e-67	237.4
	ве	,	,	237.3
277	Ribosomal_S7	Ribosomal protein S7p/S5e	3.3e-20	80.6
279	pkinase	Eukaryotic protein kinase	3.3e-77	269.9
280	WD40	WD domain, G-beta repeat	7.8e-73	255.4
281	WD40	WD domain, G-beta repeat	7.8e-73	255.4
284	zf-DHHC	DHHC zinc finger domain	4.6e-24	93.4
287	Exonuclease	Exonuclease	1.4e-67	238.0
291	SAM	SAM domain (Sterile alpha motif)	0.034	11.2
292	SAM	SAM domain (Sterile alpha motif)	0.034	11.2
294	zf-C2H2	Zinc finger, C2H2 type	1.4e-29	111.7
295	zf-C2H2	Zinc finger, C2H2 type	2.2e-125	430.0
296 297	mito_carr	Mitochondrial carrier proteins	4.1e-59	205.5
302	HMG_box	HMG (high mobility group) box	6.7e-29	109.4
	Glycos_trans f_4	Glycosyl transferase	5e-87	302.5
304	tRNA-synt_2	tRNA synthetases class II (D, K and N)	1.1e-84	294.8
305	KRAB	KRAB box	2e-44	161.0
306	rrm	RNA recognition motif.	2.7e-44	160.6
308	7tm_1	7 transmembrane receptor (rhodopsin family)	5.2e-39	126.1
309	DNA_polymera seX	DNA polymerase X family	2.4e-64	227.2
311	F-box	F-box domain.	9.5e-08	39.2
312	ig	Immunoglobulin domain	6.8e-19	65.9
313	Ets	Ets-domain	8.le-60	192.3
315	Kelch	Kelch motif	1.3e-106	367.6
317	arf	ADP-ribosylation factor family	3.2e-35	130.4
318	sugar_tr	Sugar (and other) transporter	0.0003	-73.1
320	pkinase	Eukaryotic protein kinase domain	8.1e-83	288.6
322	pkinase	Eukaryotic protein kinase domain	4.9e-81	282.6
324	Xlink	Extracellular link domain	4.5e-143	331.5
326	ARID	ARID DNA binding domain	5.1e-37	136.4
327	HMG_box	HMG (high mobility group) box	6.7e-29	109.4
328	cadherin	Cadherin domain	8.1e-81	281.9
331	chromo	'chromo' (CHRromatin	4e-18	66.7
		Urganization MOdifier)		
333	Peptidase_M2	Organization MOdifier) Glycoprotease family	1.2e-136	467.4

SEQ ID	PFAM NAME	DESCRIPTION		T sast.
NO:	TAN MANE	DESCRIPTION	p-value	PFAM SCORE
335	vwa	von Willebrand factor type A	2.3e-07	37.9
		domain		133
339	ras	Ras family	7.8e-07	-59.1
340	zf-C2H2	Zinc finger, C2H2 type	8.2e-64	225.4
342	zf-C2H2	Zinc finger, C2H2 type	2.4e-85	297.0
343	ig	Immunoglobulin domain	0.0005	18.0
346	pkinase	Eukaryotic protein kinase domain	6.5e-65	229.1
347	pkinase	Eukaryotic protein kinase domain	6.5e-65	229.1
351	EGF	EGF-like domain		
352	ank	Ank repeat	8.5e-20	79.2
354	TBC	TBC domain	2.5e-101	350.0
355	PHD	PHD-finger	5.1e-15 3.2e-07	63.3 37.4
358	DUF6	Integral membrane protein DUF6	0.033	
359	zf-C2H2	Zinc finger, C2H2 type	7.4e-20	15.8
361	ank	Ank repeat	6.6e-34	79.4
362	ArfGap	Putative GTP-ase activating	4.7e-53	126.1
_		protein for Arf	4./e-53	189.7
363	efhand	BF hand	5.4e-10	1
367	LRR	Leucine Rich Repeat	8.8e-44	46.6 158.9
368	laminin_G	Laminin G domain	1.5e-33	
369	PP2C	Protein phosphatase 2C	5.3e-20	121.7 73.9
372	LIM	LIM domain containing proteins	9.9e-15	57.1
373	KRAB	KRAB box	4.8e-23	90.0
376	ion trans	Ion transport protein	2.9e-09	-4.2
377	Beach	Beige/BEACH domain	4.9e-208	704.5
380	pkinase	Eukaryotic protein kinase	1.6e-94	327.5
381	AMP-binding	domain		
382	HECT	AMP-binding enzyme	1.4e-07	-140.3
300	inec1	HECT-domain (ubiquitin- transferase).	1.3e-07	-13.5
384	ank	Ank repeat	2.5e-101	350.0
386	ig	Immunoglobulin domain	9.5e-06	23.6
388	zf-C2H2	Zinc finger, C2H2 type	1.7e-42	154.6
389	ig	Immunoglobulin domain	2.8e-15	54.3
390	mito_carr	Mitochondrial carrier proteins	3.5e-67	233.2
392	TPR	TPR Domain	6.1e-17	69.7
393	SH3	SH3 domain	3.5e-09	43.9
394	AAA	ATPases associated with various cellular act	4.le-21	83.6
396	spectrin	Spectrin repeat	2.1e-67	237.3
397	zf-C2H2	Zinc finger, C2H2 type	0.0066	237.3
399	fn3	Fibronectin type III domain	4.1e-102	352.6
400	WD40	WD domain, G-beta repeat	0.00049	26.8
401	El_dehydrog	Dehydrogenase El component	3e-119	409.6
402	fn3	Fibronectin type III domain	0	1719.6
404	LRR	Leucine Rich Repeat	2.1e-10	48.0
405	cadherin	Cadherin domain	8.le-81	281.9
406	zf-CXXC	CXXC zinc finger	5e-15	63.4
410	RhoGRF	RhoGEF domain	1.1e-23	92.1
411	F-box	F-box domain.	4.2e-06	33.7
412	SNF2_N	SNF2 and others N-terminal domain	5.8e-16	61.6
415	CPSase_L_cha	Carbamoyl-phosphate synthase	1.5e-172	586.6
43.0	in	(CPSase)		
418	LRR	Leucine Rich Repeat	3.8e-24	93.6
419	DENN	DENN (AEX-3) domain	2e-58	207.5
420	RasGEF	RasGEF domain	8.1e-43	155.7
421	ank	Ank repeat	1.4e-153	523.7
424	G-patch	G-patch domain	1e-19	78.9
425	pkinase	Eukaryotic protein kinase domain	2.2e-31	117.1
126	Plexin_repea	Plexin repeat	0.0023	24.6
127	plexin_repea			
	* revru Lebes	Plexin repeat	0.0023	24.6

SEQ ID	Draw san			
NO:	PFAM NAME	DESCRIPTION	p-value	PFAM
<del></del>	<del> </del>			SCORE
429	zf-C3HC4			
122	21-C3HC4	Zinc finger, C3HC4 type (RING	8.6e-11	39.2
431	DEAD	finger)	<u> </u>	Į
432	SH3	DEAD/DEAH box helicase	1e-66	214.0
433		SH3 domain	3.48-16	67.2
436	GTP_CDC	Cell division protein	2.1e-114	393.5
436	Collagen	Collagen triple helix repeat	4.6e-194	658.1
439	D2-2-	(20 copies)		İ
438	Ricin_B_lect	Similarity to lectin domain of	0.0085	10.5
441	in	ricin b	İ	-
441	Alpha_adapti	Alpha adaptin carboxyl-terminal	1.2e-256	866.0
442	n_C	domai		ĺ
442	Alpha_adapti	Alpha adaptin carboxyl-terminal	1.8e-235	795.7
443	n_C PDZ	domai	1	1
443	PDZ	PDZ domain (Also known as DHR	1.9e-65	230.9
445	V 03.1	or GLGF).	1	
445	LON	ATP-dependent protease La (LON)	0.00012	-17.1
-,,,,		domain	1	
446	ig	Immunoglobulin domain	0.00011	20.1
,451	sushi	Sushi domain (SCR repeat)	1.4e-18	75.2
452	fn3	Fibronectin type III domain	1.5e-06	35.2
454	pyridoxal_de	Pyridoxal-dependent	8.3e-14	50.3
	С	decarboxylase conse		
	kinesin	Kinesin motor domain	4.9e-217	734.4.
457	neur_chan	Neurotransmitter-gated ion-	1e-175	597.1
		channel		
	Josephin	Josephin	0.0002	18.7
	bZIP	bzIP transcription factor	1.7e-07	31.8
	NTP_transfer	Nucleotidyl transferase	6.3e-06	-26.3
	ase			1
	WD40	WD domain, G-beta repeat	2e-28	107.9
	LIM	LIM domain containing proteins	0.00021	20.7
477	zf-RanBP	Zn-finger in Ran binding	0.028	21.0
		protein and others.		
	WD40	WD domain, G-beta repeat	6.5e-18	73.0
	KRAB	KRAB box	le-31	118.8
481	ArfGap	Putative GTP-ase activating	8.4e-66	232.0
		protein for Arf		
	SH2	Src homology domain 2	0.011	11.4
	Clq	Clq domain	4.3e-74	259.6
487	dsrm	Double-stranded RNA binding	1.1e-47	171.9
		motif		1 - 1 - 1 - 1
	zf-C2H2	Zinc finger, C2H2 type	4.8e-153	521.9
	Alpha_adapti	Alpha adaptin carboxyl-terminal	3.4e-222	751.6
	n_C	domai		/52.0
	SKI	Shikimate kinase	1.2e-10	48.8
	ENV_polyprot	ENV polyprotein (coat	2.6e-22	77.6
	ein	polyprotein)		//
	abhydrolase_	Phospholipase/Carboxylesterase	0.041	-48.1
	2			
	crm	RNA recognition motif.	5.4e-34	126.4
501 W	W .	WW domain	4.6e-18	73.4
	<u></u>			
	g	Immunoglobulin domain		(
504 a		Immunoglobulin domain alpha/beta hydrolase fold	1.1e-10	39.5
04 a	g	Immunoglobulin domain alpha/beta hydrolase fold	1.1e-10 0.045	39.5 -3.6
504 a	g abhydrolase	Immunoglobulin domain	1.1e-10	39.5
504 a	g abhydrolase	Immunoglobulin domain alpha/beta hydrolase fold von Willebrand factor type A domain	1.1e-10 0.045 7.1e-62	39.5 -3.6 219.0
504 a 505 v 508 N	abhydrolase rwa Wa_K_ATPase_	Immunoglobulin domain alpha/beta hydrolase fold von Willebrand factor type A	1.1e-10 0.045	39.5 -3.6
504 a 505 v 508 N C	abhydrolase wa  la_K_ATPase_  kxonuclease	Immunoglobulin domain alpha/beta hydrolase fold von Willebrand factor type A domain	1.1e-10 0.045 7.1e-62 2.3e-145	39.5 -3.6 219.0 496.3
504 a 505 v 508 N C	abhydrolase wa  la_K_ATPase_  kxonuclease	Immunoglobulin domain alpha/beta hydrolase fold von Willebrand factor type A domain Na+/K+ ATPase C-terminus Exonuclease	1.1e-10 0.045 7.1e-62 2.3e-145 1.3e-56	39.5 -3.6 219.0 496.3
504 a 505 v 508 N C 509 E	ig abhydrolase rwa Ja_K_ATPase	Immunoglobulin domain alpha/beta hydrolase fold von Willebrand factor type A domain Na+/K+ ATPase C-terminus	1.1e-10 0.045 7.1e-62 2.3e-145	39.5 -3.6 219.0 496.3
504 a 505 v 508 N C 509 E 510 G	abhydrolase wa  Wa_K_ATPase_  Exonuclease Elycos_trans	Immunoglobulin domain alpha/beta hydrolase fold von Willebrand factor type A domain Na+/K+ ATPase C-terminus  Exonuclease Glycosyl transferases group 1	1.1e-10 0.045 7.1e-62 2.3e-145 1.3e-56 2.9e-06	39.5 -3.6 219.0 496.3 201.5 27.0
504 a 505 v 508 N C 509 E 510 G f 111 G	abhydrolase wa  Wa_K_ATPase_ : xonuclease hlycos_trans _1	Immunoglobulin domain alpha/beta hydrolase fold von Willebrand factor type A domain Na+/K+ ATPase C-terminus Exonuclease	1.1e-10 0.045 7.1e-62 2.3e-145 1.3e-56	39.5 -3.6 219.0 496.3
504 a 505 v 508 N C 509 E 510 G f f	abhydrolase  Wa  Wa  Wa  Wa  Wa  Wa  Wa  Wa  Wa  W	Immunoglobulin domain alpha/beta hydrolase fold von Willebrand factor type A domain Na+/K+ ATPase C-terminus  Exonuclease Glycosyl transferases group 1 Glycosyl transferases group 1	1.1e-10 0.045 7.1e-62 2.3e-145 1.3e-56 2.9e-06	39.5 -3.6 219.0 496.3 201.5 27.0
504 a 505 v 508 N C 509 E 510 G f f 11 G f 12 G	abhydrolase  Wa  Wa  Wa  Wa  Wa  Wa  Wa  Wa  Wa  W	Immunoglobulin domain alpha/beta hydrolase fold von Willebrand factor type A domain Na+/K+ ATPase C-terminus  Exonuclease Glycosyl transferases group 1	1.1e-10 0.045 7.1e-62 2.3e-145 1.3e-56 2.9e-06	39.5 -3.6 219.0 496.3 201.5 27.0
504 a 505 v 508 N C 509 E 510 G f 111 G f f f	abhydrolase  wa  a_K_ATPase_  conuclease  clycos_trans  lycos_trans  lycos_trans  1  lycos_trans	Immunoglobulin domain alpha/beta hydrolase fold von Willebrand factor type A domain Na+/K+ ATPase C-terminus  Exonuclease Glycosyl transferases group 1 Glycosyl transferases group 1	1.1e-10 0.045 7.1e-62 2.3e-145 1.3e-56 2.9e-06	39.5 -3.6 219.0 496.3 201.5 27.0

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PPAM
NO:	1-1.2.	Busical IIOA	p-value	SCORE
515	EGF	EGF-like domain	1.9e-18	74.7
516	Surp	Surp module	4.3e-38	140.0
523	ig	Immunoglobulin domain	3.3e-06	25.0
526	UBX	UBX domain	1.1e-34	128.6
528	adh_zinc	Zinc-binding dehydrogenases	2.7e-34	127.4
530	SAM	SAM domain (Sterile alpha	0.046	10.0
		motif)		1
531	adh_short	short chain dehydrogenase	0.0025	-34.1
532	mito_carr	Mitochondrial carrier proteins	2.5e-81	281.7
533	mito_carr	Mitochondrial carrier proteins	2e-61	213.5
534	thiolase	Thiolase	3.5e-183	622.0
535	FMO-like	Plavin-binding monooxygenase- like	0	1153.7
536	SCAN	SCAN domain	4e-55	196.6
537	tRNA-synt 1	tRNA synthetases class I (I, L,	3.1e-136	466.0
	-	M and V)	3.16-136	400.0
538	tRNA-synt_1	tRNA synthetases class I (I, L, M and V)	3.le-136	466.0
539	tRNA-synt_1	tRNA synthetases class I (I, L,	1.9e-117	403.6
540	tRNA-synt 1	M and V)		
_	-	tRNA synthetases class I (I, L, M and V)	3.1e-136	466.0
541	vATP-synt_E	ATP synthase (E/31 kDa) subunit	5.9e-85	295.7
543	zf-C2H2	Zinc finger, C2H2 type	5.5e-69	242.6
544	DUF101	Protein of unknown function DUF101	8.5e-38	139.0
545	TGFb_propept	TGF-beta propeptide	1.1e-67	238.2
547	_1		1	1
548	WD40	WD domain, G-beta repeat	2.6e-32	120.8
	RHD	Rel homology domain (RHD).	1.6e-238	686.2
549	MMR_HSR1	GTPase of unknown function	5.4e-67	236.0
551	HECT	HECT-domain (ubiquitin- transferase).	4.3e-127	435.6
554	MHC_II_alpha	Class II histocompatibility	3.5e-74	259.8
555		antigen, alp		
333	zf-UBR1	Putative zinc finger in N-	3.3e-16	67.3
556	Kelch	recognin		
561	AMP-binding	Kelch motif	5.5e-29	109.7
562	PABP PABP	AMP-binding enzyme	2.8e-06	-163.7
362	PABP	Poly-adenylate binding protein, unique domai	4.9e-38	139.8
564	Gag_p30	Gag P30 core shell protein	1.2e-67	238.2
566	PWWP	PWWP domain	8.1e-16	
567	SCAN	SCAN domain	7.3e-68	66.0
569	pkinase	Eukaryotic protein kinase	1.5e-84	238.9
		domain	1.56-84	294.3
570	pkinase	Bukaryotic protein kinase domain	1.5e-84	294.3
571	CN_hydrolase	Carbon-nitrogen hydrolase	0.00081	-79.7
572	myosin_head	Myosin head (motor domain)	0.0001	1495.2
573	myosin_head	Myosin head (motor domain)	0	1490.4
575	Surp	Surp module	1.7e-23	91.5
576	Surp	Surp module	1.7e-23	
577	DNA pol B	DNA polymerase family B	0	91.5 1138.6
578	PDZ	PDZ domain (Also known as DHR	8.3e-09	42.7
579	ĺ	lor GIGEL		
<i> </i>	LRR	or GLGF).		
580	LRR neur_chan	Leucine Rich Repeat Neurotransmitter-gated ion-	4.9e-21 5.9e-177	83.3
580 ·	neur_chan	Leucine Rich Repeat Neurotransmitter-gated ion- channel		
580 ·	neur_chan	Leucine Rich Repeat Neurotransmitter-gated ion- channel Sushi domain (SCR repeat)		
580 583 584	neur_chan sushi DRAD	Leucine Rich Repeat Neurotransmitter-gated ion- channel Sushi domain (SCR repeat) DEAD/DEAH box helicase	5.9e-177	601.3
580 583 584 586	neur_chan sushi DEAD KH-domain	Leucine Rich Repeat Neurotransmitter-gated ion- channel Sushi domain (SCR repeat) DEAD/DEAH box helicase KH domain	5.9e-177	1673.0
583 584 586 587	neur_chan sushi DEAD KH-domain G-patch	Leucine Rich Repeat Neurotransmitter-gated ion- channel Sushi domain (SCR repeat) DEAD/DEAH box helicase KH domain G-patch domain	5.9e-177 0 7.3e-36	1673.0 116.3
580 583 584 586 587 589	neur_chan sushi DEAD KH-domain G-patch LIM	Leucine Rich Repeat Neurotransmitter-gated ion- channel Sushi domain (SCR repeat) DEAD/DEAH box helicase KH domain G-patch domain LIM domain containing proteins	5.9e-177 0 7.3e-36 2.9e-13	601.3 1673.0 116.3 57.5 61.2
583 584 586 587	neur_chan sushi DEAD KH-domain G-patch	Leucine Rich Repeat Neurotransmitter-gated ion- channel Sushi domain (SCR repeat) DEAD/DEAH box helicase KH domain G-patch domain	5.9e-177 0 7.3e-36 2.9e-13 2.3e-14	601.3 1673.0 116.3 57.5

Normone_rec	SEQ ID	PPAM NAME	DESCRIPTION	p-value	PFAM
	NO:				
	592	hormone_rec	nuclear hormone	3.5e-22	87.1
	593	PHD	PHD-finger	3.8e-12	53.8
Prinase   Eukaryotic protein kinase   Se-92   319.2	594	cadherin			
PG-GAP   PG-GAP repeat   4.3e-75   262.9	596	1	Eukaryotic protein kinase		
100   FG-GAP   FG-GAP repeat   4.3e-75   262.9	597	WD40	WD domain, G-beta repeat	0.00054	26.7
Q   Adapt CT	600	FG-GAP		1	
Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description	602				
Collagen   Collagen triple helix repeat   8c-42   152.4	603				1 '
(20 copies)   (20 copies)   (20 copies)   (21 copies)   (22 copies)   (23 copies)   (23 copies)   (24 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)   (25 copies)	605		domain		
PWWP		<u> </u>	(20 copies)		
Description   PRWP	606				
13	608	PWWP		2.6e-28	
RFX_DNA_bind ing   RFX_DNA_binding domain   S. 2e-54   192.9	509	PWWP	PWWP domain	2.6e-28	107.5
16	613		CAP-Gly domain	0.0046	20.1
	615		RFX DNA-binding domain	5.2e-54	192.9
17	616	kinesin	Kinesin motor domain	1.1e-81	284.8
2f-C3HC4	617	I.	<b>_i</b>	. L	
MATH   MATH domain   7.8e-05   22.2	618		Zinc finger, C3HC4 type (RING	1	
Protein-tyrosine phosphatase   1.4e-32   121.6	620	MATH		7.8e-05	22.2
Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description   Description	621	Y_phosphatas			1
BNR	622	<b>-</b> ∤		4.4e-40	146.6
TPR	623	BNR		2.18-11	51 3
TPR	624		Prokaryotic molybdopterin	,	I '
CNMP_binding	625	7700	_1	1 10 17	+
domain   domain   domain   dehydrogenase   Se-17   70.0			1		
			domain		
1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00   1.00			short chain dehydrogenase		
Pkinase					1
domain	632				
Pkinase	635			1.6e-104	360.7
domain	636	Fork_head	Fork head domain ,	5.9e-27	103.0
### efhand	637	pkinase		3.8e-70	246.5
### ### ### ### #### #### ############	642	TPR	TPR Domain	4.8e-08	40.1
SNF2_N   SNF2_and others N-terminal   1.2e-101   351.1	643	efhand	EF hand	.1—	1
PseudoU_synt h_2	647	SNF2_N		i .	1
Zf-C2H2   Zinc finger, C2H2 type   0.0087   22.7	648	h 2	1	1.9e-55	197.6
51         ank         Ank repeat         1.3e-17         71.9           52         I_LWEQ         1/LWEQ domain         9.5e-101         341.0           53         neur_chan         Neurotransmitter-gated ion-channel         4.1e-171         581.8           54         tsp_1         Thrombospondin type 1 domain         4.1e-47         169.9           59         FH2         Formin Homology 2 Domain         1e-107         371.2           61         pou         Pou domain - N-terminal to homeobox domain         5.3e-45         162.9           62         C2         C2 domain         6.7e-19         76.2           63         C2         C2 domain         6.7e-19         76.2           64         C2         C2 domain         6.7e-19         76.2           67         GST         Glutathione S-transferases         9.3e-34         114.4           68         LRR         Leucine Rich Repeat         9.3e-31         115.6           70         spectrin         Spectrin repeat         4e-57         203.2           71         I_LWEQ         I/LWEQ domain         9.5e-101         341.0           72         ABC_tran         ABC transporter         5.3e-60         212.8 <td>650</td> <td>zf-C2H2</td> <td>Zinc finger, C2H2 type</td> <td>0.0087</td> <td>22.7</td>	650	zf-C2H2	Zinc finger, C2H2 type	0.0087	22.7
Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Tabl	651				
	652		<u> </u>	1	
54         tsp_1         Thrombospondin type 1 domain         4.1e-47         169.9           59         FH2         Formin Homology 2 Domain         1e-107         371.2           61         pou         Pou domain - N-terminal to homeobox domain         5.3e-45         162.9           62         C2         C2 domain         6.7e-19         76.2           63         C2         C2 domain         6.7e-19         76.2           64         C2         C2 domain         6.7e-19         76.2           67         GST         Glutathione S-transferases.         9.3e-34         114.4           68         LRR         Leucine Rich Repeat         9.3e-31         115.6           70         spectrin         Spectrin repeat         4e-57         203.2           71         I_LWEQ         I/LWEQ domain         9.5e-101         341.0           72         ABC_tran         ABC transporter         5.3e-60         212.8	653		Neurotransmitter-gated ion-		
FH2 Formin Homology 2 Domain 1e-107 371.2  FOU DOMAIN STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE	654	tsp 1		4 10-47	169 9
Pou domain - N-terminal to homeobox domain   5.3e-45   162.9	659		Formin Homology 2 Domain		_1
62     C2     C2 domain     6.7e-19     76.2       63     C2     C2 domain     6.7e-19     76.2       64     C2     C2 domain     6.7e-19     76.2       67     GST     Glutathione S-transferases.     9.3e-34     114.4       68     LRR     Leucine Rich Repeat     9.3e-31     115.6       70     Spectrin     Spectrin repeat     4e-57     203.2       71     I LWEQ     I/LWEQ domain     9.5e-101     341.0       72     ABC_tran     ABC transporter     5.3e-60     212.8	661		Pou domain - N-terminal to		
63 C2 C2 domain 6.7e-19 76.2 64 C2 C2 domain 6.7e-19 76.2 67 GST Glutathione S-transferases. 9.3e-34 114.4 68 LRR Leucine Rich Repeat 9.3e-31 115.6 70 spectrin Spectrin repeat 4e-57 203.2 71 I_LWEQ I/LWEQ domain 9.5e-101 341.0 72 ABC_tran ABC transporter 5.3e-60 212.8	662	1 02		<del>                                     </del>	+26.3
64         C2         C2 domain         6.7e-19         76.2           67         GST         Glutathione S-transferases.         9.3e-34         114.4           68         LRR         Leucine Rich Repeat         9.3e-31         115.6           70         spectrin         Spectrin repeat         4e-57         203.2           71         I_LWEQ         I/LWEQ domain         9.5e-101         341.0           72         ABC_tran         ABC transporter         5.3e-60         212.8	663		J		
67 GST Glutathione S-transferases. 9.3e-34 114.4 68 LRR Leucine Rich Repeat 9.3e-31 115.6 70 spectrin Spectrin repeat 4e-57 203.2 71 I_LWEQ I/LWEQ domain 9.5e-101 341.0 72 ABC_tran ABC transporter 5.3e-60 212.8					_1
68         LRR         Leucine Rich Repeat         9.3e-31         115.6           70         spectrin         Spectrin repeat         4e-57         203.2           71         I_LWEQ         I/LWEQ domain         9.5e-101         341.0           72         ABC_tran         ABC transporter         5.3e-60         212.8		-l			
70 spectrin Spectrin repeat 4e-57 203.2 71 I_LWEQ I/LWEQ domain 9.5e-101 341.0 72 ABC_tran ABC transporter 5.3e-60 212.8	667				
71 I_LWEQ I/LWEQ domain 9.5e-101 341.0 72 ABC_tran ABC transporter 5.3e-60 212.8	668			d	
72 ABC_tran ABC transporter 5.3e-60 212.8	670	<del></del>		4e-57	203.2
[ ] [ ] [ ] [ ] [ ] [ ] [ ] [ ] [ ] [ ]	671		I/LWEQ domain	9.5e-101	341.0
	672	<u> </u>		5.3e-60	212.8
74 WD40 WD domain, G-beta repeat 4.8e-24 93.3	674	WD40	WD domain, G-beta repeat	4.8e-24	93.3

NO.   ND domain, G-beta repeat   4.8e-24   93.3					
676	SEQ ID	PPAM NAME	DESCRIPTION	p-value	-
1.	675	WD40	WD domain, G-beta repeat	4 80-24	
## 2.60-29   107.7.	676	LRR	Leucine Rich Repeat		
Section   Style   Sine finger, C2H2 type   S.2e-05   30.1	679	zf-CCCH	Zinc finger C-x8-C-x5-C-x3-V		
CR			type	2.66-29	107.7
681 CH Calponin homology (Ch) domain 2.4e-17 71.1 682 DSPC Dual specificity phosphatase, 4.3e-43 156.6 683 sf-C3HC4 finger, C3HC4 type (RING finger) 689 PR55 Frotein phosphatase 2A 0 1598.8 689 PR55 Protein phosphatase 2A 0 1038.8 691 homeobox Homeobox domain 8.5e-30 112.4 695 Peptidase_M2 mctallopeptidase family M24 2.5e-59 210.5 697 RhoGEF RhoGEF domain 9.5e-35 128.9 698 PHD PHD PHD-finger 0.008 9.3 699 PHD PHD PHD-finger 0.008 9.3 701 zf-C2H2 Zinc finger, C2H2 type 5.5e-123 422.0 703 zf-C2H2 Zinc finger, C2H2 type 5.5e-123 781.6 704 VAR CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CANADA CA		_1	Zinc finger, C2H2 type	5.2e-05	30.1
DSPC		_ 1.	Calponin homology (CH) domain		
catalytic doma	682	DSPC	Dual specificity phosphatase,		
Finger   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin   Synapsin	602		catalytic doma		
Synapsin   Synapsin   Synapsin   D   1890.8	683	ZI-C3HC4	Zinc finger, C3HC4 type (RING	0.051	10.8
PR55	687	Synapsin			1000
Regulatory subunit PR	689				
			regulatory subunit PR	10	1038.8
### Reput dase M2   metallopeptidase family M24   2.5e-59   210.5   ### A   A   A   A   A   A   A   A   ### A   A   A   A   A   ### A   A   A   A   ### A   A   A   ### A   A   ### A   A   ### A   A   ### A   A   ### A   A   ### A   A   ### A   A   ### A   A   ### A   A   ### A   A   ### A   A   ### A   A   ### A   A   ### A   A   ### A   A   ### A   A   ### A   A   ### A   A   ### A   A   ### A   A   ### A   ### A   A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A   ### A	691		Homeobox domain	9 50-30	112 4
A	696	Peptidase M2	metallopeptidase family M24		
PHD			, , , , , , , , , , , , , , , , , , , ,	7.50.35	210.5
PHD				9.5e-35	128 9
			PHD-finger		
702 Sulfatase Sulfatase 3e-231 781.6 703 zf-C2H2 Zinc finger, C2H2 type 5.7e-20 79.8 706 Acyl_transf Acyl transferase domain 1.1e-22 88.8 707 Acyl_transf Acyl transferase domain 1.1e-22 88.8 708 WD40 WD domain, G-beta repeat 4.8e-19 76.7 710 Ran_BP1 RanBP1 domain. 8.4e-06 -7.3 713 DEAD DEAD/DEAH box helicase 9.9e-42 134.9 714 PH PH Omain 1.6e-09 39.0 715 DBFC Dual specificity phosphatase, 1.5e-37 138.2 717 Sialyltransf Sialyltransferase family 7.5e-31 115.9 718 ig Immunoglobulin domain 1e-29 100.8 719 integrin B Integrins, beta chain 0 1125.4 720 zf-C3HC4 Zinc finger, C3HC4 type (RING 1.1e-08 32.4 721 finger) 722 Peptidase_C2 Calpain family cysteine 3e-145 495.9 723 ig Immunoglobulin domain 2.2e-05 22.4 724 P-box F-box domain. 0.007 23.0 725 Nop Putative snoRNA binding domain 8.1e-58 205.5 726 Nop Putative snoRNA binding domain 8.1e-58 205.5 727 MD40 WD domain, G-beta repeat 7.5e-26 99.3 730 darm Double-stranded RNA binding 0.027 12.1 731 dynamin Dynamin family 4.2e-16 66.9 733 zf-CCCH Zinc finger C-x8-C-x5-C-x3-H 2.8e-10 41.7 735 CDP- CDP-alcohol DEAD/DEAH box helicase 8.6e-57 182.5 739 DEAD DEAD/DEAH box helicase 8.6e-57 182.5 739 DEAD DEAD/DEAH box helicase 8.6e-57 182.5 739 DEAD DEAD/DEAH box helicase 8.6e-57 182.5 739 DEAD DEAD/DEAH box helicase 8.6e-57 182.5 739 DEAD DEAD/DEAH box helicase 8.6e-57 182.5 739 DEAD DEAD/DEAH box helicase 8.6e-57 182.5 739 DEAD DEAD/DEAH box helicase 8.6e-57 182.5 739 DEAD DEAD/DEAH box helicase 8.6e-57 182.5 739 DEAD DEAD/DEAH box helicase 8.6e-57 182.5 739 DEAD DEAD/DEAH box helicase 8.6e-57 182.5 739 DEAD DEAD/DEAH box helicase 8.6e-57 182.5 739 DEAD DEAD/DEAH box helicase 8.6e-57 182.5 739 DEAD DEAD/DEAH box helicase 8.6e-57 182.5 739 DEAD DEAD/DEAH box helicase 8.6e-57 182.5 739 DEAD DEAD/DEAH box helicase 8.6e-57 182.5 739 DEAD DEAD/DEAH box helicase 8.6e-57 182.5 739 DEAD DEAD/DEAH box helicase 8.6e-57 182.5 730 DEAD DEAD/DEAH box helicase 8.6e-57 182.5 731 Hydrolase haloacid dehalogenase-like 6.1e-11 49.8 730 DEAD DEAD DEAD/DEAH box helicase 6.1e-11 49.8 730 DEAD DEAD			Zinc finger, C2H2 type		
703   zf-C2H2   Zinc finger, C2H2 type			Sulfatase		1
Note			Zinc finger, C2H2 type	5.7e-20	1
Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran   Ran			Acyl transferase domain	1.le-22	88.8
DEAD   DEAD   DEAD/DEAH   DOX   DEAD/DEAH   DOX   DEAD/DEAH   DOX   DEAD/DEAH   DOX   DEAD/DEAH   DOX   DEAD/DEAH   DOX   DEAD/DEAH   DOX   DEAD/DEAH   DOX   DEAD/DEAH   DOX   DEAD/DEAH   DOX   DEAD/DEAH   DOX   DEAD/DEAH   DOX   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DEAD/DEAH   DE			WD domain, G-beta repeat	4.8e-19	76.7
DEAD   DEAD   DEAD/DEAH box helicase   9.9e-42   134.9				8.4e-06	-7.3
DSPC   Dual specificity phosphatase   1.6e-09   39.0				9.9e-42	
1.5e-37   138.2   1.5e-37   138.2   1.5e-37   138.2   1.5e-37   138.2   1.5e-37   138.2   138.2   138.2   138.2   138.2   138.2   138.2   138.2   138.2   138.2   138.2   138.2   138.2   138.2   138.2   138.2   138.2   138.2   138.2   138.2   138.2   139.5   138.2   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   139.5   13				1.6e-09	39.0
115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.9   115.	112	DSPC	Dual specificity phosphatase,	1.5e-37	138.2
Integrin B	717	Cialiste want	catalytic doma		1
Integrin B			Statyteransterase family		1
Zf-C3HC4					
Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Tringer   Trin			7ing finger Clude by the	_	. 1
Peptidase_C2			finger)	1.1e-08	32.4
	722	Peptidase C2	Calpain family cycleine		
Timestable   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor   Tempor			protease	3e-145	495.9
F-box		ig	Immunoglobulin domain	2 20-05	122 4
Nop		F-box	F-box domain.		
Nop		<u> </u>	Putative snoRNA binding domain		
MD40			Putative snoRNA binding domain		
Double-stranded RNA binding			WD domain, G-beta repeat	7.5e-26	
Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Trypsin   Tryp	730	darm	Double-stranded RNA binding	0.027	
Table	731	domania			1
Type			Dynamin ramily		66.9
CDP-OH P	, 00	21-cccn		2.8e-10	41.7
OH_P_transf	735	CDP-			
DEAD   DEAD   DEAD/DEAH box helicase   8.6e-57   182.5		OH P transf		4.2e-26	100.1
TSC22 TSC-22/dip/bun family 6.5e-32 119.5 TAS Ras family 2.2e-100 346.9 TAS Ras family 2.2e-100 346.9 TAS PMI_typeI Phosphomannosc isomerase type I 1.2e-243 822.9 TAS Trypsin Trypsin 6.4e-88 279.4 TAS Kazal Kazal-type serine protease 2.2e-52 187.4 TAS EF hand EF hand 6.3e-06 33.1 TAS PHD PHD-finger 4.9e-16 66.7 TAS ZINC finger, C2H2 type 3.2e-21 83.9 TAS Hydrolase haloacid dehalogenase-like hydrolase TAS Ribosomal_L3 Ribosomal L39 protein 0.00018 26.7 TAS PH PH domain 3.6e-14 55.7 TAS SCAN SCAN domain 1.4e-53 191.5 TAS ADP-ribosylation factor family 2.2e-19 77.8	738	DEAD	DEAD/DEAH box helicase	9 60-57	
Ras family   2.2e-100   346.9	739	TSC22	TSC-22/dip/bup family		
PMI_typeI	742		Ras family		
747         trypsin         Trypsin         6.4e-88         279.4           748         kazal         Kazal-type serine protease inhibitor domain         2.2e-52         187.4           749         efhand         EF hand         6.3e-06         33.1           751         PHD         PHD-finger         4.9e-16         66.7           752         zf-C2H2         Zinc finger, C2H2 type         3.2e-21         83.9           753         Hydrolase         haloacid dehalogenase-like hydrolase         6.1e-11         49.8           754         Ribosomal_L3         Ribosomal L39 protein         0.00018         26.7           755         PH         PH domain         3.6e-14         55.7           58         SCAN         SCAN domain         1.4e-53         191.5           59         PA         PA domain         0.0065         23.1           60         arf         ADP-ribosylation factor family         2.2e-19         77.8	743	PMI_typeI			
	747		Trypsin		
Inhibitor domain	748	kazal	Kazal-type serine protease		
Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   Single   S			inhibitor domain		
PHD				6.3e-06	33.1
252   zf-C2H2   Zinc finger, C2H2 type   3.2e-21   83.9			PHD-finger		
Hydrolase			Zinc finger, C2H2 type		
hydrolase	133	nydrolase	haloacid dehalogenase-like		L
9 0.00018 26.7  55 PH PH domain 3.6e-14 55.7  58 SCAN SCAN domain 1.4e-53 191.5  59 PA PA domain 0.0065 23.1  60 arf ADP-ribosylation factor family 2.2e-19 77.8	75a	Diboor 1		ļ	ŀ
55         PH         PH domain         3.6e-14         55.7           58         SCAN         SCAN domain         1.4e-53         191.5           59         PA         PA domain         0.0065         23.1           60         arf         ADP-ribosylation factor family         2.2e-19         77.8			Ribosomal L39 protein	0.00018	26.7
58         SCAN         SCAN domain         3.6e-14         55.7           59         PA         PA domain         1.4e-53         191.5           60         arf         ADP-ribosylation factor family         2.2e-19         77.8	55	· ·	Dir da di di	<u>                                      </u>	
59 PA PA domain 1.4e-53 191.5 60 arf ADP-ribosylation factor family 2.2e-19 77.8					
60 arf ADP-ribosylation factor family 2.2e-19 77.8	59				
722-1100Sylacton factor family   2.2e-19   77.8	60				
2.2e-40 147.6	61		CIDE-N domain		
			T TENN HOURAIN	2.2e-40	147.6

SEQ ID	PFAM NAME	DESCRIPTION	l nevalue	T none
NO:	, and the same	DESCRIPTION	p-value	PFAM
762	histone	Core histone H2A/H2B/H3/H4	9.9e-53	188.6
763	zf-MYND	MYND finger	4.1e-14	60.3
764	pou	Pou domain - N-terminal to	le-52	188.6
767		homeobox domain		
167	VWC	von Willebrand factor type C domain	2.9e-34	127.3
769	efhand	BF hand	4.8e-11	50.1
770	zf-C4	Zinc finger, C4 type (two . domains)	2.4e-53	181.6
772	ras	Ras family	7e-90	312.0
773	Sulfatase	Sulfatase	le-142	487.5
775	zf-C2H2	Zinc finger, C2H2 type	1.1e-12	55.5
776	zf-C2H2	Zinc finger, C2H2 type	1.1e-12	55.5
777	zf-C2H2	Zinc finger, C2H2 type	1.le-12	55.5
778	rrm	RNA recognition motif.	2.1e-32	121.1
779	G6PD ·	Glucose-6-phosphate dehydrogenase	1.5e-76	236.6
780	spectrin	Spectrin repeat		
781	mito carr	Mitochondrial carrier proteins	3.7e-29	110.3
782	SCAN	SCAN domain	4.6e-57 1.3e-24	198.5
783	PDZ	PDZ domain (Also known as DHR	1.3e-24 4.1e-07	95.2
	1	or GLGF).	4.1e-07	37.1
785	DEAD	DEAD/DEAH box helicase	6e-06	21.7
786	ras	Ras family	5.3e-39	143.0
787	RNase HII	Ribonuclease HII	2.5e-67	237.1
790	PI3 PI4 kina	Phosphatidylinositol 3- and 4-	5.4e-108	372.2
	se	kinases '	3.10 200	3,2.2
795	cadherin	Cadherin domain	2.5e-40	147.4
796	ARID	ARID DNA binding domain	1.6e-20	81.6
797 799	trypsin	Trypsin	9.9e-20	64.8
	CH	Calponin homology (CH) domain	3.7e-15	63.8
801	Gal- bind_lectin	Vertebrate galactoside-binding lectin	4.le-25	88.7
803	WD40	WD domain, G-beta repeat	0.00082	26.1
806	TBC	TBC domain	1.8e-26	101.4
807	TBC	TBC domain	1.8e-26	101.4
808	CN hydrolase	Carbon-nitrogen hydrolase	8.8e-80	278.5
811	CBFD_NFYB_HM	Histone-like transcription factor	6e-14	59.8
812	adh_short	short chain dehydrogenase	8.1e-20	79.3
814	IMP4	Domain of unknown function	3.3e-71	250.0
815	zf-C2H2	Zinc finger, C2H2 type	8.2e-66	232.1
816	Pept_tRNA_hy dro	Peptidyl-tRNA hydrolase	1.6e-37	138.0
817	ARID	ARID DNA binding domain	2.5e-18	74.3
826	IF5_eIF4_eIF 2	eIF4-gamma/eIF5/eIF2-epsilon	1.6e-32	121.5
830	ArfGap	Putative GTP-ase activating protein for Arf	1.5e-53	191.3
831	LRR	Leucine Rich Repeat	2 19-25	107
832	laminin_EGF	Laminin EGF-like (Domains III	2.1e-26 2e-57	101.1 204.2
839	rrm	and V)	ļ	
840	Y_phosphatas	RNA recognition motif. Protein-tyrosinc phosphatase	1.3e-22	88.5
	e		2.60-119	409:8
841	pkinase	Eukaryotic protein kinase domain	3.4e-100	346.3
844	Ribosomal_L2 2e	Ribosomal L22e protein family	1e-64	228.4
846	IBR	IBR domain	9e-15	62.5
849	zf-C3HC4	Zinc finger, C3HC4 type (RING	7.4e-07	26.5
050	of Caven	finger)		
	zf-C3HC4	Zinc finger, C3HC4 type (RING	0.00016	18.9
850		finger)		
851 852	SET SRCR	finger) SET domain Scavenger receptor Cysteine-	5e-30	113.2

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM
NO:	<u> </u>			SCORE
853	SRCR	rich domain		
		Scavenger receptor cysteine- rich domain	0	1025.4
857	lactamase_B	Metallo-beta-lactamase superfamily	0.012	-6.0
858	COX6A	Cytochrome c oxidase subunit	3.4e-58	206.7
859	rrm	RNA recognition motif.	5.4e-45	162.9
861	PRK	Phosphoribulokinase	5.1e-62	219.4
863	mito carr	Mitochondrial carrier proteins	2.9e-53	185.5
864	HSP90	Hsp90 protein	4.7e-158	538.5
866	ig	Immunoglobulin domain	4e-12	44.1
867	zf-C2H2	Zinc finger, C2H2 type	7e-135	461.5
872	histone	Core histone H2A/H2B/H3/H4	4.9e-41	149.8
874	CPSase L cha	Carbamoyl-phosphate synthase	2.1e-218	739.0
	in	(CPSase)	7.10.10	/33.0
879	Ribosomal_S1 2e	Ribosomal protein SI2e	2.1e-98	340.3
882	serpin	Serpins (serine protease inhibitors)	2.5e-42	145.7
883	Patatin	Patatin	1.2e-51	1.00
884	RA	Ras association (RalGDS/AF-6)	0.044	182.0
887	DUF92	domain		8.0
889		Integral membrane protein DUF92	2.7e-12	54.3
893	sugar tr	Sugar (and other) transporter  Domain of unknown function	8.2e-63	222.1
		DUF28	1.3e-43	158.3
896	IP_trans	Phosphatidylinositol transfer protein	6.5e-98	338.7
898	DEAD	DEAD/DEAH box helicase	1.5e-48	156.5
899	KE2	KE2 family protein	7e-61	215.7
900	KE2	KE2 family protein	4.3e-51	183.2
901 902	zf-C2H2	Zinc finger, C2H2 type	2.7e-57	203.8
902	ras	Ras family	2.3e-75	263.8
906	TPR GBP	TPR Domain	3.2e-22	87.2
907	GBP	Guanylate-binding protein	8.9e-253	853.1
908	WD40	Guanylate-binding protein	1.1e-239	809.6
909	PH	WD domain, G-beta repeat	2.6e-26	100.8
910	2f-C2H2		1.3e-09	39.4
913	Epimerase	Zinc finger, C2H2 type NAD dependent	2.5e-39	144.1
921	<u> </u>	epimerase/dehydratase family	5e-07	-88.5
921	TBC	TBC domain	1.5e-09	30.7
922	WD40	WD domain, G-beta repeat	1.6e-25	98.2
924		WD domain, G-beta repeat	8.2e-07	36.1
	Hydrolase	haloacid dehalogenase-like hydrolase	2.9e-05	29.1
925	UQ_con	Ubiquitin-conjugating enzyme	0.00033	-27.6
926	CH	Calponin homology (CH) domain	3.3e~53	190.2
928	WD40	WD domain, G-beta repeat	5.9e-48	172.7
929	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	3.1e-10	37.4
930	Ribul_P_3_ep im	Ribulose-phosphate 3 epimerase family	7.2e-105	361.8
931	Ribul_P_3_ep	Ribulose-phosphate 3 epimerase family	1.2e-96	334.4
36	C2	C2 domain	2.2e-62	220 =
37	NAP_family	Nucleosome assembly protein (NAP)	1.1e-22	220.7 84.6
40	abhydrolase	alpha/beta hydrolase fold		
44	Tropomyosin	Tropomyosins	0.011	3.1
		Eukaryotic protein kinase	3.2e-07	25.1
48	i okinase			1 262 2
48	pkinase	domain	3.4e-75	263.2
	WD40 Acyltransfer	domain WD domain, G-beta repeat Acyltransferase	1.8e-27 1.6e-07	104.7

SEQ ID	PPAM NAME	DESCRIPTION		
NO:	TAN MANE	DESCRIPTION	p-value	PPAM
951	SAM	SAM domain (Sterile alpha	0.014	SCORE 14.5
1		motif)	0.014	14.5
954	GFO_IDH MocA	Oxidoreductase family	1.3e-11	52.0
955	BTB	BTB/POZ domain	7e-22	86.1
956	BTB	BTB/POZ domain	7e-22	86.1
957	CDP-	CDP-alcohol	0.053	-22.2
<u> </u>	OH_P_transf	phosphatidyltransferase		
959	ras	Ras family	2.4e-97	336.8
960	ras	Ras family	8.4e-43	155.6
961	Acetyltransf	Acetyltransferase (GNAT) family	1.2e-08	42.2
962	adh_short	short chain dehydrogenase	2.4e-31	117.6
963	mutT	Bacterial mutT protein	5.6e-06	26.2
969 .	IF-2B	Initiation factor 2 subunit	8.4e-193	653.9
970		family	l .	}
975	RNase_PH	3' exoribonuclease family	9e-24	92.4
977	PDZ	WW domain	5.7e-25	96.4
"''	PDZ	PDZ domain (Also known as DHR	3.6e-21	83.7
978	Pibogomal II	or GLGF).		_1
1 7 7 8	Ribosomal_L1	Ribosomal protein L17	2.4e-20	81.0
979	LIM	Y YM done to a second district	<u> </u>	
980	Calsequestri	LIM domain containing proteins Calsequestrin	5.8e-42	152.8
	n	caracdnescriu	1.7e-297	1001.7
982	HSP20	Hsp20/alpha crystallin family	1 2 2 2 2 2	1.2.
983	oxidored q6	NADH ubiquinone oxidoreductase,	1.2e-10 4.8e-63	43.2
j	_4	20 Kd sub	4.8e-63	222.9
988	TBC	TBC domain	2.2e-50	180.8
989	TBC	TBC domain	2.2e-50	180.8
993	tRNA_int_end	tRNA intron endonuclease	0.0017	-34.2
	0		0.0017	-34.2
994	homeobox	Homeobox domain	4e-18	73.6
997	pyr_redox	Pyridine nucleotide-disulphide	0.012	11.6
		oxidoreducta		1
1000	mito_carr	Mitochondrial carrier proteins	9.7e-123	421.2
1001	RA	Ras association (RalGDS/AF-6)	1.2e-15	65.4
1004	Drine -	domain		]
1004	DUF81	Domain of unknown function	0.099	10.2
1005	actin	DUF81		
1005	actin	Actin	1.3e-174	574.3
1007	cpn60_TCP1	Actin	3.1e-130	428.6
1008	TPR	TCP-1/cpn60 chaperonin family TPR Domain	3.7e-195	661.8
1009	zf-C2H2	Zinc finger, C2H2 type	8.1e-44	159.0
1011	zf-C2H2	Zinc finger, C2H2 type	3.6e-61	216.6
1012	zf-C3HC4	Zinc finger, C3HC4 type (RING	3.6e-61	216.6
		finger)	4.7e-15	53.1
1016	tRNA-synt 2c	tRNA synthetases class II (A)	2.3e-15	+==-
1018	RhoGAP	Rhogap domain	2.3e-15 1.6e-78	55.2 274.3
1022	PGAM	Phosphoglycerate mutase family	~	<del>   </del>
1026	HMG_box	HMG (high mobility group) box	3.8e-18 8.4e-20	79.2
1027	TBC	TBC domain	7.3e-45	162.5
1028	UQ_con	Ubiquitin-conjugating enzyme	1.4e-49	178.1
1032	PDZ	PDZ domain (Also known as DHR	0.028	16.3
		or GLGF).		20.3
1034	Hydrolase	haloacid dehalogenasc-like	2e-21	84.6
4000		hydrolase		1
1037	KRAB	KRAB box	4.8e-06	32.4
1038	Cation_efflu	Cation efflux family	7.1e-42	152.5
	x		<del>-</del>	
1040	ART	NAD:arginine ADP-	4.7e-47	169.1
1040		ribosyltransferase		
1042	WD40	WD domain, G-beta repeat	1.9e-18	74.7
1043	zf-C2H2	Zinc finger, C2H2 type	3.7e-24	93.7
1045	lectin_c	Lectin C-type domain	1.9e-28	108.0
7040	Glucosamine_ iso	Glucosamine-6-phosphate	0.00013	-25.1
	*90	isomerase		

SEQ ID	PFAM NAME	DESCRIPTION		
NO:		DESCRIPTION	p-value	PFAM
1047	ligase-CoA	CoA-ligases	4.5e-80	279.4
1049	ig	Immunoglobulin domain	1.7e-09	35.6
1050	Ribosomal L2	Ribosomal protein L24e	2e-33	124.5
1054	Amidase	Amidase	4.3e-152	518.7
1055	rrm	RNA recognition motif.	3.8e-26	100.3
1058	annexin	Annexin	6.9e-14	159.2
1059	PMP22 Claudi	PMP-22/EMP/MP20/Claudin family	0.023	
1060	n		0.023	-23.6
	homeobox	Homeobox domain	3.2e-31	117.2
1062	Acyltransfer ase	Acyltransferase	0.00065	10.5
1064	AMP-binding	AMP-binding enzyme	6.6e-100	345.3
1065	LRR	Leucine Rich Repeat	3.3e-14	60.6
1066	GTP1 OBG	GTP1/OBG family	4.8e-41	
1071	iq	Immunoglobulin domain		141.8
1072	PHD	PHD-finger	8.4e-48	159.1
1074	DENN		6.8e-07	36.3
1075	SCP	DENN (AEX-3) domain	8.3e-33	121.5
1077		SCP-like extracellular protein	4.7e-41	149.8
	. OLF	Olfactomedin-like domain	2.2e-66	234.0
1078	mito_carr	Mitochondrial carrier proteins	1e-42	149.3
1079	WD40	WD domain, G-beta repeat	6.2e-45	162.7
1087	START	START domain	1.5e-48	174.7
1093	DSPc	Dual specificity phosphatase,	3.3e-63	223.4
1094	GSHPx	catalytic doma		223.4
1095		Glutathione peroxidases	9.6e-41	148.8
	DUF25	Domain of unknown function DUF25	2e-75	264.0
1096	DUF25	Domain of unknown function	6e-75	262.4
1105	Nitroreducta se	Nitroreductase family	1.3e-13	58.6
1106	PTE			
1107	DAGKC	Phosphotriesterase family	1.3e-179	610.1
	DAGKC	Diacylglycerol kinase catalytic domain	0.00049	19.6
1109	ras	Ras family	1.3e-15	40.7
1115	ArfGap	Putative GTP-ase activating protein for Arf	9.7e-47	168.7
1116	HMG14 17	HMG14 and HMG17		
1117	HMG14 17	HMG14 and HMG17	4.4e-21	83.5
1119	FAA hydrolas		9.9e-12	52.4
	е	Fumarylacetoacetate (FAA) hydrolase fam	2e-83	290.6
1120	pkinase	Eukaryotic protein kinase domain	1.4e-94	327.6
1123	abhydrolase	alpha/beta hydrolase fold	9.2e-23	00 0
1129	pro isomeras	Cyclophilin type peptidyl-		89.0
	e	prolyl cis-tr	2.2e-56	197.1
1131	DnaJ	DnaJ domain	1.6e-30	114.9
1132	WD40	WD domain, G-beta repeat	1.3e-19	78.6
1133	WD40	WD domain, G-beta repeat	1.8e-15	64.9
1134	PH	PH domain	0.0015	17.8
1136	Adap_comp_su b	Adaptor complexes medium	1.2e-256	866.0
1137	Adap_comp_su	Subunit family Adaptor complexes medium	2.5e-209	708.8
7170	b	subunit family		
1139	ras	Ras family	1.5e-86	301.0
1141	pkinase	Eukaryotic protein kinase domain	9.4e-74	258.4
1152	Acyltransfer ase	Acyltransferase	1.2e-05	29.9
1153	IRS	home	<u> </u>	
		PTB domain (IRS-1.type)	5.4e-55	196.1
1155	ig	Immunoglobulin domain	1.3e-31	106.9
1157	Asparaginase	Asparaginase	6.4e-72	252.3
1159	GMC_oxred	GMC oxidoreductases	4.7e-142	485.3
1160	zf-AN1	AN1-like Zinc finger		
	·	tinget	0.00021	27.9

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM
NO:	17-2		1	SCORE
	linker_histo	linker histone H1 and H5 family	3.8e-14	60.4
1164	DED	Death effector domain	3.9e-05	30.5
1165	IRS	PTB domain (IRS-1 type)	2.6e-43	157.3
1166	IRS	PTB domain (IRS-1 type)	2.6e-43	157.3
1168	SAM	SAM domain (Sterile alpha motif)	0.04	10.5
1170	abhydrolase	alpha/beta hydrolase fold	0.098	-7.5
1174	SAP	SAP domain	3.9e-10	47.1
1177	PP2C	Protein phosphatase 2C	5.3e-31	112.5
1178	WD40	WD domain, G-beta repeat	4.7e-35	129.9
1180	Ets	Ets-domain	1.8e-09	33.3
1181	Collagen	Collagen triple hclix repeat (20 copies)	0.00016	24.7
1182	TCL1_MTCP1	TCL1/MTCP1 family	9.5e-56	198.6
1184	RasGBF	RasGBF domain	1.7e-88	307.4
1185	mito_carr	Mitochondrial carrier proteins	1.5e-62	217.3
1187	UPAR_LY6	u-PAR/Ly-6 domain	0.0042	15.6
1188	Orn_DAP_Arg_ deC	Pyridoxal-dependent decarboxylase	6.2e-128	430.6
1193	Stathmin	Stathmin family	1.8e-90	314.0
1194	Stathmin	Stathmin family	1.8e-90	314.0
1195	Sec1	Sec1 family	3.2e-183	622.1
1196	pyr_redox	Pyridine nucleotide-disulphide oxidoreducta	3.1e-32	111.8
1197	Glyco_transf	Glycosyl transferase family 8	1.2e-09	45.5
1202	K_tetra	K+ channel tetramerisation domain	0.022	-16.8
1203	adh short	short chain dehydrogenase	8.3e-45	162.3
1206	Ubie_methylt ran	ubiE/COQ5 methyltransferase family	1.3e-121	417.4
1208	7tm_3	7 transmembrane receptor	7.2e-09	29.0
1209	ank	Ank repeat	3.9e-15	63.7
1210	vATP- synt_AC39	ATP synthase (C/AC39) subunit	2.5e-128	439.7
1212	zf-C2H2	Zinc finger, C2H2 type	5.5e-17	69.9
1213	efhand	EF hand	3.2e-07	37.4
1219	rrm	RNA recognition motif.	2.1e-40	147.7
1220	DUF6	Integral membrane protein DUF6	0.015	21.5
1222	SCAN	SCAN domain	1.5e-71	251.1
1223	G-gamma	GGL domain	3.6e-36	129.5
1227	catalase	Catalase	0	1158.9
1232	PX	PX domain	2.2e-15	64.5
1233	PX	PX domain	2.2e-15	64.5
1236	FCH	Fes/CIP4 homology domain	3.3e-09	44.0
1241	Peptidase_M2	Peptidase family M20/M25/M40	2e-63	224.1
1345	0		26-05	224.1
1243	WW	ww domain	0.044	17.9
1247	UPF0006	WW domain Metalloenzyme of unknown function UPF0006		
1247	WW UPF0006 Glycos_trans f_2	WW domain Metalloenzyme of unknown	0.044	17.9
1247 1248 1249	WW UPF0006 Glycos_trans	WW domain Metalloenzyme of unknown function UPF0006 Glycosyl transferases EF hand	0.044 6.3e-61 4.5e-10	17.9 215.8 46.9
1247 1248 1249 1254	WW UPF0006 Glycos_trans f_2	WW domain Metalloenzyme of unknown function UPF0006 Glycosyl transferases EF hand	0.044 6.3e-61 4.5e-10	17.9 215.8 46.9
1247 1248 1249 1254 1255	WW UPF0006 Glycos_trans f_2 efhand	WW domain Metalloenzyme of unknown function UPF0006 Glycosyl transferases EF hand Ubiquitin-conjugating enzyme Ras family	0.044 6.3e-61 4.5e-10 4e-11 2.1e-73	17.9 215.8 46.9 50.4 257.3
1247 1248 1249 1254	WW UPF0006  Glycos_trans f_2 efhand UQ_con	WW domain Metalloenzyme of unknown function UPF0006 Glycosyl transferases EF hand Ubiquitin-conjugating enzyme	0.044 6.3e-61 4.5e-10	17.9 215.8 46.9
1247 1248 1249 1254 1255	WW UPF0006  Glycos_trans f_2 efhand UQ_con ras formyl_trans	WW domain Metalloenzyme of unknown function UPF0006 Glycosyl transferases  EF hand Ubiquitin-conjugating enzyme Ras family Formyl transferase  Zinc finger, C3HC4 type (RING	0.044 6.3e-61 4.5e-10 4e-11 2.1e-73 2.2e-62	17.9 215.8 46.9 50.4 257.3 220.7
1247 1248 1249 1254 1255 1256	WW UPF0006  Glycos_trans f_2 efhand UQ_con ras formyl_trans f	WW domain Metalloenzyme of unknown function UPF0006 Glycosyl transferases  EF hand Ubiquitin-conjugating enzyme Ras family Formyl transferase  Zinc finger, C3HC4 type (RING finger)	0.044 6.3e-61 4.5e-10 4e-11 2.1e-73 2.2e-62 4.9e-30	17.9 215.8 46.9 50.4 257.3 220.7 108.3
1247 1248 1249 1254 1255 1256	WW UPF0006  Glycos_trans f_2 efhand UQ_con ras formyl_trans f zf-C3HC4  DiHfolate_re	WW domain Metalloenzyme of unknown function UPF0006 Glycosyl transferases  EF hand Ubiquitin-conjugating enzyme Ras family Formyl transferase  Zinc finger, C3HC4 type (RING finger) Dihydrofolate reductase	0.044 6.3e-61 4.5e-10 4e-11 2.1e-73 2.2e-62 4.9e-30 5.3e-13	17.9 215.8 46.9 50.4 257.3 220.7 108.3
1247 1248 1249 1254 1255 1256 1259	WW UPF0006  Glycos_trans f_2 efhand  UQ_con ras formyl_trans f zf-C3HC4  DiHfolate_re d G_glu_transp	WW domain Metalloenzyme of unknown function UPF0006 Glycosyl transferases  EF hand Ubiquitin-conjugating enzyme Ras family Formyl transferase  Zinc finger, C3HC4 type (RING finger) Dihydrofolate reductase  Gamma-glutamyltranspeptidase	0.044 6.3e-61 4.5e-10 4e-11 2.1e-73 2.2e-62 4.9e-30 5.3e-13 2.1e-69	17.9 215.8 46.9 50.4 257.3 220.7 108.3 46.4

NO:   1266   SCP	Value   PFAM   SCORB   108.0   3e-27   104.0   3e-85   297.9   2e-10   37.0   3e-23   89.8   5e-21   83.1   3e-41   132.0   3e-13   58.7   3e-14   49.6   7e-52   187.8
1266   SCP	-29 108.0 Be-27 104.0 Be-85 297.9 Be-10 37.0 Be-23 89.8 Be-21 83.1 Be-41 132.0 Be-13 58.7 Be-14 49.6
1267   K_tetra	Be-27 104.0 Be-85 297.9 Be-10 37.0 Be-23 89.8 Be-21 83.1 Be-41 132.0 Be-13 58.7 Be-14 49.6
domain   1269   ras   Ras family   1.3     1275   zf-C3HC4   Zinc finger, C3HC4 type (RING finger)     1276   abhydrolase   alpha/beta hydrolase fold   5.4     1277   abhydrolase   alpha/beta hydrolase fold   5.6     1279   trypsin   Trypsin   4.4     1280   PBP   Phosphatidylethanolamine-binding protein     1285   zf-C3HC4   Zinc finger, C3HC4 type (RING finger)     1287   ank   Ank repeat   1.7     1294   fn3   Fibronectin type III domain   0.0     1295   GBP   Guanylate-binding protein   0.0     1296   PMP22_Claudi   PMP-22/EMP/MP20/Claudin family   6.9	3e-85 297.9 2e-10 37.0 4e-23 89.8 5e-21 83.1 4e-41 132.0 3e-13 58.7
1269   ras	2e-10 37.0  4e-23 89.8  5e-21 83.1  4e-41 132.0  3e-13 58.7  6e-14 49.6
1275   zf-C3HC4   Zinc finger, C3HC4 type (RING finger)   1276   abhydrolase   alpha/beta hydrolase fold   5.4     1277   abhydrolase   alpha/beta hydrolase fold   5.6     1279   trypsin   Trypsin   4.4     1280   PBP   Phosphatidylethanolamine-binding protein     1285   zf-C3HC4   Zinc finger, C3HC4 type (RING finger)     1287   ank   Ank repeat   1.7     1294   fn3   Fibronectin type III domain   0.0     1295   GBP   Guanylate-binding protein   0.0     1296   PMP22_Claudi   PMP-22/EMP/MP20/Claudin family   6.9	2e-10 37.0  4e-23 89.8  5e-21 83.1  4e-41 132.0  3e-13 58.7  6e-14 49.6
finger)  1276 abhydrolase alpha/beta hydrolase fold 5.4  1277 abhydrolase alpha/beta hydrolase fold 5.6  1279 trypsin Trypsin 4.4  1280 PBP Phosphatidylethanolamine-binding protein  1285 zf-C3HC4 Zinc finger, C3HC4 type (RING finger)  1287 ank Ank repeat 1.7  1294 fn3 Fibronectin type III domain 0.0  1295 GBP Guanylate-binding protein 0.0  1296 PMP22_Claudi PMP-22/EMP/MP20/Claudin family 6.9	89.8 5e-21 83.1 4e-41 132.0 3e-13 58.7
1276	5e-21 83.1 4e-41 132.0 5e-13 58.7 6e-14 49.6
1277	5e-21 83.1 4e-41 132.0 5e-13 58.7 6e-14 49.6
1279	de-41 132.0 de-13 58.7 de-14 49.6
PBP Phosphatidylethanolamine-binding protein  1285 zf-C3HC4 Zinc finger, C3HC4 type (RING finger)  1287 ank Ank repeat 1.7  1294 fn3 Fibronectin type III domain 0.0  1295 GBP Guanylate-binding protein 0.0  1296 PMP22_Claudi PMP-22/EMP/MP20/Claudin family 6.9	Se-13 58.7 Se-14 49.6
binding protein	Se-14 49.6
1285   zf-C3HC4   Zinc finger, C3HC4 type (RING finger)   5.6     1287   ank	,
finger)  1287 ank Ank repeat 1.7  1294 fn3 Fibronectin type III domain 0.0  1295 GBP Guanylate-binding protein 0.0  1296 PMP22_Claudi PMP-22/EMP/MP20/Claudin family 6.9	,
1287	'e-52 187.8
1294 fn3 Fibronectin type III domain 0.0 1295 GBP Guanylate-binding protein 0.0 1296 PMP22_Claudi PMP-22/EMP/MP20/Claudin family 6.9	'e-52   187.8
1295 GBP Guanylate-binding protein 0.0 1296 PMP22_Claudi PMP-22/EMP/MP20/Claudin family 6.9	
1296 PMP22_Claudi PMP-22/EMP/MP20/Claudin family 6.9	
n	00026 -70.0
	e-41 149.3
1437   KNOURNESE   KNOORNASA-IIKA AAMSIA   13 9	
imbuditobe xxxc domaxii	e-14 60.7
21. Command Contesting processing 5.6	e-21 79.1
	e-43 145.2
1307 mito_carr Mitochondrial carrier proteins 2.1	.e-53 186.0
	e-17 71.6
	e-20 75.5
1313 thiored Thioredoxin 3.6	e-05 21.6
1314 Aa_trans Transmembrane amino acid 1.5	e-67 237.9
transporter protein	
1316 trypsin Trypsin 4.4	e-41 132.0
1300	e-62 219.8
3	213.0
1327 Armadillo_se Armadillo/beta-catenin-like 0.0	054 23.4
g repeats	23.1
1328 KRAB KRAB box 0.0	52 -5.6
1000	e-40 147.7
1330 Bcl-2 Apoptosis regulator proteins, 0.0	
Bcl-2 family	-1.0
1222	e-10 48.0
1335	e-36 134.6
	e-89 310.3
se diphosphate synt	310.3
100	e-59 211.0
se diphosphate synt	211.0
	e-31 118.6
catalytic doma	=-31 110.0
4358	e-12 54.5
catalytic doma	5-12 34.5
1030	0021 28.1
1340 metalthio Metallothionein 0.01	
1743	
1242 Designation of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state o	e-09 36.5
1344 Villa Comain (Dana 1.1 Idully) 1.36	2-38 122.5
1745	2-44 161.5
1347 70-4 700- 1.26	9-10 48.8
1 2 200 11/01/01/01/01	36 -177.2
dehydrogenase/isomera	<u> </u>
1349 DUF6 Integral membrane protein DUF6 0.03	
Integral membrane process bore 0.03	1088.7
1350 myosin_head Myosin_head (motor_domain) 0	
1350 myosin_head Myosin_head (motor_domain) 0 1352 Nramp Natural resistance-associated 1.2e	-202 686.6
1350 myosin_head Myosin head (motor domain) 0 1352 Nramp Natural resistance-associated 1.2e macrophage pro	2-202   686.6
1350   myosin_head   Myosin_head (motor_domain)   0	
1350 myosin_head Myosin head (motor domain) 0 1352 Nramp Natural resistance-associated macrophage pro 1353 S_100 S-100/ICaBP type calcium 5.3e binding domain	
1350   myosin_head   Myosin_head (motor domain)   0	3-23 89.9
1350   myosin_head   Myosin_head (motor domain)   0	89.9 8-65 209.0
1350   myosin_head   Myosin_head (motor domain)   0	89.9 2-65 209.0 2-15 64.4
1350   myosin_head   Myosin head (motor domain)   0	89.9 8-65 209.0 8-15 64.4

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM
NO:				SCORE
1362	SIS	SIS domain	3.8e-30	113.6
1363	SIS	SIS domain	1.3e-28	108.5
1364	ig K tetra	Immunoglobulin domain	0.00026	19.0
	<u> </u>	K+ channel tetramerisation domain	1.1e-16	68.9
1371	Collagen	Collagen triple helix repeat (20 copics)	2.2e-113	390.1
1372	DnaJ	DnaJ domain	6.6e-36	132.7
1376	KRAB	KRAB box	2.1e-38	141.0
1378	ELM2	ELM2 domain	2e-23	91.3
1380	thiored	Thioredoxin	1.2e-23	82.8
1381	ank	Ank repeat	2.3e-83	290.4
1382	BTB	BTB/POZ domain	3e-11	50.8
1384	WD40	WD domain, G-beta repeat	1.6e-19	78.3
1387	zf-C3HC4	WD domain, G-beta repeat	6.3e-24	92.9
		Zinc finger, C3HC4 type (RING finger)	1.1e-09	35.6
1389	zf-C2H2	Zinc finger, C2H2 type	5.5e-50	179.5
1390 1393	zf-C2H2	Zinc finger, C2H2 type	2.5e-85	296.9
1393	kinesin	Kincsin motor domain	7.8e-188	637.4
1398	zf-C2H2	Zinc finger, C2H2 type	1.2e-49	178.4
1402	KRAB bZIP	KRAB box	5.1e-22	86.6
1405	sugar tr	bZIP transcription factor	0.035	13.1
1406	RhoGAP	Sugar (and other) transporter	0.003	-101.5
1407	rrm	RhoGAP domain RNA recognition motif.	8.9e-47	168.8
1408	LRR	Leucine Rich Repeat	1e-35	132.1
1409	Nebulin repe	Nebulin repeat	2.1e-13 6e-54	58.0 192.6
1410	at			
1412	Ribosomal L5	Ank repeat	1.6e-17	71.6
1415	_C trypsin	ribosomal L5P family C-terminus	8.2e-58	205.5
1416	aminotran 1	Trypsin	4.7e-85	.270.4
1417		Aminotransferases class-I	4.4e-05	-91.2
	1 51	C1 DNA binding down		
L	S1 WD40	S1 RNA binding domain	1.6e-07	33.1
1419	WD40	WD domain, G-beta repeat	1.6e-C7 2.2e-09	33.1 44.6
1419	1	WD domain, G-beta repeat Cadherin domain	1.6e-C7 2.2e-09 8.3e-42	33.1 44.6 152.3
1419 1422	WD40 cadherin	WD domain, G-beta repeat Cadherin domain SH3 domain	1.6e-C7 2.2e-09 8.3e-42 2.5e-80	33.1 44.6 152.3 280.3
1419 1422 1424	WD40 cadherin SH3	WD domain, G-beta repeat Cadherin domain SH3 domain PHD-finger PHD-finger	1.6e-C7 2.2e-09 8.3e-42 2.5e-80 3.2e-17	33.1 44.6 152.3 280.3 70.6
1419 1422 1424 1425	WD40 cadherin SH3 PHD	WD domain, G-beta repeat Cadherin domain SH3 domain PHD-finger PHD-finger Putative GTP-ase activating	1.6e-C7 2.2e-09 8.3e-42 2.5e-80	33.1 44.6 152.3 280.3
1419 1422 1424 1425 1426	WD40 cadherin SH3 PHD PHD	WD domain, G-beta repeat Cadherin domain SH3 domain PHD-finger PHD-finger Putative GTP-ase activating protein for Arf Helicases conserved C-terminal	1.6e-C7 2.2e-09 8.3e-42 2.5e-80 3.2e-17 3.2e-17	33.1 44.6 152.3 280.3 70.6
1419 1422 1424 1425 1426 1427	WD40 cadherin SH3 PHD PHD ArfGap	WD domain, G-beta repeat Cadherin domain SH3 domain PHD-finger PHD-finger Putative GTP-ase activating protein for Arf Helicases conserved C-terminal domain	1.6e-C7 2.2e-09 8.3e-42 2.5e-80 3.2e-17 3.2e-17 1e-37	33.1 44.6 152.3 280.3 70.6 70.6 138.8
1419 1422 1424 1425 1426 1427	WD40 cadherin SH3 PHD PHD ArfGap helicase_C	WD domain, G-beta repeat Cadherin domain SH3 domain PHD-finger PHD-finger Putative GTP-ase activating protein for Arf Helicases conserved C-terminal domain WD domain, G-beta repeat	1.6e-C7 2.2e-09 8.3e-42 2.5e-80 3.2e-17 3.2e-17 1e-37 le-26	33.1 44.6 152.3 280.3 70.6 70.6 138.8
1419 1422 1424 1425 1426 1427 1428	WD40 cadherin SH3 PHD PHD ArfGap helicase_C WD40 inositol_P mito_carr	WD domain, G-beta repeat Cadherin domain SH3 domain PHD-finger PHD-finger Putative GTP-ase activating protein for Arf Helicases conserved C-terminal domain WD domain, G-beta repeat Inositol monophosphatase family	1.6e-C7 2.2e-09 8.3e-42 2.5e-80 3.2e-17 3.2e-17 1e-37 le-26 3.9e-07 2.5e-10	33.1 44.6 152.3 280.3 70.6 70.6 138.8 102.2
1419 1422 1424 1425 1426 1427 1428 1429 1430 1431 1433	WD40 cadherin SH3 PHD PHD ArfGap helicase_C	WD domain, G-beta repeat Cadherin domain SH3 domain PHD-finger PHD-finger Putative GTP-ase activating protein for Arf Helicases conserved C-terminal domain WD domain, G-beta repeat	1.6e-C7 2.2e-09 8.3e-42 2.5e-80 3.2e-17 3.2e-17 1e-37 le-26 3.9e-07 2.5e-10 4.3e-83	33.1 44.6 152.3 280.3 70.6 70.6 138.8 102.2 37.2 40.2 287.7
1419 1422 1424 1425 1426 1427 1428 1429 1430	WD40 cadherin SH3 PHD PHD ArfGap helicase_C WD40 inositol_P mito_carr	WD domain, G-beta repeat Cadherin domain SH3 domain PHD-finger PHD-finger Putative GTP-ase activating protein for Arf Helicases conserved C-terminal domain WD domain, G-beta repeat Inositol monophosphatase family Mitochondrial carrier proteins Ciq domain	1.6e-C7 2.2e-09 8.3e-42 2.5e-80 3.2e-17 3.2e-17 1e-37 le-26 3.9e-07 2.5e-10 4.3e-83 2.9e-16	33.1 44.6 152.3 280.3 70.6 70.6 138.8 102.2 37.2 40.2 287.7 66.2
1419 1422 1424 1425 1426 1427 1428 1429 1430 1431 1433	WD40 cadherin SH3 PHD PHD ArfGap helicase_C WD40 inositol_P mito_carr Clq WD40 Inos-1-	WD domain, G-beta repeat Cadherin domain SH3 domain PHD-finger PHD-finger PHD-finger Putative GTP-ase activating protein for Arf Helicases conserved C-terminal domain WD domain, G-beta repeat Inositol monophosphatase family Mitochondrial carrier proteins Ciq domain WD domain, G-beta repeat	1.6e-C7 2.2e-09 8.3e-42 2.5e-80 3.2e-17 1e-37 le-26 3.9e-07 2.5e-10 4.3e-83 2.9e-16 1.6e-13	33.1 44.6 152.3 280.3 70.6 70.6 138.8 102.2 37.2 40.2 287.7 66.2 58.3
1419 1422 1424 1425 1426 1427 1428 1429 1430 1431 1433 1434	WD40 cadherin SH3 PHD PHD ArfGap helicase_C WD40 inositol_P mito_carr Clq WD40 Inos-1- P_synth	WD domain, G-beta repeat Cadherin domain SH3 domain PHD-finger PHD-finger Putative GTP-ase activating protein for Arf Helicases conserved C-terminal domain WD domain, G-beta repeat Inositol monophosphatase family Mitochondrial carrier proteins Ciq domain	1.6e-C7 2.2e-09 8.3e-42 2.5e-80 3.2e-17 3.2e-17 1e-37 le-26 3.9e-07 2.5e-10 4.3e-83 2.9e-16	33.1 44.6 152.3 280.3 70.6 70.6 138.8 102.2 37.2 40.2 287.7 66.2
1419 1422 1424 1425 1426 1427 1428 1429 1430 1431 1433 1434 1435	WD40 cadherin SH3 PHD PHD ArfGap helicase_C WD40 inositol_P mito_carr C1q WD40 Inos-1- P_synth rrm	WD domain, G-beta repeat Cadherin domain SH3 domain PHD-finger PHD-finger Putative GTP-ase activating protein for Arf Helicases conserved C-terminal domain WD domain, G-beta repeat Inositol monophosphatase family Mitochondrial carrier proteins C1q domain WD domain, G-beta repeat MyO-inositol-1-phosphate synthase RNA recognition motif.	1.6e-C7 2.2e-09 8.3e-42 2.5e-80 3.2e-17 1e-37 le-26 3.9e-07 2.5e-10 4.3e-83 2.9e-16 1.6e-13	33.1 44.6 152.3 280.3 70.6 70.6 138.8 102.2 37.2 40.2 287.7 66.2 58.3
1419 1422 1424 1425 1426 1427 1428 1429 1430 1431 1433 1434 1435	WD40 cadherin SH3 PHD PHD ArfGap helicase_C WD40 inositol_P mito_carr Clq WD40 Inos-1- P_synth rrm ig	WD domain, G-beta repeat Cadherin domain SH3 domain PHD-finger PHD-finger Putative GTP-ase activating protein for Arf Helicases conserved C-terminal domain WD domain, G-beta repeat Inositol monophosphatase family Mitochondrial carrier proteins C1q domain WD domain, G-beta repeat Myo-inositol-1-phosphate synthase RNA recognition motif. Immunoglobulin domain	1.6e-C7 2.2e-09 8.3e-42 2.5e-80 3.2e-17 3.2e-17 1e-37 1e-26 3.9e-07 2.5e-10 4.3e-83 2.9e-16 1.6e-13 7e-228	33.1 44.6 152.3 280.3 70.6 70.6 138.8 102.2 37.2 40.2 287.7 66.2 58.3 770.4
1419 1422 1424 1425 1426 1427 1428 1429 1430 1431 1433 1434 1435	WD40 cadherin SH3 PHD PHD ArfGap helicase_C WD40 inositol_P mito_carr Clq WD40 Inos-1- P_synth rrm ig G_Adapt_CT	WD domain, G-beta repeat Cadherin domain SH3 domain PHD-finger PHD-finger PHD-finger Putative GTP-ase activating protein for Arf Helicases conserved C-terminal domain WD domain, G-beta repeat Inositol monophosphatase family Mitochondrial carrier proteins Clq domain WD domain, G-beta repeat Myo-inositol-1-phosphate synthase RNA recognition motif. Immunoglobulin domain Gamma-adaptin, C-terminus	1.6e-C7 2.2e-09 8.3e-42 2.5e-80 3.2e-17 3.2e-17 1e-37 1e-26 3.9e-07 2.5e-10 4.3e-83 2.9e-16 1.6e-13 7e-228	33.1 44.6 152.3 280.3 70.6 70.6 138.8 102.2 37.2 40.2 287.7 66.2 58.3 770.4
1419 1422 1424 1425 1426 1427 1428 1429 1430 1431 1433 1434 1435 1436 1438 1440	WD40 cadherin SH3 PHD PHD ArfGap helicase_C WD40 inositol_P mito_carr Clq WD40 Inos-1 P_synth rrm ig G_Adapt_CT G_Adapt_CT	WD domain, G-beta repeat Cadherin domain SH3 domain PHD-finger PHD-finger PHD-finger Putative GTP-ase activating protein for Arf Helicases conserved C-terminal domain WD domain, G-beta repeat Inositol monophosphatase family Mitochondrial carrier proteins Ciq domain WD domain, G-beta repeat Myo-inositol-1-phosphate synthase RNA recognition motif. Immunoglobulin domain Gamma-adaptin, C-terminus Gamma-adaptin, C-terminus	1.6e-C7 2.2e-09 8.3e-42 2.5e-80 3.2e-17 3.2e-17 1e-37 1e-26 3.9e-07 2.5e-10 4.3e-83 2.9e-16 1.6e-13 7e-228 1.4e-34 1.3e-12	33.1 44.6 152.3 280.3 70.6 70.6 138.8 102.2 37.2 40.2 287.7 66.2 58.3 770.4 128.3 45.6
1419 1422 1424 1425 1426 1427 1428 1429 1430 1431 1433 1434 1435	WD40 cadherin SH3 PHD PHD ArfGap helicase_C WD40 inositol_P mito_carr Clq WD40 Inos-1- P_synth rrm ig G_Adapt_CT G_Adapt_CT Kelch	WD domain, G-beta repeat Cadherin domain SH3 domain PHD-finger PHD-finger PHD-finger Putative GTP-ase activating protein for Arf Helicases conserved C-terminal domain WD domain, G-beta repeat Inositol monophosphatase family Mitochondrial carrier proteins Ciq domain WD domain, G-beta repeat Myo-inositol-1-phosphate synthase RNA recognition motif. Immunoglobulin domain Gamma-adaptin, C-terminus Gamma-adaptin, C-terminus Kelch motif	1.6e-C7 2.2e-09 8.3e-42 2.5e-80 3.2e-17 3.2e-17 1e-37 le-26 3.9e-07 2.5e-10 4.3e-83 2.9e-16 1.6e-13 7e-228 1.4e-34 1.3e-12 3.4e-67	33.1 44.6 152.3 280.3 70.6 70.6 138.8 102.2 37.2 40.2 287.7 66.2 58.3 770.4 128.3 45.6 236.7
1419 1422 1424 1425 1426 1427 1428 1429 1430 1431 1433 1434 1435 1436 1440 1441 1443	WD40 cadherin SH3 PHD PHD ArfGap helicase_C WD40 inositol_P mito_carr Clq WD40 Inos-1- P_synth rrm lg G_Adapt_CT G_Adapt_CT Kelch ARID	WD domain, G-beta repeat Cadherin domain SH3 domain PHD-finger PHD-finger PHD-finger Putative GTP-ase activating protein for Arf Helicases conserved C-terminal domain WD domain, G-beta repeat Inositol monophosphatase family Mitochondrial carrier proteins Ciq domain WD domain, G-beta repeat Myo-inositol-1-phosphate synthase RNA recognition motif. Immunoglobulin domain Gamma-adaptin, C-terminus Gamma-adaptin, C-terminus Kelch motif ARID DNA binding domain	1.6e-C7 2.2e-09 8.3e-42 2.5e-80 3.2e-17 3.2e-17 1e-37  le-26 3.9e-07 2.5e-10 4.3e-83 2.9e-16 1.6e-13 7e-228  1.4e-34 1.3e-12 3.4e-67 3.4e-67 0.00013 1.8e-21	33.1 44.6 152.3 280.3 70.6 70.6 138.8 102.2 37.2 40.2 287.7 66.2 58.3 770.4 128.3 45.6 236.7 236.7 28.7 64.7
1419 1422 1424 1425 1426 1427 1428 1429 1430 1431 1433 1434 1435 1436 1438 1440 1441 1443 1446	WD40 cadherin SH3 PHD PHD ArfGap helicase_C WD40 inositol_P mito_carr Clq WD40 Inos-1- P_synth rrm lg G_Adapt_CT G_Adapt_CT Kelch ARID zf-C2H2	WD domain, G-beta repeat Cadherin domain SH3 domain PHD-finger PHD-finger PHD-finger Putative GTP-ase activating protein for Arf Helicases conserved C-terminal domain WD domain, G-beta repeat Inositol monophosphatase family Mitochondrial carrier proteins Ciq domain WD domain, G-beta repeat Myo-inositol-1-phosphate synthase RNA recognition motif. Immunoglobulin domain Gamma-adaptin, C-terminus Gamma-adaptin, C-terminus Kelch motif ARID DNA binding domain Zinc finger, CZH2 type	1.6e-C7 2.2e-09 8.3e-42 2.5e-80 3.2e-17 3.2e-17 1e-37  le-26 3.9e-07 2.5e-10 4.3e-83 2.9e-16 1.6e-13 7e-228 1.4e-34 1.3e-12 3.4e-67 0.00013 1.8e-21 9.4e-28	33.1 44.6 152.3 280.3 70.6 70.6 138.8 102.2 37.2 40.2 287.7 66.2 58.3 770.4 128.3 45.6 236.7 236.7 28.7 84.7 105.6
1419 1422 1424 1425 1426 1427 1428 1429 1430 1431 1433 1434 1435 1436 1438 1440 1441 1443 1446 1447	WD40 cadherin SH3 PHD PHD ArfGap helicase_C WD40 inositol_P mito_carr Clq WD40 Inos-1- P_synth rrm ig G_Adapt_CT G_Adapt_CT Kelch ARID zf-C2H2 AMP-binding	WD domain, G-beta repeat Cadherin domain SH3 domain PHD-finger PHD-finger PHD-finger Putative GTP-ase activating protein for Arf Helicases conserved C-terminal domain WD domain, G-beta repeat Inositol monophosphatase family Mitochondrial carrier proteins Ciq domain WD domain, G-beta repeat Myo-inositol-1-phosphate synthase RNA recognition motif. Immunoglobulin domain Gamma-adaptin, C-terminus Gamma-adaptin, C-terminus Kelch motif ARID DNA binding domain Zinc finger, CHZ type AMP-binding enzyme	1.6e-C7 2.2e-09 8.3e-42 2.5e-80 3.2e-17 3.2e-17 1e-37  le-26 3.9e-07 2.5e-10 4.3e-83 2.9e-16 1.6e-13 7e-228 1.4e-34 1.3e-12 3.4e-67 0.00013 1.8e-21 9.4e-28 2.6e-07	33.1 44.6 152.3 280.3 70.6 70.6 138.8 102.2 37.2 40.2 287.7 66.2 58.3 770.4 128.3 45.6 236.7 236.7 236.7 26.7 84.7 105.6 -145.1
1419 1422 1424 1425 1426 1427 1428 1429 1430 1431 1433 1434 1435 1436 1438 1440 1441 1443 1446 1447 1448	WD40 cadherin SH3 PHD PHD ArfGap helicase_C WD40 inositol_P mito_carr C1q WD40 Inos-1- P_synth rrm ig G_Adapt_CT G_Adapt_CT Kelch ARID zf-C2H2 AMP-binding rrm	WD domain, G-beta repeat Cadherin domain SH3 domain PHD-finger PHD-finger Putative GTP-ase activating protein for Arf Helicases conserved C-terminal domain WD domain, G-beta repeat Inositol monophosphatase family Mitochondrial carrier proteins Clq domain WD domain, G-beta repeat Myo-inositol-1-phosphate synthase RNA recognition motif. Immunoglobulin domain Gamma-adaptin, C-terminus Gamma-adaptin, C-terminus Kelch motif ARID DNA binding domain Zinc finger, CZH2 type AMP-binding enzyme RNA recognition motif.	1.6e-C7 2.2e-09 8.3e-42 2.5e-80 3.2e-17 3.2e-17 1e-37  le-26 3.9e-07 2.5e-10 4.3e-83 2.9e-16 1.6e-13 7e-228 1.4e-34 1.3e-12 3.4e-67 0.00013 1.8e-67 0.00013 1.8e-21 9.4e-28 2.6e-07 6.5e-21	33.1 44.6 152.3 280.3 70.6 70.6 138.8 102.2 37.2 40.2 297.7 66.2 58.3 770.4 128.3 45.6 236.7 236.7 28.7 84.7 105.6 -145.1 82.9
1419 1422 1424 1425 1426 1427 1428 1429 1430 1431 1433 1434 1435 1436 1438 1440 1441 1443 1446 1447	WD40  cadherin SH3 PHD PHD ArfGap  helicase_C  WD40 inositol_P mito_carr C1q WD40 Inos-1- P_synth rrm ig G_Adapt_CT G_Adapt_CT Kelch ARID zf-C2H2 AMP-binding rrm ig	WD domain, G-beta repeat Cadherin domain SH3 domain PHD-finger PHD-finger PHD-finger Putative GTP-ase activating protein for Arf Helicases conserved C-terminal domain WD domain, G-beta repeat Inositol monophosphatase family Mitochondrial carrier proteins Clq domain WD domain, G-beta repeat Myo-inositol-1-phosphate synthase RNA recognition motif. Immunoglobulin domain Gamma-adaptin, C-terminus Gamma-adaptin, C-terminus Kelch motif ARID DNA binding domain Zinc finger, CZH2 type RNA recognition motif. Immunoglobulin domain	1.6e-C7 2.2e-09 8.3e-42 2.5e-80 3.2e-17 3.2e-17 1e-37 le-26 3.9e-07 2.5e-10 4.3e-83 2.9e-16 1.6e-13 7e-228 1.4e-34 1.3e-12 3.4e-67 0.00013 1.8e-21 9.4e-28 2.6e-07 6.5e-21 5.6e-44	33.1 44.6 152.3 280.3 70.6 70.6 138.8 102.2 37.2 40.2 287.7 66.2 58.3 770.4 128.3 45.6 236.7 236.7 28.7 84.7 105.6 -145.1 82.9 146.7
1419 1422 1424 1425 1426 1427 1428 1429 1430 1431 1433 1434 1435 1436 1438 1440 1441 1443 1446 1447 1448 1451	WD40  cadherin SH3 PHD PHD ArfGap  helicase_C  WD40 inositol_P mito_carr C1q WD40 Inos-1 P_synth rrm ig G_Adapt_CT G_Adapt_CT Kelch ARID zf-C2H2 AMP-binding rrm ig Sialyltransf	WD domain, G-beta repeat Cadherin domain SH3 domain PHD-finger PHD-finger PHD-finger Putative GTP-ase activating protein for Arf Helicases conserved C-terminal domain WD domain, G-beta repeat Inositol monophosphatase family Mitochondrial carrier proteins Clq domain WD domain, G-beta repeat Myo-inositol-1-phosphate synthase RNA recognition motif. Immunoglobulin domain Gamma-adaptin, C-terminus Gamma-adaptin, C-terminus Kelch motif ARID DNA binding domain Zinc finger, CZHZ type AMP-binding enzyme RNA recognition motif. Immunoglobulin domain Sialyltransferase family	1.6e-C7 2.2e-09 8.3e-42 2.5e-80 3.2e-17 1e-37 1e-37 1e-26 3.9e-07 2.5e-10 4.3e-83 2.9e-16 1.6e-13 7e-228 1.4e-34 1.3e-12 3.4e-67 0.00013 1.8e-21 9.4e-28 2.6e-07 6.5e-21 5.6e-44 5.4e-21	33.1 44.6 152.3 280.3 70.6 70.6 138.8 102.2 37.2 40.2 287.7 66.2 58.3 770.4 128.3 45.6 236.7 236.7 28.7 84.7 105.6 -145.1 82.9 146.7 83.2
1419 1422 1424 1425 1426 1427 1428 1429 1430 1431 1433 1434 1435 1436 1438 1440 1441 1443 1446 1447 1448 1451 1451	WD40  cadherin SH3 PHD PHD ArfGap  helicase_C  WD40 inositol_P mito_carr C1q WD40 Inos-1- P_synth rrm ig G_Adapt_CT G_Adapt_CT Kelch ARID zf-C2H2 AMP-binding rrm ig	WD domain, G-beta repeat Cadherin domain SH3 domain PHD-finger PHD-finger PHD-finger Putative GTP-ase activating protein for Arf Helicases conserved C-terminal domain WD domain, G-beta repeat Inositol monophosphatase family Mitochondrial carrier proteins Clq domain WD domain, G-beta repeat Myo-inositol-1-phosphate synthase RNA recognition motif. Immunoglobulin domain Gamma-adaptin, C-terminus Gamma-adaptin, C-terminus Kelch motif ARID DNA binding domain Zinc finger, CZHZ type AMP-binding enzyme RNA recognition motif. Immunoglobulin domain Sialyltransferase family Aldose 1-epimerase	1.6e-C7 2.2e-09 8.3e-42 2.5e-80 3.2e-17 3.2e-17 1e-37  le-26  3.9e-07 2.5e-10 4.3e-83 2.9e-16 1.6e-13 7e-228  1.4e-34 1.3e-12 3.4e-67 0.00013 1.8e-21 9.4e-28 2.6e-07 6.5e-21 5.6e-44 5.4e-21 1.9e-35	33.1 44.6 152.3 280.3 70.6 70.6 138.8 102.2 37.2 40.2 287.7 66.2 58.3 770.4 128.3 45.6 236.7 236.7 29.7 84.7 105.6 -145.1 82.9 146.7 83.2 131.2
1419 1422 1424 1425 1426 1427 1428 1429 1430 1431 1433 1434 1435 1436 1440 1441 1443 1446 1447 1448 1451 1451	WD40 cadherin SH3 PHD PHD ArfGap helicase_C WD40 inositol_P mito_carr Clq WD40 Inos-1- P_synth rrm ig G_Adapt_CT G_Adapt_CT Kelch ARID zf-C2H2 AMP-binding rrm ig Sialyltransf Aldose_epim	WD domain, G-beta repeat Cadherin domain SH3 domain PHD-finger PHD-finger PHD-finger PHD-finger Putative GTP-ase activating protein for Arf Helicases conserved C-terminal domain WD domain, G-beta repeat Inositol monophosphatase family Mitochondrial carrier proteins Ciq domain WD domain, G-beta repeat Myo-inositol-1-phosphate synthase RNA recognition motif. Immunoglobulin domain Gamma-adaptin, C-terminus Gamma-adaptin, C-terminus Kelch motif ARID DNA binding domain Zinc finger, C2H2 type AMP-binding enzyme RNA recognition motif. Immunoglobulin domain Sialyltransferase family Aldose 1-epimerase C2 domain	1.6e-C7 2.2e-09 8.3e-42 2.5e-80 3.2e-17 3.2e-17 1e-37  le-26 3.9e-07 2.5e-10 4.3e-83 2.9e-16 1.6e-13 7e-228  1.4e-34 1.3e-12 3.4e-67 0.00013 1.8e-21 9.4e-28 2.6e-07 6.5e-21 5.6e-44 5.4e-21 1.9e-35 4e-18	33.1 44.6 152.3 280.3 70.6 70.6 138.8 102.2 37.2 40.2 287.7 66.2 58.3 770.4 128.3 45.6 236.7 236.7 29.7 84.7 105.6 -145.1 82.9 146.7 83.2 131.2 73.6
1419 1422 1424 1425 1426 1427 1428 1429 1430 1431 1433 1434 1435 1436 1440 1441 1443 1446 1447 1448 1451 1455 1455 1460	WD40 cadherin SH3 PHD PHD ArfGap helicase_C WD40 inositol_P mito_carr Clq WD40 Inos-1- P_synth rrm ig G_Adapt_CT G_Adapt_CT Kelch ARID zf-C2H2 AMP-binding rrm ig Sialyltransf Aldose_epim C2	WD domain, G-beta repeat Cadherin domain SH3 domain PHD-finger PHD-finger PHD-finger Putative GTP-ase activating protein for Arf Helicases conserved C-terminal domain WD domain, G-beta repeat Inositol monophosphatase family Mitochondrial carrier proteins Clq domain WD domain, G-beta repeat Myo-inositol-1-phosphate synthase RNA recognition motif. Immunoglobulin domain Gamma-adaptin, C-terminus Gamma-adaptin, C-terminus Kelch motif ARID DNA binding domain Zinc finger, CZHZ type AMP-binding enzyme RNA recognition motif. Immunoglobulin domain Sialyltransferase family Aldose 1-epimerase	1.6e-C7 2.2e-09 8.3e-42 2.5e-80 3.2e-17 3.2e-17 1e-37  le-26  3.9e-07 2.5e-10 4.3e-83 2.9e-16 1.6e-13 7e-228  1.4e-34 1.3e-12 3.4e-67 0.00013 1.8e-21 9.4e-28 2.6e-07 6.5e-21 5.6e-44 5.4e-21 1.9e-35	33.1 44.6 152.3 280.3 70.6 70.6 138.8 102.2 37.2 40.2 287.7 66.2 58.3 770.4 128.3 45.6 236.7 236.7 29.7 84.7 105.6 -145.1 82.9 146.7 83.2 131.2

SEQ ID	PFAM NAME	DESCRIPTION		
NO:	TIME NAME	DESCRIPTION	p-value	PPAM
	h 2	<del></del>		SCORE
1474	DENN	DENN (AEX-3) domain	1,-	
1475	Cation efflu	Cation efflux family	1.3e-44 4.6e-49	161.6
1	x	cataon cellar lamily	4.6e-49	176.4
1477	TBC	TBC domain	8e-47	1,20
1478	rrm	RNA recognition motif.	2e-21	169.0
1480	İq	Immunoglobulin domain	5.5e-06	84.6
1484	Telo bind al	Telomere-binding protein alpha		24.3
1	pha	subuni	0.028	-225.9
1485	zf-C2H2	Zinc finger, C2H2 type	1.8e-68	
1486	pkinase	Eukaryotic protein kinase	9.5e-13	240.9 49.9
	1.	domain	3.5e-13	49.9
1488	helicase C	Helicases conserved C-terminal	1.4e-15	65.2
	_	domain	1.46-15	05.2
1489	DUF89	Protein of unknown function	0.079	-132.4
1		DUF89	0.079	-132.4
1490	ECH	Enoyl-CoA hydratase/isomerase	5.2e-41	140 2
		family	3.26-41	149.7
1491	guanylate_cy	Adenylate and Guanylate cyclase	5.9e-46	166.1
1	c	catalyt	3.95-40	100.1
1492	LRR	Leucine Rich Repeat	3.4e-19	77.2
1495	zf-C3HC4	Zinc finger, C3HC4 type (RING	7.1e-10	36.3
ŀ		finger)	/.16-10	36.3
1497	pkinase	Eukaryotic protein kinase	le-22	85.8
		domain	1	03.8
1500	SH3	SH3 domain	9.3e-05	27.2
1502	homeobox	Homeobox domain	0.084	13.8
1503	homeobox	Homeobox domain	0.084	13.8
1505	EGF	EGF-like domain	2.7e-23	90.8
1506	UCH-2	Ubiquitin carboxyl-terminal	2.7e-21	84.2
l		hydrolase family	1.76-21	04.2
1508	Peptidase_M2	Peptidase family M20/M25/M40	2.8e-28	101.8
		, ,	1	101.0
1511	PX	PX domain	1.9e-11	51.5
1512	Sulfatase	Sulfatase	2.8e-35	130.7
1516	Syntaxin	Syntaxin	0.011	-62.3
1518	aminotran_3	Aminotransferases class-III	9.7e-106	305.6
		pyridoxal-pho		1.545.0
1520	ig	Immunoglobulin domain	0.075	11.0
1521	RA	Ras association (RalGDS/AF-6)	0.013	13.3
		domain		1 ~ 3 . 3
1523	RhoGAP	RhoGAP domain	2.5e-05	18.7
1528	WD40	WD domain, G-beta repeat	5.4e-24	93.1
1535	IMS	impB/mucB/samB family	7.8e-95	328.5
1538	FYVE	FYVE zinc finger	3.2e-27	101.5
1539	DAGKC	Diacylglycerol kinase catalytic	6e-07	36.5
		domain		1 33.3
1540	Ocular_alb	Ocular albinism type 1 protein	<del></del>	1184.7
1653	SAP	SAP domain	6e-06	33.2
1654	Amino_oxidas	Flavin containing amine oxidase	3.2e-43	157.0
	e	3		1 -570
1655	Amino_oxidas	Plavin containing amine oxidase	3.2e-43	157.0
	e	-3	00 33	1 *37.0
1656	RhoGEF	RhoGEF domain	1.4e-24	95.1
1657	MMR_HSR1	GTPase of unknown function	0.0011	-45.5
1659	UCH-2	Ubiquitin carboxyl-terminal	2.5e-11	51.1
		hydrolase family	50-II	
1660	actin	Actin	6.6e-21	69.9
1661	BAH	BAH domain	1.7e-82	287.5
1662	vwa	von Willebrand factor type A	0	
		domain	•	1909.4
1663	WD40	WD domain, G-beta repeat	1 46 67	227 0
1667	zf-C2H2	Zinc finger, C2H2 type	1.4e-67	237.9
1669	Nol1_Nop2_Su	NOL1/NOP2/sun family	1.3e-93	324.4
	n	, word, built tallity	1.3e-23	84.3
1671	SH2	Src homology domain 2	E-42-15-	
		June 1037 Granuatit &	5.4e-15	46.9

SEQ ID	T PFAM NAME	I DUGGO TOMOS TO		
NO:	PFAM NAME	DESCRIPTION	p-value	PFAM
1672	chromo	'chromo' (CHRromatin	2.1e-18	67.7
i	1	Organization MOdifier)	2.20 20	"""
1674	zf-CCCH	Zinc finger C-x8-C-x5-C-x3-H	0.0025	17.6
ļ	İ	type	10.0025	17.0
1676	Glyco_hydro_	Glycosyl hydrolase family 47	1.8e-187	636.2
	47			(
1677	Glyco_hydro_	Glycosyl hydrolase family 47	4.5e-74	259.5
200	47		₫	
1680	WD40	WD domain, G-beta repeat	1.le-27	105.5
1681	WD40	WD domain, G-beta repeat	1.le-27	105.5
1683	MMR_HSR1	GTPase of unknown function	1.8e-78	274.1
1691	rrm	RNA recognition motif.	1.8e-37	137.9
1692	rrm	RNA recognition motif.	1.8e-37	137.9
1693	AAA	ATPases associated with various cellular act	1.3e-81	284.5
1697	Ferric_reduc	Ferric reductase like		
2021	t t	transmembrane com	8.4e-82	285.2
1698	Ferric reduc			
1000	t t	Ferric reductase like	3.5e-53	190.1
1699	zf-C2H2	transmembrane com	1	. 1
1700	arf	Zinc finger, C2H2 type	4.48-34	126.6
1702		ADP-ribosylation factor family	9e-19	75.8
1702	GTP_EFTU	Elongation factor Tu family	0.014	11.4
	SCAN	SCAN domain	1.8e-54	194.4
1707	pkinase	Eukaryotic protein kinase	1.2e-88	307.9
	<u> </u>	domain	ļ	(
1709	WD40	WD domain, G-beta repeat	0.0035	24.0
1710	LRR	Leucine Rich Repeat	1.2e-30	115.3
1711	WW	WW domain	7.6e-12	52.8
1712	ank	Ank repeat	4.2e-34	126.7
1713	zf-CCCH	Zinc finger C-x8-C-x5-C-x3-H	2.6e-09	38.3
		type	1 2.00	30.5
1714	zf-CCCH	Zinc finger C-x8-C-x5-C-x3-H	2.6e-09	38.3
		type	1	1 30.3
1715	ras	Ras family	4.4e-41	149.9
1718	HMG box	HMG (high mobility group) box	8.3e-21	82.6
1719	TBC	TBC domain	1.1e-45	165.2
1721	HLH	Helix-loop-helix DNA-binding	9.2e-10	45.9
	}	domain	3.20-10	13.7
1723	dsrm	Double-stranded RNA binding	2.9e-05	30.9
	1	motif	2.50-05	30.3
1724	RrnaAD	Ribosomal RNA adenine	0.045	9.2
		dimethylases	0.015	7.2
1725	CIDE-N	CIDE-N domain	5.9e-40	146.2
1726	HAT	HAT (Half-A-TPR) repeats	2.9e-44	160.5
1728	efhand	EF hand	5.1e-20	79.9
1733	Hist_deacety	Histone deacetylase family	1.7e-104	360.6
	1	deductyrase samily	1.76-104	360.6
1735	LRR	Leucine Rich Repeat	4 60 36	100.0
1739	PI-PLC-X	Phosphatidylinositol-specific	4.6e-34	126.6
	}	phospholipase	0.0023	16.1
1743	ras	Ras family		
			3.7e-10	-21.3
1744	ras	Pag familia		
1744	ras	Ras family	3.7e-10	-21.3
1745	RasGEF	RasGEF domain	3.2e-49	-21.3 176.9
1745 1746	RasGEF adh_short	RasGEF domain short chain dehydrogenase	3.2e-49 7.1e-08	-21.3 176.9 34.6
1745 1746 1751	RasGEF adh_short zf-C2H2	RasGEF domain short chain dehydrogenase Zinc finger, C2H2 type	3.2e-49 7.1e-08 9e-39	-21.3 176.9 34.6 142.2
1745 1746 1751 1754	RasGEF adh_short zf-C2H2 fn3	RasGEF domain short chain dehydrogenase Zinc finger, C2H2 type Fibronectin type III domain	3.2e-49 7.1e-08 9e-39 5.5e-101	-21.3 176.9 34.6 142.2 348.9
1745 1746 1751 1754	RasGEF adh_short zf-C2H2 fn3 zf-C2H2	RasgEF domain short chain dehydrogenase Zinc finger, C2H2 type Fibronectin type III domain Zinc finger, C2H2 type	3.2e-49 7.1e-08 9e-39 5.5e-101 6.3e-93	-21.3 176.9 34.6 142.2 348.9 322.1
1745 1746 1751 1754 1756	RasGEF adh_short zf-C2H2 fn3 zf-C2H2 rrm	RasgEF domain short chain dehydrogenase Zinc finger, C2H2 type Fibronectin type III domain Zinc finger, C2H2 type RNA recognition motif.	3.2e-49 7.1e-08 9e-39 5.5e-101 6.3e-93 0.017	-21.3 176.9 34.6 142.2 348.9
1745 1746 1751 1754 1756 1758	RasGEF adh_short zf-C2H2 fn3 zf-C2H2 rrm Nop	RasGEF domain short chain dehydrogenase Zinc finger, C2H2 type Fibronectin type III domain Zinc finger, C2H2 type RNA recognition motif. Putative snoRNA binding domain	3.2e-49 7.1e-08 9e-39 5.5e-101 6.3e-93	-21.3 176.9 34.6 142.2 348.9 322.1
1745 1746 1751 1754 1756 1758 1760	RasGEF adh_short zf-C2H2 fn3 zf-C2H2 rrm Nop Nop	RasGEF domain short chain dehydrogenase Zinc finger, C2H2 type Fibronectin type III domain Zinc finger, C2H2 type RNA recognition motif. Putative snoRNA binding domain Putative snoRNA binding domain	3.2e-49 7.1e-08 9e-39 5.5e-101 6.3e-93 0.017	-21.3 176.9 34.6 142.2 348.9 322.1 21.2
1745 1746 1751 1754 1756 1758 1760 1761	RasGEF adh_short zf-C2H2 fn3 zf-C2H2 rrm Nop Nop MMR HSR1	RasGEF domain short chain dehydrogenase Zinc finger, C2H2 type Fibronectin type III domain Zinc finger, C2H2 type RNA recognition motif. Putative snoRNA binding domain Putative snoRNA binding domain GTPase of unknown function	3.2e-49 7.1e-08 9e-39 5.5e-101 6.3e-93 0.017 6.1e-95	-21.3 176.9 34.6 142.2 348.9 322.1 21.2
1745 1746 1751 1754 1756 1758 1760 1761 1765	RasGEF adh_short zf-C2H2 fn3 zf-C2H2 rrm Nop Nop MMR_HSR1 CN_hydrolase	RasGEF domain short chain dehydrogenase Zinc finger, C2H2 type Fibronectin type III domain Zinc finger, C2H2 type RNA recognition motif. Putative snoRNA binding domain Putative snoRNA binding domain GTPase of unknown function Carbon-nitrogen hydrolase	3.2e-49 7.1e-08 9e-39 5.5e-101 6.3e-93 0.017 6.1e-95 6.1e-95 6.4e-41	-21.3 176.9 34.6 142.2 348.9 322.1 21.2 328.8 328.8
1745 1746 1751 1754 1756 1758 1760 1761 1765 1765	RasGEF adh_short zf-C2H2 fn3 zf-C2H2 rrm Nop Nop MMR HSR1 CN_hydrolase ank	RasGEF domain short chain dehydrogenase Zinc finger, C2H2 type Fibronectin type III domain Zinc finger, C2H2 type RNA recognition motif. Putative snoRNA binding domain Putative snoRNA binding domain GTPase of unknown function Carbon-nitrogen hydrolase Ank repeat	3.2e-49 7.1e-08 9e-39 5.5e-101 6.3e-93 0.017 6.1e-95 6.1e-95 6.4e-41 3e-06	-21.3 176.9 34.6 142.2 348.9 322.1 21.2 328.8 328.8 149.4 -43.9
1745 1746 1751 1754 1756 1758 1760 1761 1765 1769 1779	RasGEF adh_short zf-C2H2 fn3 zf-C2H2 rrm Nop Nop MMR_HSR1 CN_hydrolase ank Oxysterol_BF	RasGEF domain short chain dehydrogenase Zinc finger, C2H2 type Fibronectin type III domain Zinc finger, C2H2 type RNA recognition motif. Putative snoRNA binding domain Putative snoRNA binding domain GTPase of unknown function Carbon-nitrogen hydrolase Ank repeat Oxysterol-binding protein	3.2e-49 7.1e-08 9e-39 5.5e-101 6.3e-93 0.017 6.1e-95 6.1e-95 6.4e-41 3e-06 4.1e-07	-21.3 176.9 34.6 142.2 348.9 322.1 21.2 328.8 328.8 149.4 -43.9
1745 1746 1751 1754 1756 1758 1760 1761 1765 1765	RasGEF adh_short zf-C2H2 fn3 zf-C2H2 rrm Nop Nop MMR HSR1 CN_hydrolase ank	RasGEF domain short chain dehydrogenase Zinc finger, C2H2 type Fibronectin type III domain Zinc finger, C2H2 type RNA recognition motif. Putative snoRNA binding domain Putative snoRNA binding domain GTPase of unknown function Carbon-nitrogen hydrolase	3.2e-49 7.1e-08 9e-39 5.5e-101 6.3e-93 0.017 6.1e-95 6.1e-95 6.4e-41 3e-06	-21.3 176.9 34.6 142.2 348.9 322.1 21.2 328.8 328.8 149.4 -43.9

SEQ ID NO:	PFAM NAME	DESCRIPTION .	p-value	PFAM SCORE
1785	rrm	RNA recognition motif.	6.4e-14	59.7

TRADOCS:1416227.1(%CRN01!.DOC)

TABLE 5

SEQ ID NO:  1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24	POSITION OF SIGNAL IN AMINO ACID SEQUENCE 1-21 1-31 1-33 1-19 1-26 1-26 1-26 1-26 1-27 1-28 1-19 1-23 1-25 1-18 1-18 1-18 1-19 1-27 1-16 1-19 1-20 1-21	MaxS (MAXIMUM SCORE)  0.991 0.995 0.949 0.970 0.971 0.971 0.971 0.982 0.991 0.989 0.955 0.932 0.938 0.941 0.972 0.964 0.914 0.953 0.935 0.935 0.935 0.935 0.991	MeanS (MEAN SCORE)  0.955 0.944 0.736 0.951 0.863 0.863 0.863 0.863 0.901 0.955 0.899 0.803 0.625 0.876 0.811 0.939 0.777 0.657 0.840 0.701 0.850 0.895
2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25	ACID SEQUENCE  1-21  1-31  1-33  1-19  1-26  1-26  1-26  1-26  1-27  1-18  1-18  1-19  1-27  1-16  1-19  1-20  1-22  1-33  1-19  1-31	0.991 0.995 0.949 0.970 0.971 0.971 0.971 0.982 0.991 0.989 0.955 0.932 0.938 0.941 0.972 0.964 0.914 0.953 0.995 0.995 0.995	0.955 0.944 0.736 0.951 0.863 0.863 0.863 0.863 0.901 0.955 0.899 0.803 0.625 0.876 0.811 0.939 0.777 0.657 0.840 0.701 0.850 0.855
2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25	1-21 1-31 1-33 1-19 1-26 1-26 1-26 1-26 1-26 1-27 1-10 1-21 1-23 1-25 1-18 1-18 1-19 1-10 1-10 1-10 1-10 1-10 1-10 1-10	0.995 0.949 0.970 0.971 0.971 0.971 0.971 0.982 0.991 0.989 0.955 0.932 0.938 0.941 0.972 0.964 0.914 0.953 0.935 0.935 0.935	0.944 0.736 0.951 0.863 0.863 0.863 0.863 0.901 0.955 0.899 0.803 0.625 0.876 0.811 0.939 0.777 0.657 0.840 0.701 0.850 0.895
2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25	1-31 1-33 1-19 1-26 1-26 1-26 1-26 1-46 1-21 1-23 1-25 1-18 1-18 1-19 1-27 1-16 1-19 1-20 1-22 1-33 1-19 1-31	0.995 0.949 0.970 0.971 0.971 0.971 0.971 0.982 0.991 0.989 0.955 0.932 0.938 0.941 0.972 0.964 0.914 0.953 0.935 0.935 0.935	0.944 0.736 0.951 0.863 0.863 0.863 0.863 0.901 0.955 0.899 0.803 0.625 0.876 0.811 0.939 0.777 0.657 0.840 0.701 0.850 0.895
3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24	1-33 1-19 1-26 1-26 1-26 1-26 1-26 1-46 1-21 1-23 1-25 1-18 1-18 1-19 1-27 1-16 1-19 1-20 1-22 1-33 1-19 1-31	0.949 0.970 0.971 0.971 0.971 0.971 0.982 0.991 0.989 0.955 0.932 0.938 0.941 0.972 0.964 0.914 0.953 0.935 0.935 0.935	0.736 0.951 0.863 0.863 0.863 0.863 0.901 0.955 0.899 0.803 0.625 0.876 0.811 0.939 0.777 0.657 0.840 0.701 0.850 0.895
4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24	1-19 1-26 1-26 1-26 1-26 1-26 1-27 1-28 1-29 1-23 1-25 1-18 1-18 1-25 1-17 1-27 1-16 1-19 1-20 1-31	0.970 0.971 0.971 0.971 0.982 0.982 0.991 0.989 0.955 0.932 0.938 0.941 0.972 0.964 0.914 0.953 0.935 0.935	0.951 0.863 0.863 0.863 0.901 0.955 0.899 0.803 0.625 0.876 0.811 0.939 0.777 0.657 0.840 0.701 0.850 0.895
5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24	1-26 1-26 1-26 1-26 1-26 1-46 1-21 1-23 1-25 1-18 1-18 1-19 1-20 1-31	0.971 0.971 0.971 0.981 0.982 0.991 0.989 0.955 0.932 0.938 0.941 0.972 0.964 0.914 0.953 0.935 0.935	0.951 0.863 0.863 0.863 0.901 0.955 0.899 0.803 0.625 0.876 0.811 0.939 0.777 0.657 0.840 0.701 0.850 0.895
6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25	1-26 1-26 1-26 1-26 1-46 1-21 1-23 1-25 1-18 1-18 1-25 1-17 1-27 1-16 1-19 1-20 1-22 1-33 1-19 1-31	0.971 0.971 0.971 0.981 0.982 0.991 0.989 0.955 0.932 0.938 0.941 0.972 0.964 0.914 0.953 0.935 0.935	0.863 0.863 0.863 0.863 0.901 0.955 0.899 0.803 0.625 0.876 0.811 0.939 0.777 0.657 0.657 0.840 0.701 0.850 0.895
7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24	1-26 1-26 1-26 1-26 1-46 1-21 1-23 1-25 1-18 1-18 1-25 1-17 1-27 1-16 1-19 1-20 1-22 1-33 1-19 1-31	0.971 0.971 0.982 0.991 0.989 0.985 0.932 0.938 0.941 0.972 0.964 0.914 0.953 0.935 0.935	0.863 0.863 0.863 0.901 0.955 0.899 0.803 0.625 0.876 0.811 0.939 0.777 0.657 0.840 0.701 0.850 0.895
7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24	1-26 1-26 1-46 1-21 1-23 1-25 1-18 1-18 1-25 1-17 1-27 1-16 1-19 1-20 1-22 1-33 1-19 1-31	0.971 0.971 0.982 0.991 0.989 0.955 0.932 0.938 0.941 0.972 0.964 0.914 0.953 0.935 0.935 0.935	0.863 0.863 0.901 0.955 0.899 0.803 0.625 0.876 0.811 0.939 0.777 0.657 0.840 0.701 0.850 0.895
8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24	1-26 1-46 1-21 1-23 1-25 1-18 1-18 1-25 1-17 1-27 1-16 1-19 1-20 1-22 1-33 1-19 1-31	0.971 0.982 0.991 0.989 0.955 0.932 0.938 0.941 0.972 0.964 0.914 0.953 0.935 0.935	0.863 0.901 0.955 0.899 0.803 0.625 0.876 0.811 0.939 0.777 0.657 0.840 0.701 0.850 0.895
9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24	1-46 1-21 1-23 1-25 1-18 1-18 1-25 1-17 1-27 1-16 1-19 1-20 1-22 1-33 1-19 1-31	0.982 0.991 0.989 0.955 0.932 0.938 0.941 0.972 0.964 0.914 0.953 0.935 0.935	0.901 0.955 0.899 0.803 0.625 0.811 0.939 0.777 0.657 0.840 0.701 0.850 0.895
10 11 12 13 14 15 16 17 18 19 20 21 22 23 24	1-21 1-23 1-25 1-18 1-18 1-25 1-17 1-27 1-16 1-19 1-20 1-22 1-33 1-19 1-31	0.991 0.989 0.955 0.932 0.938 0.941 0.972 0.964 0.914 0.953 0.935 0.935	0.955 0.899 0.803 0.625 0.811 0.939 0.777 0.657 0.840 0.701 0.850 0.895
11 12 13 14 15 16 17 18 19 20 21 22 23 24	1-23 1-25 1-18 1-18 1-25 1-17 1-27 1-16 1-19 1-20 1-22 1-33 1-19 1-31	0.989 0.955 0.932 0.938 0.941 0.972 0.964 0.914 0.953 0.935 0.935	0.899 0.803 0.625 0.876 0.811 0.939 0.777 0.657 0.840 0.701 0.850 0.895
12 13 14 15 16 17 18 19 20 21 22 23 24	1-25 1-18 1-18 1-25 1-17 1-27 1-16 1-19 1-20 1-22 1-33 1-19 1-31	0.955 0.932 0.938 0.941 0.972 0.964 0.914 0.953 0.935 0.974 0.961	0.803 0.625 0.876 0.811 0.939 0.777 0.657 0.840 0.701 0.850 0.895
13 14 15 16 17 18 19 20 21 22 23 24	1-18 1-18 1-25 1-17 1-27 1-16 1-19 1-20 1-22 1-33 1-19 1-31	0.932 0.938 0.941 0.972 0.964 0.914 0.953 0.935 0.974 0.961	0.625 0.876 0.811 0.939 0.777 0.657 0.850 0.701 0.850 0.895
14 15 16 17 18 19 20 21 22 23 24	1-18 1-25 1-17 1-27 1-16 1-19 1-20 1-22 1-33 1-19 1-31	0.938 0.941 0.972 0.964 0.914 0.953 0.935 0.974 0.961	0.876 0.811 0.939 0.777 0.657 0.840 0.701 0.850 0.895
15 16 17 18 19 20 21 22 23 24	1-25 1-17 1-27 1-16 1-19 1-20 1-22 1-33 1-19 1-31	0.941 0.972 0.964 0.914 0.953 0.935 0.974	0.811 0.939 0.777 0.657 0.840 0.701 0.850 0.895
16 17 18 19 20 21 22 23 24	1-17 1-27 1-16 1-19 1-20 1-22 1-33 1-19	0.941 0.972 0.964 0.914 0.953 0.935 0.974	0.811 0.939 0.777 0.657 0.840 0.701 0.850 0.895
17 18 19 20 21 22 22 23 24	1-17 1-27 1-16 1-19 1-20 1-22 1-33 1-19	0.972 0.964 0.914 0.953 0.935 0.974 0.961	0.939 0.777 0.657 0.840 0.701 0.850 0.895
18 19 20 21 22 23 24 25	1-27 1-16 1-19 1-20 1-22 1-33 1-19 1-31	0.964 0.914 0.953 0.935 0.974 0.961	0.777 0.657 0.840 0.701 0.850 0.895
18 19 20 21 22 23 24 25	1-16 1-19 1-20 1-22 1-33 1-19	0.914 0.953 0.935 0.974 0.961	0.657 0.840 0.701 0.850 0.895
19 20 21 22 23 24 25	1-19 1-20 1-22 1-33 1-19 1-31	0.953 0.935 0.974 0.961	0.840 0.701 0.850 0.895
20 21 22 23 24 25	1-20 1-22 1-33 1-19 1-31	0.935 0.974 0.961	0.701 0.850 0.895
21 22 23 24 25	1-22 1-33 1-19 1-31	0.974	0.850
22 23 24 25	1-33 1-19 1-31	0.961	0.895
23 24 25	1-19		.1
24 25	1-31	0.991	<del> </del>
25	1		0.959
		0.995	0.944
	1-22	0.976	0.935
26	1-27	0.996	0.928
27	1-24	0.953	0.739
28	1-21	0.906	0.688
29	1-31	0.986	0.841
30	1-28	0.980	
31	1-19		0.893
32	1-22	0.993	0.976
35		0.998	0.909
36	1-33	0.949	0.736
	1-33	0.949	0.736
46	1-19	0.570	0.951
67	1-25	0.968	0.848
71	1-18	0.949	0.845
72	1-30	0.991	0.919
75	1-29	0.958	0.854
88	1-20	0.986	0.945
94	1-33	0.994	0.943
97	1-46	0.964	0.595
103	1-49	0.983	0.570
108	1-26		
111	1-23	0.978	0.885
126		0.989	0.899
129	1-25	0.955	0.803
	1-19	0.963	0.918
138	1-29	0.971	0.844
143	1-18	0.914	0.628
148	1-20	0.969	0.904
156	1-25	0.941	0.811
158	1-22	0.979	0.927
160	1-17	0.972	0.939
161	1-48	0.903	
162	1-25		0.571
168	1-16	0.937	0.729
171		0.939	0.826
	1-27	0.964	0.777
178	1-21	0.945	0.825
180	1-27	0.981	0.941
	1-28	0.982	0.936
190	1-19	0.953	0.840
	1-22	0.975	0.916
	1-22	0.963	0.916

SEQ ID NO:	POSITION OF SIGNAL IN AMINO	MaxS (MAXIMUM SCORE)	MeanS (MEAN SCORE)
	ACID SEQUENCE		
199	1-20	0.935	0.701
200	1-23	0.977	0.773
206	1-30	0.984	0.890
207	1-19	0.990	0.924
208	1-22	0.974	0.850
210	1-40	0.940	0.670
211	1-28	0.971	0.849
216	1-24	0.986	0.956
218	1-33	0.961	0.895
219	1-19	0.970	0.871
221	1-19	0.904	0.553
222	1-21	0.917	0.555
230	1-19	0.991	0.959
231	1-26	0.953	0.800
232	1-25	0.988	0.826
239	1-23	0.969	0.828
240	1-17	0.982	0.955
241	1-17	0.982	0.955
245	1-30	0.970	0.722
248	1-22	0.976 "	0.935
249	1-23	0.968	0.940
252	1-18	0.971	0.923
261	1-24	0.883	0.587
265	1-18	0.939	0.868
272	1-24	0.953	0.739
283	. 1-21	0.906	0.688
284	1-29	0.997	0.854
290	1-31	0.986	0.841
302	1-28	0.980	0.893
304	1-16	0.907	0.635
312	1-19	0.993	0.976
313	1-17	0.930	0.753
323	1-22	0.998	0.909
324	1-17	0.982	0.954
328	1-19	0.971	0.865
329	1-22	0.963	0.924
330	1-33	0.978	0.841
331	1-24	0.520	0.712
332	1-24	0.975	0.881
333	1-19	0.984	0.941
334	1-20	0.899	0.567
335	1-27	0.942	0.813
336	1-20	0.952	0.850
337	1-38	0.942	0.653
338	1-27	0.973	0.772
339	1-36	0.979	0.804
340	1-27	0.888	0.597
343	1-19	0.971	0.865
344	1-22	0.994	0.928
345	1-17	0.966	0.687
346	1-19	0.936	0.822
347	1-22	0.963	0.924
349	1-24	0.982	
351	1-21	0.918	0.966
352	1-31		0.815
354	1-31	0.988	0.912
355	1-29	0.974	0.839
356	1-16		0.632
357	1-33	0.994	0.969
360	1-33	0.935	0.726
361		0.938	0.827
362	1-25	0.954	0.674
363	1-22	0.929	0.788
364	1-21	0.881	0.715
365	1-33	0.978	0.841
	1-33	0.978	0.841

SEQ ID NO:	POSITION OF	I Mana The Manager	Tv. 6 7 6 6
S=Q 25 110.	SIGNAL IN AMINO	MaxS (MAXIMUM SCORE)	MeanS (MEAN SCORE)
1	ACID SEQUENCE	SCORS	SCORE)
366	1-21	0.916	0.820
367	1-19	0.936	0.822
368	1-29	0.972	0.874
370	1-24	0.920	0.712
371	1-24	0.961	0.712
372	1-27	0.919	
373	1-19	0.986	0.768
375	1-32		0.945
376		0.994	0.932
377	1-34	0.987	0.810
378	1-17	0.995	0.950
380	1-49	0.971	0.749
381	1-20	0.968	0.874
382	1-20	0.928	0.782
	1-19	0.986	0.934
383	1-28	0.965	0.829
384	1-39	0.970	0.551
386	1-24	0.975	0.881
388	1-30	0.989	0.868
389	1-19	0.984	0.941
390	1-26	0.971	0.782
392	1-20	0.981	0.900
393	16	0.968	0.890
394	1-23	0.937	0.701
397	1-22	0.985	0.854
399	1-46	0.977	0.698
401	1-20	0.899	0.567
402	1-22	0.967	0.931
403	1-27	0.992	0.934
404	1-19	0.991	0.973
405	1-23	0.994	0.921
407	1-35	0.987	0.658
408	1-39	0.976	0.551
409	1-33	0.897	0.570
410	1-25	0.990	0.962
411	1-38	0.977	0.827
412	1-20	0.944	0.768
413	1-20	0.988	0.965
414	1-46	0.993	0.638
415	1-23	0.981	0.940
417	1-29	0.941	0.672
418	1-20	0.952	0.850
419	1-19	0.986	0.967
420	1-29	0.965	0.861
421	1-22	0.889	0.785
422	1-48	0.982	0.862
424	1-19	0.979	
428	1-38	0.942	0.933
430	1-18		0.653
432	1-33	0.947	0.595
433	1-26	0.957	0.789
434	1-27	0.979	0.904
435	1-24	0.962	0.777
436	1-24	0.998	0.977
443		0.973	0.772
448	1-15	0.966	0.940
453	1-36	0.979	0.804
	1-41	0.958	0.609
455	1-33	0.943	0.606
457	1-27	0.888	0.597
462	1-16	0.925	0.681
486	1-27	0.972	0.845
495	1-24	0.917	0.636
498	1-26	0.993	0.890
505	1-20	0.976	0.926
507	1-17	0.966	0.687
510	1-23	0.930	0.593

SEQ ID NO:	POSITION OF	MaxS (MAXIMUM	Manne Carres
	SIGNAL IN AMINO	SCORE)	MeanS (MEAN SCORE)
	ACID SEQUENCE	000.037	SCORE,
511	1-23	0.930	0.593
512	1-23	0.930	0.593
515	1-18	0.978	0.956
523	1-19	0.936	0.822
529	1-22	0.963	0.924
545	1-24	0.982	0.966
550	1-30	0.933	0.713
552	1-21	0.973	0.912
554	1-23	0.969	0.784
571	1-21	0.918	0.815
574	1-31	0.988	0.912
580	1-39	0.925	0.556
594	1-31	0.974	0.839
608	1-29	0.932	0.632
609	1-29	0.932	0.632
610	1-21	0.990	0.948
621	1-15	0.994	0.969
623	1-33	0.935	
653	1-27	0.938	0.726
668	1-22	0.929	
677	1-16	0.948	0.788
685	1-21	1 1 1 1 1 1 1	0.807
699	1-22	0.861	0.715
702	1-31	0.975	0.816
707	1-16	0.968	0.898
713	1-16	0.850	0.562
718		0.966	0.743
719	1-19	0.936	0.822
729	1-20	0.961	0.824
735	1-29	0.972	0.874
746	1-46	0.903	0.598
747	1-14	0.916	0.730
748	1-22	0.965	0.876
759	1-29	0.968	0.785
767	1-24	0.961	0.773
	1-27	0.919	0.768
768	1-33	0.900	0.585
773	1-42	0.959	0.702
779	1-19	0.986	0.945
797	1-19	0.944	0.759
798	1-19	0.900	0.568
820	1-17	0.995	0.950
827	1-49	0.971	0.749
848	1-20	0.968	0.874
864	1-20	0.928	0.782
866	1-19	0.986	0.934
873	1-23	0.948	0.886
881	1-28	0.965	0.829
887	1-39	0.970	0.551
927	1-30	0.989	0.868
934	1-48	0.988	0.777
939	1-39	0.994	0.889
944	1-26	0.971	0.782
950	1-29	0.957	0.845
963	1-20	0.981	0.900
964	1-20	0.886	0.558
973	1-16	0.968	0.890
980	1-34	0.961	0.749
981	1-20	0.953	0.822
984	1-12	0.938	
1015	1-22	0.985	0.780
1040	1-46	0.977	
1052	1-18	0.969	0.698
1059	1-20		0.842
1065	1-33	0.927	0.867
1069	1-22	0.983	0.918
		0.993	0.935

SEQ ID NO:	POSITION OF	1.00	
SEQ ID NO:		MaxS (MAXIMUM	11120
1	SIGNAL IN AMINO	SCORE)	SCORE)
1075	ACID SEQUENCE		
1080	1-27	0.992	0.934
1092	1-19	0.931	0.829
	1-19	0.991	0.973
1094	1-46	0.992	0.653
1095	1-30	0.974	0.929
1105	1-23	0.994	0.921
1123	1-35	0.987	0.658
1138	1-32	0.954	0.613
1140	1-39	0.989	0.789
1142	1-33	0.897	0.570
1152	1-25	0.990	0.962
1170	1-38	0.977	0.827
1176	1-20	0.944	
1187	1-20	0.988	0.768
1189	1-35		0.965
1192	1-46	0.967	0.839
1193		0.993	0.638
1197	1-16	0.925	0.710
	1-29	0.985	0.853
1208	1-23	0.981	0.940
1225	1-29	0.941	0.672
1245	1-19	0.986	0.967
1258	1-29	0.965	0.861
1265	1-22	0.889	0.785
1266	1-20	0.944	0.809
1276	1-48	0.982	0.862
1292	1-19	0.979	0.933
1296	1-21	0.984	0.944
1297	1-19	0.984	0.953
1332	1-38	0.942	<u></u>
1358	1-18	0.947	0.653
1371	1-33	0.957	0.595
1380	1-26		0.789
1397	1-27	0.979	0.904
1399	1-23	0.962	0.777
1404	1-24	0.997	0.960
1410		0.998	0.977
1414	1-15	0.946	0.845
1415	1-24	0.913	0.588
	1-19	0.982	0.929
1416	1-12	0.931	0.891
1418	1-30	0.933	0.563
1420	1-20	0.881	0.561
1421	1-19	0.990	0.968
1423	1-17	0.968	0.863
1424	1-21	0.885	0.591
1425	1-24	0.913	0.588
1426	1-24	0.913	0.588
1428	1-25	0.957	0.899
1430	1-34	0.977	<del></del>
1431	1-28	0.979	0.819
1432	1-36	J	0.923
1433	1-32	0.957	0.613
1434	1-39	0.921	0.753
1435		0.983	0.621
1436	1-25	0.910	0.631
1437	1-42	0.988	0.868
	1-22	0.998	0.980
1442	1-20	0.918	0.753
1448	1-12	0.931	0.891
1462	1-18	0.968	0.888
1490	1-20	0.881	0.561
1518	1-17	0.968	0.863
1525	1-21	0.885	0.591
1547	1-28	0.974	
1561	1-25	0.967	0.891
1580	1-17		0.899
1593	1-28	0.923	0.824
		0.979	0.923

SEQ ID NO:	POSITION OF SIGNAL IN AMINO ACID SEQUENCE	MaxS (MAXIMUM SCORE)	MeanS (MEAN SCORE)
1596	1-16	0.929	0.709
1601	1-36	0.957	0.613
1606	1-22	0.979	0.831
1607	1-20	0.974	0.770
1608	1-32	0.921	0.753
1614	1-33	0.969	0.829
1616	1-20	0.959	0.869
1625	1-39	0.983	0.621
1632	1-25	0.910	0.631
1636	1-33	0.897	0.591
1639	1-42	0.988	0.868
1645	1-20	0.927	0.568
1647	1-17	0.923	0.742
1648	1-22	0.998	0.980

TRADOCS:1416234.1(%CR%01!.DOC)

TABLE 6

TABLE 6					
SEQ ID NO:	SEQ ID	SEQ ID NO:	SEQ ID	Priority	SEQ ID
of full-	NO: of	of contig	NO:	docket number_	NO:in
length	full-	nucleotide	Of contig	corresponding	U.S.S.N.
nucleotide	length	sequence	peptide	SEQ ID NO: in	09/488,725
sequence	peptide	1	sequence	priority	
	sequence			application	
1	1787	3573	5359	784CIP2_1	1103
2	1788	3574	5360	784CIP2_2	2673
3	1789	357,5	5361	784CIP2_3	4117
4	1790	3576	5362	784CIP2_4	5556
5	1791	3577	5363	784CIP2 5	5562
6	1792	3578	5364	784CIP2 6	5562
7	1793	3579	5365	784CIP2 7	5562
8	1794	3580	5366	784CIP2 8	5562
9	1795	3581	5367	784CIP2 9	5563
10	1796	3582	5368	784CIP2 10	5564
11	1797	3583	5369	784CIP2 11	5565
12	1798	3584	5370	784CIP2 12	5689
13	1799	3585	5371	784CIP2 13	5729
14	1800	3586	5372	784CIP2 14	5745
15	1801	3587	5373	784CIP2_14	5777
16	1802	3588	5374	784CIP2_15	5777
17	1803	3589	5375		
18	1804	3590	5376	784CIP2_17 784CIP2_18	5789
19	1805	3590	5376	784CIP2_18 784CIP2_19	5792 5804
20	1806	3592	5378		1
21	1807	3593	5379		5805
22	1808	3594	5380	784CIP2_21	5805
23	1809	3595	5381	784CIP2_22	5844
24	1810	3596	5382	784CIP2_23 784CIP2_24	5844
25	1811	3597		1	5850
26	1812	3598	5383	784CIP2_25	5867
27	1813	3599	5384	784CIP2_26	5973
28	1814	3600	5385	784CIP2_27	5995
29	1815		5386	784CIP2_28	5995
30	1815	3601	5387	784CIP2_29	6005
31		3602	5388	784CIP2_30	6007
32	1817	3603	5389	784CIP2_31	6007
33	1818	3604	5390	784CIP2_32	6009
34	1819	3605	5391	784CIP2_33	6012
	1820	3606	5392	784CIP2_34	6015
35 36	1821	3607	5393	784CIP2_35	6016
37	1822	3608	5394	784CIP2_36	6016
37	1823	3609	5395	784CIP2_37	6018
	1824	3610	5396	784CIP2_38	6018
39	1825	3611	5397	784CIP2_39	6018
40	1826	3612	5398	784CIP2_40	6023
41	1827	3613	5399	784CIP2_41	6070
42	1828	3614	5400	784CIP2_42	6081
43	1829	3615	5401	784CIP2_43	6089
44	1830	3616	5402	784CIP2_44	6118
45	1831	3617	5403	784CIP2_45	6118
46	1832	3618	5404	784CIP2_46	6130
47	1833	3619	5405	784CIP2_47	6177
48	1834	3620	5406	784CIP2_48	6189
49	1835	3621	5407	784CIP2 49	6191
50	1836	3622	5408	784CIP2 50	6204
51	1837	3623	5409	784CIP2 51 ·	6204
52	1838	3624	5410	784CIP2 52	6284
53	1839	3625	5411	784CIP2 53	6367
54	1840	3626	5412	784CIP2 54	6436
55	1841	3627	5413	784CIP2 55	6442
56	1842	3628	5414	784CIP2_55	
57	1843	3629	5415	784CIP2_56	6445 6457
58	1844	3630	5416	784CIP2_57	
59	1845	3631	5417	784CIP2_58	6458
				,04CT57_2A	6458

SEQ ID NO:	SEQ ID	SEQ ID NO:	SEQ ID	I not auch.	T 250 55
of full-	NO: of	of contig	NO:	Priority docket number	SEQ ID NO:in
length	full-	nucleotide	of contig	corresponding	U.S.S.N.
nucleotide	length	sequence	peptide	SEQ ID NO: in	09/488,725
sequence	peptide		sequence	priority	11,100,120
	sequence		1	application	
60	1846	3632	5418	784CIP2_60	6462
61	1847	3633	5419	784CIP2_61	6472
62	1848	3634	5420	784CIP2_62	6499
63	1849	3635	5421	784CIP2_63	6499
64	1850	3636	5422	784CIP2_64	6505
66	1851	3637	5423	784CIP2_65	6534
67	1852 1853	3638	5424	784CIP2_66	6534
6B	1853	3639	5425	784CIP2_67	6540
69	1855	3640	5426	784CIP2_68	6550
70	1856	3641 3642	5427	784CIP2_69	6550
71	1857	3643	542B 5429	784CIP2_70	6592
72	1858	3644	5429	784CIP2_71	6645
73	1859	3645	5431	784CIP2_72	6671
74	1860	3646	5432	784CIP2_73 784CIP2_74	6763
75	1861	3647	5433	784CIP2_74 784CIP2_75	6763
76	1862	3648	5434	784CIP2_75	6786
77	1863	3649	5435	784CIP2 76	6824
78	1864	3650	5436	784CIP2_77	6830 6831
79	1865	3651	5437	784CIP2 79	6832
80	1866	3652	5438	784CIP2 80	6834
81	1857	3653	5439	784CIP2 81	6834
82	1858	3654	5440	784CIP2 82	6835
83	1869	3655	5441	784CIP2 83	6837
84	1870	3656	5442	784CIP2 84	6843
85	1871	3657	5443	784CIP2 85	6859
86	1872	3658	5444	784CIP2 86	6915
87	1873	3659	5445	784CIP2_B7	6932
88	1874	3660	5446	784CIP2_88	6957
90	1875	3661	5417	784CIP2_89	6961
91	1876	3662	5448	784CIP2_90	6973
92	1877	3663	5449	784CIP2_91	6973
93	1879	3664	5450	784CIP2_93	7007
94	1880	3665	5451	784CIP2_94	7018
95	1881	3666 3667	5452	784CIP2_95	7019
96	1882	3668	5453 5454	784CIP2_96	7020
97	1883	3669	5454	784CIP2_97	7020
98	1884	3670	5456	784CIP2_98 784CIP2_99	7021
99	1885	3671	5457	784CIP2_99	7023 7027
100	1886	3672	5458	784CIP2_100	7028
101	1887	3673	5459	784CIP2 102	7029
102	1888	3674	5460	784CIP2 103	7031
103	1889	3675	5461	784CIP2 104	7032
104	1890	3676	5462	784CIP2 105	7033
105	1891	3677	5463	784CIP2_106	7035
106	1892	367B	5464	784CIP2_107	7036
107	1893	3679	5465	784CIP2_108	7039
108	1894	3680	5466	784CIP2_109	7043
109	1895	3681	5467	784CIP2_110	7044
110	1896	3682	5468	784CIP2_111	7046
111	1897	3683	5469	784CIP2_112	7054
112	1898	3684	5470	784CIP2_113	7061
113	1899	3685	5471	784CIP2_114	7077
115	1900 1901	3686	5472	784CIP2_115	7092
116	1901	3687	5473	784CIP2_116	7094
117	1902	3688	5474	784CIP2_117	7106
118	1904	3689	5475	784CIP2_118	7107
119	1905	3690 3691	5476	784CIP2_119	7111
120	1906	3692	5477 · 5478	784CIP2_120	7123
121	1907	3693	5478	784CIP2_121	7142
				784CIP2_122	7142

SEQ ID NO:	SEQ ID	SEQ ID NO:	SEQ ID	Priority	T 0 = 0 + 0
of full-	NO: of	of contig	NO:	docket number	SEQ ID No:in
length	full-	nucleotide	of contig	corresponding	U.S.S.N.
nucleotide	length	sequence	peptide	SEQ ID No: in	09/488,725
sequence	peptide		sequence	priority	1 , 100, 100
	sequence			application	
122	1908	3694	5480	784CIP2 123	7154
123	1909	3695	5481	784CIP2_124	7160
124	1910	3696	5482	784CIP2 125	7169
125	1911	3697	5483	784CIP2 126	7185
126	1912	3698	5484	784CIP2 127	7197
127	1913	3699	5485	784CIP2_128	7219
128	1914	3700	5486	784CIP2_129	7226
129	1915	3701	5487	784CIP2_130	7229
130	1916	3702	5488	784CIP2_131	7234
131	1917	3703	5489	784CIP2_132	7235
132	1918	3704	5490	784CIP2_133	7235
133	1919	3705	5491	784CIP2_134	7238
134	1920	3706	5492	784CIP2_135	7247
135	1921	3707	5493	784CIP2_136	7261
136	1922	3708	5494	784CIP2_137	7262
137	1923	3709	5495	784CIP2_138	7267
138	1924	3710	5496	784CIP2_139	7272
139	1925	3711	5497	784CIP2_140	7273
140	1926	3712	5498 .	784CIP2_141	7282
141	1927	3713	5499	784CIP2_142	7288
142	1928	3714	5500	784CIP2_143	7291
143	1929	3715	5501	784CIP2_144	7293
144	1930	3716	5502	784CIP2_145	7294
146	1931	3717	5503	784CIP2_146	7299
147	1932	3718	5504	784CIP2_147	7300
148	1933	3719	5505	784CIP2_148	7312
149	1934	3720	5506	784CIP2_149	7313
150	1935	3721	5507	784CIP2_150	7315
151	1936 1937	3722	5508	784CIP2_151	7318
152	1937	3723	5509	784CIP2_152	7321
153	1939	3724 3725	5510	784CIP2_153	7330
154	1940	3725	5511	784CIP2_154	7331
155	1941	3727	5512	784CIP2_155	7333
156	1942	3728	5513 5514	784CIP2_156	7350
157	1943	3729	5514	784CIP2_157	7352
158	1944	3730	5516	784CIP2_158	7384
159	1945	3731	5517	784CIP2_159 784CIP2_160	7403
160	1946	3732	5518	784CIP2_160 784CIP2_161	7431
161	1947	3733	5519	784CIP2_161 784CIP2_162	7411
162	1948	3734	5520	784CIP2_162 784CIP2_163	7453
163	1949	3735	5521	784CIP2_163 784CIP2_164	7467
164	1950	3736	5522	784CIP2_164 784CIP2_165	7471 7493
165	1951	3737	5523	784CIP2_165 784CIP2_166	7502
166	1952	3738	5524	784CIP2_167	7511
167	1953	3739	5525	784CIP2 168	7511
168	1954	3740	5526	784CIP2 169	7520
169	1955	3741	5527	784CIP2_189	7541
170	1956	3742	5528	784CIP2_170	7570
171	1957	3743	5529	784CIP2 172	7578
172	1958	3744	5530	784CIP2 173	7583
173	1959	3745	5531	784CIP2_173	7592
174	1960	3746	5532	784CIP2_174	7601
175	1961	3747	5533	784CIP2 176	7602
176	1962	3748	5534	784CIP2_176	7608
177	1963	3749	5535	784CIP2_177	7615
178	1964	3750	5536	784CIP2 179	7617
179	1965	3751	5537	784CIP2_179 784CIP2_181	7624
180	1966	3752	5538	784CIP2 182	7626
181	1967	3753	5539	784CIP2_182	7640
182	1968	3754	5540	784CIP2 184	7641
183	1969	3755	5541	784CIP2 185	7641
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185	1971	3757	5543	784CIP2 187	7642
186	1972	3758	5544	784CIP2 188	7649
187	1973	3759	5545	784CIP2 189	7656
188	1974	3760	5546	784CIP2 190	7657
189	1975	3761	5547	784CIP2 191	7657
190	1976	3762	5548	784CIP2 192	7662
191	1977	3763	5549	784CIP2 193	7668
192	1978	3764	5550	784CIP2 194	7673
193	1979	3765	5551	784CIP2 195	7690
194	1980	3766	5552	784CIP2 196	7700
195	1981	3767	5553	784CIP2 197	7709
196	1982	3768	5554	784CIP2 198	7736
197	1983	3769	5555	784CIP2 199	7737
198	1984	3770	5556	784CIP2 200	7744
199	1985	3771	5557	784CIP2 201	7771
200	1986	3772	5558	784CIP2 202	7786
201	1987	3773	5559	784CIP2 203	7791
202	1988	3774	5560	784CIP2 204	7797
203	1989	3775	5561	784CIP2 205	7806
204	1990	3776	5562	784CIP2_205	7812
205	1991	3777	5563	784CIP2 207	7812
206	1992	3778	5564	784CIP2_207	7812
207	1993	3779	5565	784CIP2_208	7822
208	1994	3780	5566	784CIP2_209	7827
209	1995	3781	5567	784CIP2_210	7830
210	1995	3782	5568	784CIP2 211	7835
211	1997	3783	5569	784CIP2_212 784CIP2_214	
212	1998	3784	5570	784CIP2_214 784CIP2_215	7840
213	1999	3785	5571	784CIP2_215	7858
214	2000	3786	5572	784CIP2_216 784CIP2_217	7858
215	2001	3787	5573	784CIP2_217	7861
216	2002	3788	5574	784CIP2_218	7866 7868
217	2003	3789	5575	784CIP2_219	1
218	2004	3790	5576	784CIP2_220	7896
219	2005	3791	5577	784CIP2_221 784CIP2_222	7898 7900
220	2006	3792	5578	784CIP2_222	
221	2007	3793	5579	784CIP2_223	7906 7908
222	2008	3794	5580	784CIP2_224 784CIP2_225	
223	2009	3795	5581	784CIP2 225	7909
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225	2011	3797	5583	784CIP2_227	7932
226	2012	3798	5584	784CIP2_228	7940
227	2013	3799	5585	784CIP2_229 784CIP2_230	7940
228	2014	3800	5586		7984
229	2015	3801	5587	784CIP2_231 784CIP2_232	7984
230	2016	3802	5588	784CIP2_232 784CIP2_233	8001
231	2017	3803	5589		8021
232	2018	3804		784CIP2_234	8029
233	2019	3805	5590	784CIP2_235	8033
234	2020	3806	5591 5592	784CIP2_236	8040
235	2021	3807	5593	784CIP2_237	8052
236	2022	3808		784CIP2_238	8096
237	2023	3809	5594	784CIP2_239	8096
238	2024	3810	5595	784CIP2_240	8113
239	2025		5596	784CIP2_241	8126
240	2026	3811	5597	784CIP2_242	8132
241	2027	3812	5598	784CIP2_243	8137
242	2028	3813	5599	784CIP2_244	8137
243	2029	3814	5600	784CIP2_245	8159
244		3815	5501	784CIP2_246	8159
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247	2033	3819	5605	784CIP2 250	8200
248	2034	3820	5606	784CIP2 251	8212
249	2035	3821	5607	784CIP2 252	8220
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251	2037	3823	5609	784CTP2 254	8254
252	2038	3824	5610	784CIP2_255	8255
253	2039	3825	5611	784CIP2 256	8288
254	2040	3826	5612	784CIP2 257	8296
255	2041	3827	5613	784CIP2 258	8329
256	2042	3828	5614	784CIP2 259	8362
257	2043	3829	5615	784CIP2 260	8429
258	2044	3830	5616	784CIP2_261	8436
259	2045	3831	5617	784CIP2_262	8448
260	2046	3832	5618	784CIP2_263	8472
261	2047	3833	5619	784CIP2_264	8502
262	2048	3834	5620	784CIP2_265	8504
263	2049	3835	5621	784CIP2_266	8507
264	2050	3836	5622	784CIP2_268	8509
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266	2052	3838	5624	784CIP2_270	8519
267	2053	3839	5625	784CIP2_271	8530
268 269	2054	3840	5626	784CIP2_272	8532
270	2055	3841	5627	784CIP2_273	8532
L	2056	3842	5628	784CIP2_274	8539
271 272	2057	3843	5629	784CIP2_275	8541
273	2058	3844	5630	784CIP2_276	8543
274	2059	3845	5631	784CIP2_277	8593
275	2060	3846	5632	784CIP2_278	8595
276	2061 2062	3847	5633	784CIP2_279	8615
277	2063	3848	5634	784CIP2_280	8620
278	2063	3849 3850	5635	784CIP2_281	8621
279	2065	3851	5636	784CIP2_282	8623
280	2066	3852	5637	784CIP2_283	8625
281	2067	3853	5638	784CIP2_284	8628
282	2068	3854	5639 5640	784CIP2_285	8628
283	2069	3855	5641	784CIP2_286	8629
284	2070	3856	5642	784CIP2_287	8630
285	2071	3857	5643	784CIP2_288	8631
286	2072	3858	5644	784CIP2_289 784CIP2_290	8633
287	2073	3859	5645	784CIP2_290 784CIP2_291	8634
288	2074	3860	5646	784CIP2_291 784CIP2_292	8635 8636
289	2075	3861	5647	784CIP2_292	8659
290	2076	3862	5648	784CIP2_293	8660
291	2077	3863	5649	784CIP2 295	8667
292	2078	3864	5650	784CIP2_296	8667
293	2079	3865	5651	784CIP2_297	8685
294	2080	3866	5652	784CIP2 298	8805
295	2081	3867	5653	784CIP2_298	8896
296	2082	3868	5654	784CIP2 300	8978
297	2083	3869	5655	784CIP2_301	9046
298	2084	3870	5656	784CIP2 302	9048
299	2085	3871	5657	784CIP2 303	9116
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301	2087	3873	5659	784CIP2 305	9201
302	2088	3874	5660	784CIP2 306	9307
303	2089	3875	5661	784CIP2 307	9321
304	2090	3876	5662	784CIP2 308	9397
305	2091	3877	5663	784CIP2 309	9405
306	2092	3878	5664	784CIP2 310	9406
307	2093	3879	5665	784CIP2_311	9422

SEQ ID NO:	SEQ ID	SEQ ID NO:	SEQ ID	Priority	Lego to
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310	2096	3882	5668	784CIP2_314	9632
311	2097	3883	5669	784CIP2_315	9661
312	2098	3884	5670	784CIP2_316	9664
313	2099	3885	5671	784CIP2_317	9691
314	2100	3886	5672	784CIP2_318	9700
315	2101	3887	5673	784CIP2_319	9716
316	2102	3888	5674	784CIP2_320	9721
317	2103	3889	5675	784CIP2_321	9870
318	2104	3890	5676	784CIP2_322	9887
319	2105	3891	5677	784CIP2_323	9923
320	2106	3892	5678	784CIP2_324	9938
321	2107	3893	5679	784CIP2_325	9964
322	2108	3894	5680	784CIP2_326	10007
323	2109	3895	5681	784CIP2_327	10009
324	2110	3896	5682	784CIP2_328	10046
325	2111	3897	5683	784CIP2_329	10156
326	2112	3898	5684	784CIP2_330	10276
327	2113	3899	5685	784CIP2_331	10283
328	2114	3900	5686	784CIP2B_1	152
329 330	2115	3901	5687	784CIP2B_2	167
	2116	3902	5688	784CIP2B_3	205
331 332	2117	3903	5689	784CIP2B_4	210
333	2118	3904	5690	784CIP2B_5	225
333	2119	3905	5691	784CIP2B_6	226
335	2120	3906	5692	784CIP2B_7	264
336	2121	3907	5693	784CIP2B_8	268
337	2122	3908	5694	784CIP2B_9	293
338	2123	3909	5695	784CIP2B_10	293
339	2124 2125	3910	5696	784CIP2B_11	293
340	2126	3911 3912	5697 5698	784CIP2B_12	302
341	2127	3913	5699	784CIP2B_13	311
342	2128	3914	5700	784CIP2B_14	352
343	2129	3915	5701	784CIP2B_15	358
344	2130	3916	5702	784CIP28_16 784CIP2B 17	368
345	2131	3917	. 5703	784CIP2B 17	393 477
346	2132	3918	5704	784CIP2B_18 784CIP2B_19	508
347	2133	3919	5705	784CIP2B_19	508
348	2134	3920	5706	784CIP2B_20 784CIP2B_21	515
349	2135	3921	5707	784CIP2B_21 784CIP2B_22	578
350	2136	3922	5708	784CIP2B 23	588
351	2137	3923	5709	784CIP2B_23	591
352	2138	3924	5710	784CIP2B_24	593
353	2139	3925	5711	784CIP2B_25	594
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355	2141	3927	5713	784CIP2B 28	620
356	2142	3928	5714	784CIP2B 29	654
357	2143	3929	5715	784CIP2B 30	692
358	2144	3930	5716	784CIP2B 31	753
359	2145	3931	5717	784CIP2B 32	758
360	2146	3932	5718	784CIP2B 33	787
361	2147	3933	5719	784CIP2B 34	833
362	2148	3934	5720	784CIP2B 35	838
363	2149	3935	5721	784CIP2B 36	870
364	2150	3936	5722	784CIP2B 37	891
365	2151	3937	5723	784CIP2B 38	891
366	2152	3938	5724	784CIP2B 39	921
367	2153	3939	5725	784CIP2B 40	924
368	2154	3940	5726	784CIP2B 41	932
369	2155	3941	5727	784CIP2B_42	942

SEQ ID NO:	SEQ ID	SEQ ID NO:	SEQ ID	Priority	SEQ ID
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length	full-	nucleotide	of contig	corresponding	U.S.S.N.
nucleotide	length	sequence	peptide	SEQ ID NO: in	09/488,725
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371	2156	3942	5728	784CIP2B_43	958
372	2157	3943	5729	784CIP2B_44	968
373	2158 2159	3944 3945	5730	784CIP2B_45	992
374	2160	3946	5731 5732	784CIP2B_46	1025
375	2161	3946	5733	784CIP2B_47	1074
376	2162	3948	5734	784CIP2B_48	1104
377	2163	3949	5735	784CIP2B_49 784CIP2B_50	1114
378	2164	3950	5736	784CIP2B_50	1144
379	2165	3951	5737	784CIP2B 52	1318
380	2166	3952	5738	784CIP2B 53	1318
381	2167	3953	5739	784CIP2B_53	1319
382	2168	3954	5740	784CIP2B_55	1436
383	2169	3955	5741	784CIP2B 56	1464
384	2170	3956	5742	784CIP2B 57	1584
385	2171	3957	5743	784CIP2B 58	1617
386	2172	3958	5744	784CIP2B 59	1724
387	2173	3959	5745	784CIP2B 60	1728
388	2174	3960	5746	784CIP2B 61	1772
389	2175	3961	5747	784CIP2B 62	1809
390	2176	3962	5748	784CIP2B 63	1868
391	2177	3963	5749	784CIP2B 64	1898
392	2178	3964	5750	784CIP2B_65	1926
393	2179	3965	5751	784CIP2B_66	1965
394	2180	3966	5752	784CIP2B_67	1967
395	2181	3967	5753	784CIP2B_68	1995
396	2182	3968	5754	784CIP2B_69	2005.
397	2183	3969	5755	784CIP2B_70	2027
398	2184	3970	5756	784CIP2B_71	2055
399 400	2185	3971	. 5757	784CIP2B_72	2103
401	2186	3972	5758	784CIP2B_73	2106
402	2187 2188	3973	5759	784CIP2B_74	2166
403	2189	3974 3975	5760	784CIP2B_75	2175
404	2190	3975	5761 5762	784CIP2B_76	2176
405	2191	3977	5763	784CIP2B_78 784CIP2B_79	2236
406	2192	3978	5764	784CIP2B_79 784CIP2B_80	2250
407	2193	3979	5765	784CIP2B_80	2300 . 2323
408	2194	3980	5766	784CIP2B 82	2323
409	2195	3981	5767	784CIP2B_62	2371
410	2196	3982	5768	784CIP2B 84	2399
411	2197	3983	5769	784CIP2B 85	2411
412	2198	3984	5770	784CIP2B 86	2428
413	2199	3985	5771	784CIP2B 87	2430
414	2200	3986	5772	784CIP2B 88	2439
415	2201	3987	5773	784CIP2B_89	2447
416	2202	3988	5774	784CIP2B 90	2461
417	2203	3989	5775	784CIP2B_91	2487
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419	2205	3991	5777	784CIP2B_93	2512
420	2206	3992	5778	784CIP2B_94	2564
421	2207	3993	5779	784CIP2B_95	2678
422	2208	3994	5780	784CIP2B_96	2816
423	2209	3995	5781	784CIP2B_97	2818
424	2210	3996	5782	784CIP2B_98	2819
425	2211	3997	5783	784CIP2B_99	2943
426	2212	3998	5784	784CIP2B_100	3137
427	2213	3999	5785	784CIP2B_101	3137
428	2214	4000	5786	784CIP2B_102	3160
747	2215	4001	5787	784CIP2B_103	3323
430	2216	4 4 4 4			
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SEQ ID NO:	SEQ ID	SEQ ID NO:	SEQ ID	Priority	SEQ ID
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length	full-	nucleotide	of contig	corresponding	U.S.S.N.
nucleotide sequence	length	sequence	peptide	SEQ ID NO: in	09/488,725
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433	2218	4004	5790	784CIP2B_106	3417
434	2219	4005	5791	784CIP2B_107	3418
434	2220	4006	5792	784CIP2B_108	3442
	2221	4007	5793	784CIP2B_109	3442
436	2222	4008	5794	784CIP2B_110	3444
437	2223	4009	5795	784CIP2B_111	3855
438	2224	4010	5796	784CIP2B_112	3863
439	2225	4011	5797	784CIP2B_113	4090
440	2226	4012	5798	784CIP2B_114	4105
441	2227	4013	5799	784CIP2B_115	4142
442	2228	4014	5800	784CIP2B_116	4142
443	2229	4015	5801	784CIP2B_117	4149
444	2230	4016	5802	784CIP2B_118	4196
445	2231	4017	5803	784CIP2B 119	4202
446	2232	4018	5804	784CIP2B 120	4274
447	2233	4019	5805	784CIP2B 121	4304
448	2234	4020	5806	784CIP2B 122	4306
449	2235	4021	5807	784CIP2B 123	4311
450	2236	4022	5808	784CIP2B 124	4321
451	2237	4023	5809	784CIP2B 125	4323
452	2238	4024	5810	784CIP2B 126	4332
453	2239	4025	5811	784CIP2B 127	4488
454	2240	4026	5812	784CIP2B 128	4588
455	2241	4027	5813	784CIP2B 129	5569
456	2242	4028	5814	784CIP2B 130	5573
457	2243	4029	5815	784CIP2B 131	5577
458	2244	4030	5816	784CIP2B 132	5579
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460	2246	4032	5818	784CIP2B 134	5583
461	2247	4033	5819	784CIP2B_134	5584
462	2248	4034	5820	784CIP2B 136	5585
463	2249	4035	5821	784CIP2B 137	5591
464	2250	4036	5822	784CIP2B 138	5593
465	2251	4037	5823	784CIP2B 139	5594
466	2252	4038	5824	784CIP2B 140	5594
467	2253	4039	5825	784CIP2B 141	5598
468	2254	4040	5826	784CIP2B_141	5602
469	2255	4041	5827	784CIP2B 143	
470	2256	4042	5828	784CIP2B_143	5605
471	2257	4043	5829	784CIP2B 145	5608
472	2258	4044	5830	784CIP2B_145	5617
473	2259	4045	5831	784CIP2B_146	5620
474	2260	4046	5832	784CIP2B_147 784CIP2B_148	5622 5623
475	2261	4047	5833	784CIP2B_148 784CIP2B_149	
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477	2263	4049	5835	784CIP2B_150	5625
478	2264	4050		784CIP2B_151	5627
479	2265	4051	5836	784CIP2B_152	5628
480	2266		5837	784CIP2B_153	5630
481	2267	4052	5838	784CIP2B_154	5632
482	2268	4053	5839	784CIP2B_155	5640
483	2269	4054	5840	784CIP2B_156	5641
484	2270	4055	5841	784CIP2B_157	5643
485		4056	5842	784CIP2B_158	5647
	2271	4057	5843	784CIP2B_159	5649
486	2272	4058	5844	784CIP2B_160	5658
487	2273	4059	5845	784CIP2B_161	5659
488	2274	4060	5846	784CIP2B_162	5667
489	2275	4061	5847	784CIP2B_163	5672
490	2276	4062	5848	784CIP2B_164	5674
_491	2277	4063	5849	784CIP2B_165	5678
492	2278	4064	5850	784CIP2B_166	5680
493	2279	4065	5851	784CIP2B 167	5684

SEQ ID NO:	Tero to	LOGO TO NO	1000	C5-/	
of full-	SEQ ID NO: of	SEQ ID NO:	SEQ ID	Priority	SEQ ID
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	2283	4069	5855	784CIP2B_171	5699
498	2284	4070	5856	784CIP2B_172	5712
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500	2286	4072	5858	784CIP2B_174	5720
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503	2289	4075	5861	784CIP2B 177	5734
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506	2292	4078	5864	784CIP2B 180	5740
507	2293	4079	5865	784CIP2B 181	5744
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510	2296	4082	5868	784CIP2B 183	5750
511	2297	4083	5869	784CIP2B 184	
512	2298	4084			5750
513	2299	4085	5870	784CIP2B_186	5750
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		4087	5873	784CIP2B_189	5767
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517	2303	4089	5875	784CIP2B_191	5783
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519	2305	4091	5877	784CIP2B_193	5788
520	2306	4092	5878	784CIP2B 194	5798
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526	2312	4098	5884	784CIP2B 201	5842
527	2313	4099	5885	784CIP2B 202	5853
528	2314	4100	5886	784CIP2B 203	5861
529	2315	4101	5887	784CIP2B 204	5864
530	2316	4102	5888	784CIP2B 205	5865
531	2317	4103	5889	784CIP2B 206	5871
532	2318	4104	5890	784CIP2B 207	5873
533	2319	4105	5891	784CIP2B 208	5873
534	2320	4106	5892	784CIP2B 209	5875
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542	2328	4114	5900	784CIP2B_217	5895
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544	2330	4116	5902	784CIP2B_219	5902
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546	2332	4118	5904	784CIP2B_221	5918
547	2333	4119	5905	784CIP2B 222	5921
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549	2335	4121	5907	784CIP2B 224	5932
550	2336	4122	5908	784CIP2B 225	5939
551	2337	4123	5909	784CIP2B_225	5945
552	2338	4124	5910	784CIP2B_226	5946
553	2339	4125	5911	784CIP2B 228	
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559	2345	4131	5917	784CIP2B_235	5979
560	2346	4132	5918	784CIP2B_236	5980
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567	2352	4138	5924	784CIP2B 242	6003
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570	2356	4141	5927	784CIP2B_245	6028
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574	2360	4145	5931	784CIP2B_249 784CIP2B_250	6031
575	2361	4147	5932		6032
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580	2366	4152	5938	784CIP2B_255	6046
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582	2368	4154	5940	784CIP2B 258	6051
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585	2371	4157	5943	784CIP2B 261	6063
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588	2374	4160	5946	784CIP2B 264	6068
589	2375	4161	5947	784CIP2B 265	6073
590	2376	4162	5948	784CIP2B 266	6076
591	2377	4163	5949	784CIP2B 267	6076
592	2378	4164	5950	784CIP2B 268	6077
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595	2381	4167	5953	784CIP2B 272	6088
596	2382	4168	5954	784CIP2B 273	6091
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615	2401	4187	5973	784CIP2B_292	6148
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nucleotide	length	sequence	peptide	SEQ ID NO: in	09/488,725
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626	2411		5983	784CIP2B_302	6194
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630	2416	4202	5988	784CIP2B_308	6214
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632	2418	4204	5990	784CIP2B_310	6219
633	2419	4205	5991	784CIP2B_311	6226
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635	2421	4207	5993	784CIP2B_313	6234
636	2422	4208	5994	784CIP2B 314	6237
637	2423	4209	5995	784CIP2B 315	6238
638	2424	4210	5996	784CIP2B 316	6239
639	2425	4211	5997	784CIP2B 317	6239
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644	2430	4216	6002	784CIP2B 322	6250
645	2431	4217	6003	784CIP2B 323	6252
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652	2438	4224	6010	784CIP2B 330	
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674	2460	4246	6032	784CIP2B 356	6348
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sequence	peptide		sequence	priority	05/400,725
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682	2468	4254	6040	784CIP2B_364	6371
683	2469	4255	6041	784CIP2B_365	6376
684	2470	4256	6042	784CIP2B_366	6379
685	2471	4257	6043	784CIP2B_367	6380
686	2472	4258	6044	784CIP2B_368	6381
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688	2474	4260	6046	784CIP2B_370	6395
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695	2480	4266	6052	784CIP2B_376	6411
696		4267	6053	784CIP2B_377	6416
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698	2483		6055	784CIP2B_379	. 6422
699	2485	4270	6056	784CIP2B_380	6423
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701	2487	4273	6058	784CIP2B_382	: 6427
702	2498	4274	6060	784CIP2B_383	6428
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705	2491	4277	6063	784CIP2B_386	6432 6432
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707	2493	4279	6065	784CIP2B 389	6441
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736	2522	4308	6094	784CIP2B 419	
737	2523	4309	6095	784CIP2B_420	6577 6593
738	2524	4310	6096	784CIP2B 422	6595
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745	2531	4317	6103	1 ·	6631
746	2532	4317		784CIP2B_429	6632
747	2533		6104	784CIP2B_430	6633
748		4319	6105	784CIP2B_431	6634
	2534	4320	6106	784CIP2B_432	6638
749	2535	4321	6107	784CIP2B_433	6641
750	2536	4322	6108	784CIP2B_434	6644
751	2537	4323	6109	784CIP2B_435	6646
752	2538	4324	6110	784CIP2B_436	664B
753	2539	4325	6111	784CIP2B_437	6652
754	2540	4326	6112	784CIP2B 438	6654
755	2541	4327	6113	784CIP2B 439	6657
756	2542	4328	6114	784CIP2B 440	6658
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760	2546	4332	6118	784CIP2B 444	6669
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767	2553	4339	6125	784CIP2B_451	6699
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770 .	2556	4342	6128	784CIP2B_454	6713
771	2557	4343	6129	784CIP2B_455	6716
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773	2559	4345	6131	784CIP2B_457	6726
774	2560	4346	6132	784CIP2B 458	6727
775	2561	4347	6133	784CIP2B 459	6730
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779	2565	4351	6137	784CIP2B 463	6733
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785	2571	4357	6143	784CIP2B_468 784CIP2B 469	
786	2572	4358		784CIP2B 470	6761
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788			6145	784CIP2B_471	6768
789	2574 2575	4360	5146	784CIP2B_472	6773
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794	2580	4366	6152	784CIP2B_478	6826
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799	2585	4371	6157	784CIP2B 484	6857
800	2586	4372	6158	784CIP2B 485	6861
801	2587	4373	6159	784CIP2B 485	6873
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Description	SEQ ID NO:	SEQ ID	SEQ ID NO:	SEQ ID	Priority	SEQ ID
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833         2619         4405         6191         784CTP2B 518         7017           834         2620         4406         6192         784CTP2B 519         7025           835         2621         4407         6193         784CTP2B 521         7025           836         2622         4408         6194         784CTP2B 521         7025           837         2623         4409         6195         784CTP2B 521         7025           838         2624         4410         6195         784CTP2B 523         7051           839         2625         4411         6197         784CTP2B 524         7055           840         2626         4412         6198         784CTP2B 525         7060           841         2627         4413         6199         784CTP2B 525         7067           843         2629         4415         6201         784CTP2B 527         7067           844         2630         4415         6201         784CTP2B 527         7067           844         2630         4415         6201         784CTP2B 527         7067           845         2631         4417         6203         784CTP2B 530         7073				L	<u> </u>	
834         2620         4406         6192         784CIP2B 519         7025           835         2621         4407         6193         784CIP2B 520         7025           836         2622         4408         6194         784CIP2B 521         7025           837         2623         4409         6195         784CIP2B 522         7050           838         2624         4410         6196         784CIP2B 523         7051           839         2625         4411         6197         784CIP2B 525         7050           841         2626         4412         6198         784CIP2B 525         7060           841         2627         4413         6199         784CIP2B 525         7060           842         2628         4414         6200         784CIP2B 527         7067           843         2629         4415         6201         784CIP2B 528         7071           844         2630         4416         6202         784CIP2B 529         7072           845         2631         4417         6203         784CIP2B 530         7073           846         2632         4418         6204         784CIP2B 531         7066						
835         2621         4407         6193         784CIP2B 520         7025           836         2622         4408         6194         784CIP2B 521         7025           837         2623         4409         6195         784CIP2B 522         7050           838         2624         4410         6196         784CIP2B 523         7051           839         2625         4411         6197         784CIP2B 524         7055           840         2626         4412         6198         784CIP2B 525         7060           841         2627         4413         6199         784CIP2B 525         7067           843         2629         4415         6200         784CIP2B 527         7067           843         2629         4415         6201         784CIP2B 527         7067           843         2629         4415         6201         784CIP2B 529         7071           844         2630         4416         6202         784CIP2B 530         7073           845         2631         4417         6203         784CIP2B 531         7076           847         2633         4418         6204         784CIP2B 531         7076						
836         2622         4408         6194         784CIP2B_521         7025           837         2623         4409         6195         784CIP2B_522         7050           838         2624         4410         6196         784CIP2B_523         7051           839         2625         4411         6197         784CIP2B_524         7055           840         2626         4412         6198         784CIP2B_524         7055           841         2627         4413         6199         784CIP2B_526         7064           842         2628         4414         6200         784CIP2B_527         7067           843         2629         4415         6201         784CIP2B_528         7071           844         2630         4416         6202         784CIP2B_528         7071           845         2631         4417         6203         784CIP2B_538         7073           846         2632         4418         6204         784CIP2B_531         7076           847         2633         4419         6205         784CIP2B_531         7076           847         2633         4419         6205         784CIP2B_533         7089	835					
837         2623         4409         6195         784CIP2B 522         7050           838         2624         4410         6196         784CIP2B 523         7051           839         2625         4411         6197         784CIP2B 524         7055           840         2626         4412         6198         784CIP2B 525         7060           841         2627         4413         6199         784CIP2B 526         7064           842         2628         4414         6200         784CIP2B 527         7067           843         2629         4415         6201         784CIP2B 528         7071           844         2630         4416         6202         784CIP2B 529         7072           845         2631         4417         6203         784CIP2B 530         7073           846         2632         4418         6204         784CIP2B 531         7076           847         2633         4419         6205         784CIP2B 532         7088           848         2634         4420         6206         784CIP2B 533         7089           849         2635         4421         6207         784CIP2B 533         7089	836				<del></del>	
838         2624         4410         6196         784CIP2B 523         7051           839         2625         4411         6197         784CIP2B 524         7055           840         2626         4412         6198         784CIP2B 525         7060           841         2627         4413         6199         784CIP2B 525         7060           842         2628         4414         6200         784CIP2B 527         7067           843         2629         4415         6201         784CIP2B 528         7071           844         2630         4416         6202         784CIP2B 529         7072           845         2631         4417         6203         784CIP2B 530         7073           846         2632         4418         6204         784CIP2B 531         7076           847         2633         4419         6205         784CIP2B 532         7088           848         2634         4420         6206         784CIP2B 533         7089           849         2635         4421         6207         784CIP2B 534         7091           850         2636         4422         6208         784CIP2B 535         7104	837	2623				I
839         2625         4411         6197         784CIP2B 524         7055           840         2626         4412         6198         784CIP2B 525         7060           841         2627         4413         6199         784CIP2B 526         7064           842         2628         4414         6200         784CIP2B 527         7067           843         2629         4415         6201         784CIP2B 529         7071           844         2630         4416         6202         784CIP2B 539         7072           845         2631         4417         6203         784CIP2B 530         7073           846         2632         4418         6204         784CIP2B 531         7076           847         2633         4419         6205         784CIP2B 532         7088           848         2634         4420         6206         784CIP2B 533         7089           849         2635         4421         6207         784CIP2B 535         7091           850         2636         4422         6208         784CIP2B 535         7091           851         2637         4423         6209         784CIP2B 536         7104	838	2624				L
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841         2627         4413         6199         784CIP2B 526         7064           842         2628         4414         6200         784CIP2B_527         7067           843         2629         4415         6201         784CIP2B_528         7071           844         2630         4416         6202         784CIP2B_529         7072           845         2631         4417         6203         784CIP2B_530         7073           846         2632         4418         6204         784CIP2B_531         7076           847         2633         4419         6205         784CIP2B_532         7088           848         2634         4420         6206         784CIP2B_532         7088           849         2635         4421         6207         784CIP2B_534         7091           850         2636         4422         6208         784CIP2B_535         7091           851         2637         4423         6209         784CIP2B_535         7091           852         2638         4424         6210         784CIP2B_536         7104           852         2638         4425         6211         784CIP2B_539         7105	840	2626				
842         2628         4414         6200         784CIP2B 527         7067           843         2629         4415         6201         784CIP2B 528         7071           844         2630         4416         6202         784CIP2B 529         7072           845         2631         4417         6203         784CIP2B 530         7073           846         2632         4418         6204         784CIP2B 531         7076           847         2633         4419         6205         784CIP2B 532         7088           848         2634         4420         6206         784CIP2B 532         7088           849         2635         4421         6207         784CIP2B 534         7091           850         2636         4422         6208         784CIP2B 535         7091           851         2637         4423         6209         784CIP2B 536         7104           852         2638         4424         6210         784CIP2B 537         7105           853         2639         4425         6211         784CIP2B 538         7105           854         2640         4426         6212         784CIP2B 539         7109	841	2627	4413			
843         2629         4415         6201         784CIP2B 528         7071           844         2630         4416         6202         784CIP2B 529         7072           845         2631         4417         6203         784CIP2B 530         7073           846         2632         4418         6204         784CIP2B 531         7076           847         2633         4419         6205         784CIP2B 532         7088           848         2634         4420         6206         784CIP2B 533         7089           849         2635         4421         6207         784CIP2B 534         7091           850         2636         4422         6208         784CIP2B 535         7091           851         2637         4423         6209         784CIP2B 536         7104           852         2638         4424         6210         784CIP2B 536         7105           853         2639         4425         621         784CIP2B 536         7105           853         2639         4425         621         784CIP2B 539         7105           854         2640         4426         621         784CIP2B 539         7109	842	2628	4414			
844         2630         4416         6202         784CIP2B 529         7072           845         2631         4417         6203         784CIP2B 530         7073           846         2632         4418         6204         784CIP2B 531         7076           847         2633         4419         6205         784CIP2B 532         7088           848         2634         4420         6206         784CIP2B 533         7089           849         2635         4421         6207         784CIP2B 534         7091           850         2636         4422         6208         784CIP2B 535         7091           851         2637         4423         6209         784CIP2B 535         7091           852         2638         4424         6210         784CIP2B 536         7104           852         2638         4424         6210         784CIP2B 537         7105           853         2639         4425         6212         784CIP2B 538         7105           854         2640         4426         6212         784CIP2B 539         7109           855         2641         4427         6213         784CIP2B 540         7109	843	2629	4415	6201		
845         2631         4417         6203         784CIP2B 530         7073           846         2632         4418         6204         784CIP2B 531         7076           847         2633         4419         6205         784CIP2B 532         7088           848         2634         4420         6206         784CIP2B 533         7089           849         2635         4421         6207         784CIP2B 534         7091           850         2636         4422         6208         784CIP2B 535         7091           851         2637         4423         6209         784CIP2B 536         7104           852         2638         4424         6210         784CIP2B 536         7105           853         2639         4425         6211         784CIP2B 537         7105           854         2640         4426         6212         784CIP2B 539         7109           855         2641         4427         6213         784CIP2B 539         7109           855         2641         4427         6213         784CIP2B 540         7109           856         2642         4428         6214         784CIP2B 541         7119		2630	4416	6202		
846         2632         4418         6204         784CIP2B_531         7076           847         2633         4419         6205         784CIP2B_532         7088           848         2634         4420         6206         784CIP2B_533         7089           849         2635         4421         6207         784CIP2B_534         7091           850         2636         4422         6208         784CIP2B_535         7091           851         2637         4423         6209         784CIP2B_536         7104           852         2638         4424         6210         784CIP2B_537         7105           853         2639         4425         6212         784CIP2B_538         7105           854         2540         4426         6212         784CIP2B_539         7109           855         2641         4427         6213         784CIP2B_540         7109           856         2642         4428         6214         784CIP2B_541         7119           857         2643         4429         6215         784CIP2B_542         7120           858         2644         4430         6216         784CIP2B_544         7121	845	2631	4417	6203		
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848         2634         4420         6206         784CIP2B_533         7089           849         2635         4421         6207         784CIP2B_534         7091           850         2636         4422         6208         784CIP2B_535         7091           851         2637         4423         6209         784CIP2B_536         7104           852         2638         4424         6210         784CIP2B_537         7105           853         2639         4425         6211         784CIP2B_536         7105           854         2540         4426         6212         784CIP2B_539         7109           855         2641         4427         6213         784CIP2B_540         7109           856         2642         4428         6214         784CIP2B_541         7119           857         2643         4429         6215         784CIP2B_542         7120           858         2644         4430         6216         784CIP2B_543         7121           859         2645         4431         6217         784CIP2B_544         7126           860         2646         4432         6218         784CIP2B_546         7130	847	2633	4419	6205	784CIP2B 532	7088
849         2635         4421         6207         784CIP2B_534         7091           850         2636         4422         6208         784CIP2B_535         7091           851         2637         4423         6209         784CIP2B_536         7104           852         2638         4424         6210         784CIP2B_537         7105           853         2639         4425         6212         784CIP2B_538         7105           854         2640         4426         6212         784CIP2B_539         7109           855         2641         4427         6213         784CIP2B_540         7109           856         2642         4428         6214         784CIP2B_541         7119           857         2643         4429         6215         784CIP2B_542         7120           858         2644         4430         6216         784CIP2B_543         7121           859         2645         4431         6217         784CIP2B_544         7126           860         2646         4432         6218         784CIP2B_545         7127           861         2647         4433         6219         784CIP2B_546         7130			4420	6206		
850         2636         4422         6208         784CIP2B_535         7091           851         2637         4423         6209         784CIP2B_536         7104           852         2638         4424         6210         784CIP2B_537         7105           853         2639         4425         621         784CIP2B_538         7105           854         2640         4426         6212         784CIP2B_539         7109           855         2641         4427         6213         784CIP2B_539         7109           856         2642         4428         6214         784CIP2B_540         7109           857         2643         4429         6215         784CIP2B_542         7120           858         2644         4430         6216         784CIP2B_543         7121           859         2645         4431         6217         784CIP2B_544         7126           860         2646         4432         6218         784CIP2B_545         7127           861         2647         4433         6219         784CIP2B_546         7130           862         2648         4434         6220         784CIP2B_547         7131			4421	6207		
851         2637         4423         6209         784CIP2B_536         7104           852         2638         4424         6210         784CIP2B_537         7105           853         2639         4425         6211         784CIP2B_538         7105           854         2540         4426         6212         784CIP2B_539         7109           855         2641         4427         6213         784CIP2B_540         7109           856         2642         4428         6214         784CIP2B_541         7119           857         2643         4429         6215         784CIP2B_542         7120           858         2644         4430         6216         784CIP2B_543         7121           859         2645         4431         6217         784CIP2B_544         7126           860         2646         4432         6218         784CIP2B_545         7127           861         2647         4433         6219         784CIP2B_546         7130           862         2648         4434         6220         784CIP2B_548         7144           863         2649         4435         6221         784CIP2B_549         7159				6208		
852         2638         4424         6210         784CIP2B_537         7105           853         2639         4425         6211         784CIP2B_538         7105           854         2540         4426         6212         784CIP2B_539         7109           855         2641         4427         6213         784CIP2B_540         7109           856         2642         4428         6214         784CIP2B_541         7119           857         2643         4429         6215         784CIP2B_542         7120           858         2644         4430         6216         784CIP2B_543         7121           859         2645         4431         6217         784CIP2B_544         7126           860         2646         4432         6218         784CIP2B_545         7127           861         2647         4433         6219         784CIP2B_546         7130           862         2648         4434         6220         784CIP2B_548         7144           863         2649         4435         6221         784CIP2B_548         7144           864         2650         4436         6222         784CIP2B_549         7159			4423	6209	784CIP2B_536	
853         2639         4425         621_         784CIP2B_538         7105           854         2640         4426         6212         784CIP2B_539         7109           855         2641         4427         6213         784CIP2B_540         7109           856         2642         4428         6214         784CIP2B_541         7119           857         2643         4429         6215         784CIP2B_542         7120           858         2644         4430         6216         784CIP2B_543         7121           859         2645         4431         6217         784CIP2B_544         7126           860         2646         4432         6218         784CIP2B_545         7127           861         2647         4433         6219         784CIP2B_546         7130           862         2648         4434         6220         784CIP2B_547         7131           863         2649         4435         6221         784CIP2B_548         7144           864         2650         4436         6222         784CIP2B_549         7159			4424	6210	784CIP2B_537	
854         2640         4426         6212         784CIP2B_539         7109           855         2641         4427         6213         784CIP2B_540         7109           856         2642         4428         6214         784CIP2B_541         7119           857         2643         4429         6215         784CIP2B_542         7120           858         2644         4430         6216         784CIP2B_543         7121           859         2645         4431         6217         784CIP2B_544         7126           860         2646         4432         6218         784CIP2B_545         7127           861         2647         4433         6219         784CIP2B_546         7130           862         2648         4434         6220         784CIP2B_547         7131           863         2649         4435         6221         784CIP2B_548         7144           864         2650         4436         6222         784CIP2B_549         7159			4425	6211	784CIP2B 538	
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858         2644         4430         6216         784CIP2B_543         7121           859         2645         4431         6217         784CIP2B_544         7126           860         2646         4432         6218         784CIP2B_545         7127           861         2647         4433         6219         784CIP2B_546         7130           862         2648         4434         6220         784CIP2B_547         7131           863         2649         4435         6221         784CIP2B_548         7144           864         2650         4436         6222         784CIP2B_549         7159				6214	784CIP2B 541	
858     2644     4430     6216     784CIP2B_543     7121       859     2645     4431     6217     784CIP2B_544     7126       860     2646     4432     6218     784CIP2B_545     7127       861     2647     4433     6219     784CIP2B_546     7130       862     2648     4434     6220     784CIP2B_547     7131       863     2649     4435     6221     784CIP2B_548     7144       864     2650     4436     6222     784CIP2B_549     7159			4429	6215	784CIP2B_542	7120
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860     2646     4432     6218     784CIP2B 545     7127       861     2647     4433     6219     784CIP2B 546     7130       862     2648     4434     6220     784CIP2B 547     7131       863     2649     4435     6221     784CIP2B 548     7144       864     2650     4436     6222     784CIP2B 549     7159			4431	6217	784CIP2B 544	
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862 2648 4434 6220 784CIP2B_547 7131 863 2649 4435 6221 784CIP2B_548 7144 864 2650 4436 6222 784CIP2B_549 7159				6219	784CIP2B_546	
864 2650 4436 6222 784CIP2B 549 7159				6220	784CIP2B_547	
965 4430 6222 784CIP2B 549 7159				6221		7144
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	000	2651	4437	6223	784CIP2B_550	7163

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885         2671         4457         6243         784CIP2B_570         7260           886         2672         4458         6244         784CIP2B_571         7265           887         2673         4459         6244         784CIP2B_573         7275           888         2674         4460         6246         784CIP2B_573         7275           889         2675         4461         6247         784CIP2B_574         7279           890         2676         4462         6248         784CIP2B_574         7279           891         2677         4463         6249         784CIP2B_576         7283           891         2677         4463         6249         784CIP2B_576         7283           893         2679         4465         6250         784CIP2B_577         7287           893         2679         4465         6252         784CIP2B_579         7308           895         2681         4466         6252         784CIP2B_579         7308           895         2681         4467         6253         784CIP2B_581         7309           897         2683         4469         6255         784CIP2B_581         7319						
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887         2673         4459         6245         784CIP2B_572         7268           888         2674         4460         6246         784CIP2B_573         7275           889         2675         4461         6247         784CIP2B_574         7279           890         2676         4462         6248         784CIP2B_575         7283           891         2677         4463         6249         784CIP2B_576         7283           892         2678         4464         6250         784CIP2B_577         7287           893         2679         4465         6251         784CIP2B_579         7301           894         2680         4466         6252         784CIP2B_580         7301           895         2681         4467         6253         784CIP2B_581         7309           897         2683         4469         6255         784CIP2B_581         7309           899         2684         4471         6257         784CIP2B_583         7320           899         2685         4471         6257         784CIP2B_583         7326           900         2686         4472         6258         784CIP2B_586         7334	1					
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894         2680         4466         6252         784CTP2B_579         7308           895         2681         4467         6253         784CTP2B_580         7308           896         2682         4468         6254         784CTP2B_581         7309           897         2683         4469         6255         784CTP2B_582         7319           898         2684         4470         6256         784CTP2B_583         7320           899         2685         4471         6257         784CTP2B_584         7326           900         2686         4472         6258         784CTP2B_586         7326           901         2687         4473         6259         784CTP2B_586         7334           902         2688         4474         6260         784CTP2B_586         7337           903         2689         4475         6261         784CTP2B_587         7337           903         2690         4476         6262         784CTP2B_589         7344           905         2691         4477         6263         784CTP2B_590         7355           906         2692         4478         6264         784CTP2B_592         7363						
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896						
897         2683         4469         6255         784CIP2B_582         7319           898         2684         4470         6256         784CIP2B_583         7320           899         2685         4471         6257         784CIP2B_584         7326           900         2686         4471         6258         784CIP2B_585         7326           901         2687         4473         6259         784CIP2B_586         7334           902         2688         4474         6260         784CIP2B_588         7337           903         2689         4475         6261         784CIP2B_589         7334           905         2691         4476         6262         784CIP2B_589         7334           905         2691         4477         6263         784CIP2B_589         7344           905         2691         4477         6263         784CIP2B_589         7345           906         2692         4478         6264         784CIP2B_591         7363           907         2693         4479         6265         784CIP2B_593         7365           908         2694         4480         6266         784CIP2B_593         7368						
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905         2691         4477         '6263         784CIP2B 590         7355           906         2692         4478         6264         784CIP2B 591         7363           907         2693         4479         6265         784CIP2B 592         7363           908         .2694         4480         6266         784CIP2B 593         7365           909         2695         4481         6267         784CIP2B 595         7368           910         2696         4482         6268         784CIP2B 595         7369           911         2697         4483         6269         784CIP2B 595         7372           912         2698         4484         6270         784CIP2B 595         7375           913         2699         4485         6271         784CIP2B 600         7381           914         2700         4486         6272         784CIP2B 601         7363           915         2701         4487         6273         784CIP2B 602         7367           916         2702         4488         6274         784CIP2B 603         7391           917         2703         4489         6275         784CIP2B 604         7393 <td>904</td> <td>2690</td> <td>4476</td> <td></td> <td></td> <td></td>	904	2690	4476			
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908         .2694         4480         6266         784CIP2B_593         7365           909         2695         4481         6267         784CIP2B_594         7368           910         2696         4482         6268         784CIP2B_595         7369           911         2697         4483         6269         784CIP2B_596         7372           912         2698         4484         6270         784CIP2B_599         7375           913         2699         4485         6271         784CIP2B_600         7381           914         2700         4486         6272         784CIP2B_600         7381           915         2701         4487         6273         784CIP2B_602         7387           916         2702         4488         6274         784CIP2B_603         7391           917         2703         4489         6275         784CIP2B_604         7393           918         2704         4490         6276         784CIP2B_605         7395           919         2705         4491         6277         784CIP2B_606         7397           920         2706         4492         6278         784CIP2B_608         7405	907	2693	4479		-	
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911         2697         4483         6269         784CIP2E_596         7372           912         2698         4484         6270         784CIP2B_599         7375           913         2699         4485         6271         784CIP2B_600         7381           914         2700         4486         6272         784CIP2B_601         7383           915         2701         4487         6273         784CIP2B_602         7387           916         2702         4488         6274         784CIP2B_603         7391           917         2703         4489         6275         784CIP2B_603         7393           918         2704         4490         6276         784CIP2B_605         7395           919         2705         4491         6277         784CIP2B_606         7397           920         2706         4492         6278         784CIP2B_606         7397           921         2707         4493         6279         784CIP2B_608         7405           922         2708         4494         6280         784CIP2B_609         7406           923         2709         4495         6281         784CIP2B_610         7406		2696	4482	6268	784CIP2B 595	7369
913         2699         4485         6271         784CIP2B 600         7381           914         2700         4486         6272         784CIP2B 601         7383           915         2701         4487         6273         784CIP2B 602         7387           916         2702         4488         6274         784CIP2B 603         7391           917         2703         4489         6275         784CIP2B 604         7393           918         2704         4490         6276         784CIP2B 605         7395           919         2705         4491         6277         784CIP2B 606         7397           920         2706         4492         6278         784CIP2B 607         7399           921         2707         4493         6279         784CIP2B 608         7405           922         2708         4494         6280         784CIP2B 609         7406           923         2709         4495         6281         784CIP2B 610         7406           924         2710         4496         6282         784CIP2B 611         7409           925         2711         4497         6283         784CIP2B 612         7410		2697	4483	6269		
913         2699         4485         6271         784CIP2B_600         7381           914         2700         4486         6272         784CIP2B_601         7383           915         2701         4487         6273         784CIP2B_602         7387           916         2702         4488         6274         784CIP2B_603         7391           917         2703         4489         6275         784CIP2B_604         7393           918         2704         4490         6276         784CIP2B_605         7395           919         2705         4491         6277         784CIP2B_606         7397           920         2706         4492         6278         784CIP2B_607         7399           921         2707         4493         6279         784CIP2B_608         7405           922         2708         4494         6280         784CIP2B_609         7406           923         2709         4495         6281         784CIP2B_611         7409           925         2711         4496         6282         784CIP2B_611         7409           925         2711         4497         6283         784CIP2B_612         7410		2698		6270	784CIP2B_599	7375
914         2700         4486         6272         784CIP2B_601         7383           915         2701         4487         6273         784CIP2B_602         7387           916         2702         4488         6274         784CIP2B_603         7391           917         2703         4489         6275         784CIP2B_604         7393           918         2704         4490         6276         784CIP2B_605         7395           919         2705         4491         6277         784CIP2B_606         7397           920         2706         4492         6278         784CIP2B_607         7399           921         2707         4493         6279         784CIP2B_608         7405           922         2708         4494         6280         784CIP2B_609         7406           923         2709         4495         6281         784CIP2B_610         7406           924         2710         4496         6282         784CIP2B_611         7409           925         2711         4497         6283         784CIP2B_612         7410           926         2712         4498         6284         784CIP2B_613         7411			4485	6271	784CIP2B 600	
916         2702         4488         6274         784CIP2B 603         7391           917         2703         4489         6275         784CIP2B 604         7393           918         2704         4490         6276         784CIP2B 605         7395           919         2705         4491         6277         784CIP2B 606         7397           920         2706         4492         6278         784CIP2B 607         7399           921         2707         4493         6279         784CIP2B 608         7405           922         2708         4494         6280         784CIP2B 609         7406           923         2709         4495         6281         784CIP2B 610         7406           924         2710         4496         6282         784CIP2B 611         7409           925         2711         4497         6283         784CIP2B 612         7410           926         2712         4498         6284         784CIP2B 613         7411			4486	6272	784CIP2B 601	
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918         2704         4490         6276         784CIP2B 605         7395           919         2705         4491         6277         784CIP2B 606         7397           920         2706         4492         6278         784CIP2B 607         7399           921         2707         4493         6279         784CIP2B 608         7405           922         2708         4494         6280         784CIP2B 609         7406           923         2709         4495         6281         784CIP2B 610         7406           924         2710         4496         6282         784CIP2B 611         7409           925         2711         4497         6283         784CIP2B 612         7410           926         2712         4498         6284         784CIP2B 613         7411			4488	6274	784CIP2B_603	
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921         2707         4493         6279         784CIP2B 608         7405           922         2708         4494         6280         784CIP2B 609         7406           923         2709         4495         6281         784CIP2B 610         7406           924         2710         4496         6282         784CIP2B 611         7409           925         2711         4497         6283         784CIP2B 612         7410           926         2712         4498         6284         784CIP2B 613         7411			4491	6277	784CIP2B 606	7397
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930		2714	4500	6286	784CIP2B 615	7418
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934 2720 4506 6292 784CIP23 621 7425 935 2721 4507 6293 784CIP23 621 7427 936 2722 4508 6294 784CIP23 623 7428 937 2723 4508 6294 784CIP23 623 7428 938 2724 4510 6295 784CIP23 625 7435 938 2724 4510 6295 784CIP23 625 7435 939 2725 4511 6297 784CIP23 625 7437 940 2726 4512 6298 784CIP23 627 7439 940 2726 4512 6298 784CIP23 627 7439 941 2727 4513 6298 784CIP23 627 7439 941 2727 4513 6298 784CIP23 628 7440 942 645 645 645 645 645 645 645 645 645 645			4504	6290	784CIP2B_619	7423
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936 2722 4508 6294 784CIP28 623 7428 937 2723 4508 6295 784CIP28 624 7430 938 2724 4510 6295 784CIP28 624 7430 939 2725 4511 6297 784CIP28 626 7437 939 2725 4511 6297 784CIP28 626 7437 940 2726 4512 6298 784CIP28 626 7437 940 2726 4512 6298 784CIP28 626 7437 941 2727 4513 6299 784CIP28 628 7440 942 2728 4514 6300 784CIP28 628 7440 943 2728 4515 6301 784CIP28 629 7442 943 2729 4515 6301 784CIP28 630 7450 944 2730 4516 6302 784CIP28 631 7451 945 2731 4517 6303 784CIP28 632 7452 946 2732 4518 6304 784CIP28 633 7457 948 2733 4519 6305 784CIP28 634 7457 948 2734 4520 6306 784CIP28 637 7451 949 2735 4521 6307 784CIP28 637 7459 949 2735 4521 6307 784CIP28 637 7463 950 2736 4522 6308 784CIP28 637 7463 951 2737 4523 6309 784CIP28 637 7463 952 2738 4524 6310 784CIP28 637 7468 953 2739 4526 6312 784CIP28 639 7468 953 2739 4526 6312 784CIP28 639 7468 953 2739 4526 6312 784CIP28 639 7468 955 2741 4527 6313 784CIP28 640 7473 955 2743 4529 6315 784CIP28 640 7473 955 2743 4529 6315 784CIP28 640 7473 955 2743 4529 6315 784CIP28 647 7481 955 2743 4529 6315 784CIP28 647 7481 956 2746 4531 6310 784CIP28 647 7481 957 2746 4530 6316 784CIP28 647 7481 958 2744 4530 6316 784CIP28 647 7487 958 2744 4530 6316 784CIP28 647 7487 958 2746 4531 6317 784CIP28 647 7487 958 2746 4531 6317 784CIP28 647 7487 959 2765 4531 6317 784CIP28 647 7487 959 2765 4531 6317 784CIP28 647 7487 959 2765 4531 6317 784CIP28 647 7487 959 2765 4531 6317 784CIP28 647 7487 959 2765 4531 6317 784CIP28 647 7487 959 2765 4531 6317 784CIP28 647 7487 959 2765 4531 6317 784CIP28 647 7487 959 2765 4531 6317 784CIP28 647 7487 959 2765 4531 6317 784CIP28 647 7487 959 2765 4531 6317 784CIP28 647 7487 959 2765 4531 6317 784CIP28 647 7487 959 2765 4531 6317 784CIP28 647 7487 959 2765 4531 6317 784CIP28 657 7551 960 2766 4532 6318 784CIP28 657 7551 960 2766 4536 6332 784CIP28 657 7551 977 2763 4545 6333 784CIP28 657 7551 979 2755 4543 6333 784CIP28 657 7551 979 2756 4548 6331 784CIP28 657 7551 979 2756 4548 6331 784CIP28 657 7551 979 2756 4548 6331 784CIP28 667 7557 979 2756 45			4506	6292	784CIP2B_621	7426
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945         2731         4517         6303         784CIP2B 632         7452           946         2732         4518         6304         784CIP2B 633         7454           947         2733         4519         6305         784CIP2B 635         7459           948         2734         4520         6306         784CIP2B 635         7459           949         2735         4521         6306         784CIP2B 635         7461           950         2736         4522         6308         784CIP2B 637         7463           951         2737         4523         6309         784CIP2B 638         7466           952         2738         4524         6310         784CIP2B 638         7466           952         2738         4525         6311         784CIP2B 630         7473           953         2739         4525         6311         784CIP2B 640         7473           955         2741         4527         6313         784CIP2B 641         7481           955         2741         4527         6313         784CIP2B 641         7481           956         2742         4528         6314         784CIP2B 644         7483			4516	6302	784CIP2B_631	7451
947 2733 4519 6305 784C1P2B 634 7457 948 2734 4520 6306 784C1P2B 635 7459 949 2735 4521 6307 784C1P2B 635 7461 950 2736 4522 6308 784C1P2B 637 7463 951 2737 4523 6309 784C1P2B 637 7463 951 2737 4523 6309 784C1P2B 638 7466 952 2738 4524 6310 784C1P2B 638 7466 953 2739 4524 6310 784C1P2B 640 7473 953 2739 4525 6311 784C1P2B 640 7473 955 2740 4526 6312 784C1P2B 641 7481 955 2741 4527 6313 784C1P2B 641 7482 956 2742 4528 6314 784C1P2B 643 7482 957 2743 4529 6315 784C1P2B 643 7482 958 2744 4530 6316 784C1P2B 645 7485 959 2745 4531 6317 784C1P2B 645 7485 959 2745 4531 6317 784C1P2B 646 7486 960 2746 4532 6318 784C1P2B 646 7486 960 2746 4532 6318 784C1P2B 647 7487 961 2747 4533 6319 784C1P2B 648 7491 962 2748 4534 6320 784C1P2B 648 7491 962 2748 4536 6312 784C1P2B 648 7491 963 2749 4535 6321 784C1P2B 649 7492 964 2750 4536 6322 784C1P2B 659 7494 964 2750 4536 6322 784C1P2B 651 7498 966 2752 4638 6324 784C1P2B 657 7594 966 2753 4539 6325 784C1P2B 657 7594 969 2755 4541 6337 784C1P2B 657 7594 969 2755 4541 6337 784C1P2B 657 7594 969 2756 4542 6328 784C1P2B 657 7594 970 2756 4542 6338 784C1P2B 657 7594 971 2757 4543 6327 784C1P2B 657 7519 972 2758 4541 6327 784C1P2B 657 7519 973 2759 4545 6331 784C1P2B 657 7519 974 2750 4554 6532 784C1P2B 657 7519 975 2751 4537 6323 784C1P2B 657 7519 970 2756 4542 6328 784C1P2B 657 7519 971 2757 4543 6330 784C1P2B 657 7519 972 2758 4544 6330 784C1P2B 657 7519 973 2759 4545 6331 784C1P2B 666 7539 974 2760 4546 6332 784C1P2B 667 7533 975 2751 4553 6331 784C1P2B 667 7533 977 2763 4549 6331 784C1P2B 667 7533 978 2766 4542 6328 784C1P2B 657 7521 979 2758 4541 6330 784C1P2B 667 7539 979 2756 4543 6330 784C1P2B 667 7539 979 2756 4543 6330 784C1P2B 667 7539 979 2756 4545 6331 784C1P2B 667 7539 979 2765 4555 6311 784C1P2B 667 7539 980 2766 4552 6338 784C1P2B 667 7559 981 2767 4553 633 784C1P2B 667 7559 982 2768 4554 6340 784C1P2B 667 7559 982 2768 4555 6341 784C1P2B 667 7559 983 2766 4552 6338 784C1P2B 667 7559 984 2770 4556 6342 784C1P2B 667 7557				1	784CIP2B_632	7452
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985 2771 4557 6343 784CIP23 672 7582 986 2772 4558 6344 784CIP2B 673 7587 987 2773 4559 6345 784CIP2B 674 7589 988 2774 4560 6346 784CIP2B 675 7597				<del></del>		
986 2772 4558 6344 784CIP2B 673 7587 987 2773 4559 6345 784CIP2B 674 7589 988 2774 4560 6346 784CIP2B 675 7597	985					
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000	988	2774				
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994	2780	4566	6352	784CIP2B_680	
995	2781	4567	6353	784CIP23_681	7623 7629
996	2782	4568	6354	784CIP2B_683	
997	2783	4569	6355	784CIP2B 683	7630
998	2784	4570	6356	784CIP2B_684	7633 7635
999	2785	4571	6357	784CIP2B 686	1
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1001	2787	4573	6359	784CIP2B_687	7639
1002	2788	4574	1	784CIP2B_688	7646
1002	2789	4574	6360	784CIP2B_689	7647
1003	2790		6361	784CIP2B_690	7648
1005	2791	4576	6362	784CIP2B_691	7658
1005	L	4577	6363	784CIP2B_692	7664
1007	2792	4578	6364	784CIP2B_693	7664
1007	2793	4579	6365	784CIP2B_695	7674
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	2796	4582	6368	784CIP2B_698	7681
1011	2797	4583	6369	784CIP2B_699	7688
1012	2798	4584	6370	784CIP2B_700	'/693
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	2800	4586	6372	784CIP2B_702	7715
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1016	2802	4588	6374	784CIP2B_704	7718
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1059	2845	4631	6417	784CIP2B_748	7862
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1074	2859 2860	4645	6431	784CIP2B_762	7923
1075	2860	4646	6432	784CIP2B_763	7924
1076	2862	4647	6433	784CIP2B_764	7925
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1080	2866	4651 4652	6437	784CIP2B_768	7934
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1082	2868	4654	6439 6440	784CIP2B_770	7942
1083	2869	4655	6441	784CIP2B_771	7945
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1087	2873	4659	6445	784CIP2B_775 784CIP2B_776	7952
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1089	2875	4661	6447	784CIP2B_777 784CIP2B_778	7954
1090	2876	4662	6448	784CIP2B 779	7957
1091	2877	4663	6449	784CIP2B 780	7958
1092	2878	4664	6450	784CIP2B 781	7961
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1109	2895	4681	6467	784CIP2B 798	8020
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1111	2897	4683	6469	784CIP2B 800	8022
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1172	2958	4744		784CIP2B_860	8209
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1174	2960		6531	784CIP2B_862	8214
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1189	2975	4761	6547	784CIP2B_877	8260
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	2979	4765	6551	784CIP2B_882	8274
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1199	2985	4771	6557	784CIP2B_888	8289
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1253	3039	4825	6611	784CIP2B_942	8434
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1255	3041	4827	6613	784CIP2B_944 784CIP2B_945	8439
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1263	3049	4835		784CIP2B_952	8464
1264	3050	4836	6621 6622	784CIP2B_953	8465
1265	3051	4837	6623	784CIF2B_954	8467
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1427   3213   4999   6785   784C1PZC 14   2185     1429   3211   5000   6786   784C1PZC 15   2089     1429   3215   5001   6787   784C1PZC 16   2901     1430   3215   5002   6788   784C1PZC 17   2902     1431   3217   5003   6789   784C1PZC 17   2902     1431   3217   5003   6789   784C1PZC 18   2905     1432   3218   5004   6790   784C1PZC 19   2948     1433   3219   5005   6791   784C1PZC 19   2948     1434   3220   5006   6792   784C1PZC 19   2948     1434   3220   5006   6792   784C1PZC 21   2959     1435   3221   5007   6793   784C1PZC 22   2965     1436   3222   5008   6794   784C1PZC 22   2965     1437   3223   5009   6795   784C1PZC 22   2965     1438   3224   5010   6796   784C1PZC 24   2970     1440   3226   5012   6798   784C1PZC 24   2970     1441   3227   5013   6797   784C1PZC 26   2987     1440   3226   5012   6798   784C1PZC 27   2991     1441   3227   5013   6799   784C1PZC 27   2991     1442   3228   5014   6800   784C1PZC 28   2991     1443   3229   5015   6801   784C1PZC 29   3017     1444   3230   5016   6802   784C1PZC 29   3017     1445   3231   5017   6803   784C1PZC 31   3050     1446   3232   5018   6804   784C1PZC 33   3357     1446   3232   5018   6801   784C1PZC 33   3357     1446   3233   5019   6805   784C1PZC 34   3432     1449   3235   5021   6806   784C1PZC 34   3432     1449   3235   5021   6806   784C1PZC 34   3432     1449   3235   5021   6807   784C1PZC 34   3432     1449   3235   5021   6807   784C1PZC 34   3432     1449   3236   5019   6805   784C1PZC 34   3432     1449   3237   5023   6809   784C1PZC 34   3432     1449   3236   5019   6805   784C1PZC 34   3432     1450   3236   5020   6806   784C1PZC 34   3432     1460   3236   5022   6808   784C1PZC 34   3438     1451   3237   5023   6809   784C1PZC 34   3466     1453   3234   5020   6806   784C1PZC 35   3488     1458   3244   5020   6806   784C1PZC 36   3438     1458   3244   5020   6806   784C1PZC 36   3488     1458   3245   5031   6807   784C1PZC 36   3488     1468   3235   5036   6812   784C1PZC 55   3531     1468				6783	784CIP2C_12	1955
1428   3214   \$5000   \$6786   784CLPZC 15   2889     1429   3215   \$5001   \$6786   784CLPZC 15   2889     1430   3215   \$5002   \$6788   784CLPZC 16   2901     1431   3217   \$5003   \$6789   784CLPZC 17   2902     1431   3217   \$5003   \$6789   784CLPZC 18   2905     1432   3218   \$5004   \$6790   784CLPZC 18   2904     1433   3219   \$5005   \$6791   784CLPZC 19   2948     1434   3220   \$5006   \$6792   784CLPZC 20   2958     1435   3221   \$5007   \$6792   784CLPZC 20   2958     1436   3222   \$5009   \$6793   784CLPZC 22   2965     1437   3223   \$5009   \$6794   784CLPZC 22   2965     1438   3224   \$5009   \$6795   784CLPZC 23   2966     1439   3224   \$5010   \$6796   784CLPZC 24   2970     1439   3224   \$5010   \$6796   784CLPZC 25   2985     1440   3226   \$5012   \$6798   784CLPZC 27   2991     1441   3227   \$5013   \$6799   784CLPZC 27   2991     1442   3228   \$5014   \$6800   784CLPZC 27   2991     1443   3229   \$5015   \$6801   784CLPZC 28   2981     1444   3220   \$5016   \$6802   784CLPZC 29   3017     1446   3232   \$5017   \$6803   784CLPZC 31   3050     1445   3231   \$5017   \$6803   784CLPZC 31   33357     1446   3232   \$5018   \$6804   784CLPZC 31   33357     1448   3234   \$5020   \$6806   784CLPZC 33   33359     1449   3233   \$5019   \$6807   784CLPZC 36   3439     1449   3233   \$5019   \$6807   784CLPZC 36   3439     1450   3236   \$5022   \$6808   784CLPZC 36   3439     1451   3237   \$5023   \$6809   784CLPZC 36   3439     1452   3238   \$5024   \$6801   784CLPZC 36   3439     1453   3234   \$5020   \$6806   784CLPZC 36   3439     1451   3237   \$5036   \$6807   784CLPZC 36   3439     1452   3238   \$5024   \$6810   784CLPZC 36   3439     1453   3234   \$5020   \$6806   784CLPZC 36   3439     1459   3241   \$5020   \$6808   784CLPZC 36   3439     1460   3246   \$5025   \$6911   784CLPZC 49   3466     1458   3241   \$5026   \$6912   784CLPZC 49   3466     1458   3241   \$503   \$6919   784CLPZC 49   3466     1458   3244   \$503   \$6919   784CLPZC 55   3551     1466   3252   \$5038   \$6824   784CLPZC 57   3536     1467   3263   \$5044   \$683						1955
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1430   3215   SODO						2889
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1432 3218 5004 5790 784C1P2C_19 2948 1433 3219 5005 6791 784C1P2C_19 2948 1434 3220 5006 6792 784C1P2C_21 2959 1435 3221 5007 6793 784C1P2C_21 2959 1435 3221 5007 6793 784C1P2C_22 2959 1435 3221 5007 6793 784C1P2C_22 2966 1437 3223 5009 6795 784C1P2C_23 2966 1439 3224 5010 6796 784C1P2C_24 2970 1439 3224 5010 6796 784C1P2C_24 2970 1439 3225 5011 6797 784C1P2C_27 2993 1440 3226 5012 6798 784C1P2C_27 2993 1441 3227 5013 6799 784C1P2C_28 2993 1441 3227 5013 6799 784C1P2C_28 2993 1442 3228 5014 6800 784C1P2C_28 2993 1443 3229 5015 6801 784C1P2C_28 2993 1444 3229 5015 6801 784C1P2C_28 2993 1444 3220 5016 6802 784C1P2C_31 3050 1445 3231 5017 6803 784C1P2C_31 3050 1446 3222 5018 6807 784C1P2C_33 3357 1446 3222 5018 6804 784C1P2C_33 3359 1447 3233 5019 6805 784C1P2C_33 3359 1448 3224 5020 6806 784C1P2C_33 3359 1449 3235 5021 6807 784C1P2C_33 3359 1449 3235 5021 6807 784C1P2C_33 3359 1449 3235 5020 6806 784C1P2C_33 3491 1450 3236 5022 6806 784C1P2C_35 3438 1451 3237 5023 6809 784C1P2C_36 3439 1452 3238 5024 6810 784C1P2C_36 3439 1453 3239 5025 6811 784C1P2C_43 3466 1453 3239 5025 6811 784C1P2C_43 3466 1453 3239 5025 6811 784C1P2C_43 3466 1453 3239 5025 6811 784C1P2C_43 3466 1458 3244 5020 6602 784C1P2C_36 3488 1459 3244 5020 6603 784C1P2C_36 3449 1456 3224 5028 6814 784C1P2C_43 3466 1453 3239 5025 6811 784C1P2C_43 3466 1453 3239 5025 6811 784C1P2C_43 3466 1453 3239 5025 6811 784C1P2C_43 3466 1458 3244 5030 6816 784C1P2C_43 3468 1458 3244 5030 6816 784C1P2C_45 3488 1459 3245 5031 6817 784C1P2C_45 3488 1459 3245 5031 6817 784C1P2C_45 3488 1459 3245 5031 6817 784C1P2C_45 3488 1459 3245 5036 6812 784C1P2C_45 3488 1459 3245 5036 6812 784C1P2C_65 3531 1468 3259 5036 6827 784C1P2C_56 3531 1469 3255 5041 6827 784C1P2C_56 3531 1469 3255 5041 6827 784C1P2C_56 3531 1469 3255 5041 6827 784C1P2C_56 3531 1469 3255 5041 6826 784C1P2C_56 3531 1470 3256 5046 6832 784C1P2C_56 3531 1479 3256 5046 6832 784C1P2C_56 3531 1479 3256 5046 6832 784C1P2C_66 3551 1479 3263 5049 6835 784C1P2C_66 3551 1479 3266 5052 6838 784C1P2C_66 3551 1479 3266 5			1	1		2902
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1456         3242         5028         6814         784CIP2C 45         3488           1457         3243         5029         6815         784CIP2C 46         3488           1458         3244         5030         6816         784CIP2C 47         3491           1459         3245         5031         6817         784CIP2C 48         3493           1460         3246         5032         6818         784CIP2C 49         3494           1461         3247         5033         6819         784CIP2C 50         3495           1462         3248         5034         6820         784CIP2C 51         3496           1463         3249         5035         6821         784CIP2C 52         3503           1464         3250         5036         6822         784CIP2C 52         3503           1465         3251         5037         6823         784CIP2C 54         3504           1466         3252         5038         6824         784CIP2C 55         3511           1467         3253         5039         6825         784CIP2C 56         3531           1468         3254         5040         6826         784CIP2C 57         3536			<u> </u>			
1457         3243         5029         6815         784CIP2C_46         3488           1458         3244         5030         6816         784CIP2C_47         3491           1459         3245         5031         6817         784CIP2C_48         3493           1460         3246         5032         6818         784CIP2C_49         3494           1461         3247         5033         6819         784CIP2C_50         3495           1462         3248         5034         6820         784CIP2C_51         3496           1463         3249         5035         6821         784CIP2C_52         3503           1464         3250         5036         6822         784CIP2C_52         3503           1465         3251         5037         6823         784CIP2C_54         3504           1466         3252         5038         6824         784CIP2C_55         3531           1466         3252         5038         6824         784CIP2C_55         3531           1467         3253         5039         6825         784CIP2C_56         3531           1468         3254         5040         6826         784CIP2C_57         3536						
1458         3244         5030         6816         784CIP2C_47         3491           1459         3245         5031         6817         784CIP2C_48         3493           1460         3246         5032         6818         784CIP2C_49         3494           1461         3247         5033         6819         784CIP2C_50         3495           1462         3248         5034         6820         784CIP2C_51         3496           1463         3249         5035         6821         784CIP2C_52         3503           1464         3250         5036         6822         784CIP2C_53         3503           1465         3251         5037         6823         784CIP2C_53         3503           1465         3251         5037         6823         784CIP2C_53         3504           1466         3252         5038         6824         784CIP2C_55         3511           1467         3253         5039         6825         784CIP2C_56         3531           1468         3254         5040         6826         784CIP2C_56         3531           1470         3256         5042         6828         784CIP2C_58         3548	1457					
1459         3245         5031         6817         784CIP2C 48         3493           1460         3246         5032         6818         784CIP2C 49         3494           1461         3247         5033         6819         784CIP2C 50         3495           1462         3248         5034         6820         784CIP2C 51         3496           1463         3249         5035         6821         784CIP2C 52         3503           1464         3250         5036         6822         784CIP2C 53         3503           1465         3251         5037         6823         784CIP2C 54         3504           1466         3252         5038         6824         784CIP2C 55         3511           1467         3253         5039         6825         784CIP2C 56         3531           1468         3254         5040         6826         784CIP2C 57         3536           1469         3255         5041         6827         784CIP2C 57         3536           1470         3256         5042         6828         784CIP2C 59         3548           1471         3257         5043         6829         784CIP2C 59         3548						
1460         3246         5032         6818         784CIP2C 49         3494           1461         3247         5033         6819         784CIP2C_50         3495           1462         3248         5034         6820         784CIP2C_51         3496           1463         3249         5035         6821         784CIP2C_52         3503           1464         3250         5036         6822         784CIP2C_53         3503           1465         3251         5037         6823         784CIP2C_53         3504           1466         3252         5038         6824         784CIP2C_55         3511           1467         3253         5039         6825         784CIP2C_56         3531           1468         3254         5040         6826         784CIP2C_57         3536           1469         3255         5041         6827         784CIP2C_58         3546           1470         3256         5042         6828         784CIP2C_58         3548           1471         3257         5043         6829         784CIP2C_60         3551           1472         3258         5044         6830         784CIP2C_61         3553	1459				L	
1461         3247         5033         6819         784CIP2C_50         3495           1462         3248         5034         6820         784CIP2C_51         3496           1463         3249         5035         6821         784CIP2C_52         3503           1464         3250         5036         6822         784CIP2C_53         3503           1465         3251         5037         6823         784CIP2C_54         3503           1466         3252         5038         6824         784CIP2C_55         3511           1467         3253         5039         6825         784CIP2C_55         3511           1468         3254         5040         6826         784CIP2C_58         3546           1470         3255         5041         6827         784CIP2C_58         3546           1470         3256         5042         6828         784CIP2C_58         3548           1471         3257         5043         6829         784CIP2C_59         3548           1471         3257         5043         6829         784CIP2C_60         3551           1472         3258         5044         6830         784CIP2C_61         3553	1460					
1462         3248         5034         6820         784CIP2C 51         3496           1463         3249         5035         6821         784CIP2C 52         3503           1464         3250         5036         6822         784CIP2C 53         3503           1465         3251         5037         6823         784CIP2C 54         3504           1466         3252         5038         6824         784CIP2C 55         3511           1467         3253         5039         6825         784CIP2C 56         3531           1468         3254         5040         6826         784CIP2C 57         3536           1469         3255         5041         6827         784CIP2C 58         3546           1470         3256         5042         6828         784CIP2C 59         3548           1471         3257         5043         6829         784CIP2C 60         3551           1472         3258         5044         6830         784CIP2C 61         3553           1473         3259         5045         6831         784CIP2C 62         3564           1474         3260         5046         6832         784CIP2C 62         3564	1461	3247				
1463         3249         5035         6821         784CIP2C 52         3503           1464         3250         5036         6822         784CIP2C 53         3503           1465         3251         5037         6823         784CIP2C 54         3504           1466         3252         5038         6824         784CIP2C 55         3511           1467         3253         5039         6825         784CIP2C 56         3531           1468         3254         5040         6826         784CIP2C 57         3536           1469         3255         5041         6827         784CIP2C 58         3546           1470         3256         5042         6828         784CIP2C 59         3548           1471         3257         5043         6829         784CIP2C 59         3548           1471         3257         5043         6829         784CIP2C 60         3551           1472         3258         5044         6830         784CIP2C 61         3553           1473         3259         5045         6831         784CIP2C 62         3564           1474         3260         5046         6832         784CIP2C 63         3572	1462	3248				
1464         3250         5036         6822         784CIP2C 53         3503           1465         3251         5037         6823         784CIP2C 54         3504           1466         3252         5038         6824         784CIP2C 55         3511           1467         3253         5039         6825         784CIP2C 56         3531           1468         3254         5040         6826         784CIP2C 57         3536           1469         3255         5041         6827         784CIP2C 58         3546           1470         3256         5042         6828         784CIP2C 59         3548           1471         3257         5043         6829         784CIP2C 50         3551           1472         3258         5044         6830         784CIP2C 60         3551           1473         3259         5045         6831         784CIP2C 61         3553           1474         3260         5046         6832         784CIP2C 63         3567           1475         3261         5047         6833         784CIP2C 64         3572           1476         3262         5048         6834         784CIP2C 65         3573	1463	3249	5035			
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1466         3252         5038         6824         784CIP2C 55         3511           1467         3253         5039         6825         784CIP2C 56         3531           1468         3254         5040         6826         784CIP2C 57         3536           1469         3255         5041         6827         784CIP2C 58         3546           1470         3256         5042         6828         784CIP2C 59         3548           1471         3257         5043         6829         784CIP2C 60         3551           1472         3258         5044         6830         784CIP2C 61         3553           1473         3259         5045         6831         784CIP2C 61         3553           1474         3260         5046         6832         784CIP2C 61         3553           1474         3260         5046         6832         784CIP2C 63         3567           1475         3261         5047         6833         784CIP2C 64         3572           1476         3262         5048         6834         784CIP2C 65         3573           1477         3263         5049         6835         784CIP2C 66         3574	1465	3251	5037			
1467         3253         5039         6825         784CIP2C 56         3531           1468         3254         5040         6826         784CIP2C 57         3536           1469         3255         5041         6827         784CIP2C 58         3546           1470         3256         5042         6828         784CIP2C 59         3548           1471         3257         5043         6829         784CIP2C 60         3551           1472         3258         5044         6830         784CIP2C 61         3553           1473         3259         5045         6831         784CIP2C 61         3553           1473         3259         5045         6831         784CIP2C 61         3553           1474         3260         5046         6832         784CIP2C 61         3553           1475         3261         5047         6833         784CIP2C 63         3567           1476         3262         5048         6834         784CIP2C 65         3573           1477         3263         5049         6835         784CIP2C 66         3574           1478         3264         5050         6836         784CIP2C 66         3574	1466	3252				
1468         3254         5040         6826         784CIP2C 57         3536           1469         3255         5041         6827         784CIP2C 58         3546           1470         3256         5042         6828         784CIP2C 59         3548           1471         3257         5043         6829         784CIP2C 60         3551           1472         3258         5044         6830         784CIP2C 61         3553           1473         3259         5045         6831         784CIP2C 62         3564           1474         3260         5046         6832         784CIP2C 62         3567           1475         3261         5047         6833         784CIP2C 64         3572           1476         3262         5048         6834         784CIP2C 65         3573           1477         3263         5049         6835         784CIP2C 66         3574           1478         3264         5050         6836         784CIP2C 67         3583           1479         3265         5051         6837         784CIP2C 69         3623           1480         3266         5052         6638         784CIP2C 69         3623	1467	3253	5039			
1469         3255         5041         6827         784CIP2C 58         3546           1470         3256         5042         6828         784CIP2C 59         3548           1471         3257         5043         6829         784CIP2C 60         3551           1472         3258         5044         6830         784CIP2C 61         3553           1473         3259         5045         6831         784CIP2C 62         3564           1474         3260         5046         6832         784CIP2C 63         3567           1475         3261         5047         6833         784CIP2C 64         3572           1476         3262         5048         6834         784CIP2C 65         3573           1477         3263         5049         6835         784CIP2C 65         3574           1478         3264         5050         6836         784CIP2C 67         3583           1479         3265         5051         6837         784CIP2C 68         3615           1480         3266         5052         6838         784CIP2C 69         3623           1481         3267         5053         6839         784CIP2C 70         3629	1468	3254	5040			
1470         3256         5042         6828         784CIP2C 59         3548           1471         3257         5043         6829         784CIP2C 60         3551           1472         3258         5044         6830         784CIP2C 61         3553           1473         3259         5045         6831         784CIP2C 62         3564           1474         3260         5046         6832         784CIP2C 63         3567           1475         3261         5047         6833         784CIP2C 64         3572           1476         3262         5048         6834         784CIP2C 65         3573           1477         3263         5049         6835         784CIP2C 66         3574           1478         3264         5050         6836         784CIP2C 67         3583           1479         3265         5051         6837         784CIP2C 68         3615           1480         3266         5052         6838         784CIP2C 69         3623           1481         3267         5053         6839         784CIP2C 70         3629           1482         3268         5054         6840         784CIP2C 71         3666	1469	3255				
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1473         3259         5045         6831         784CIP2C 62         3564           1474         3260         5046         6832         784CIP2C 63         3567           1475         3261         5047         6833         784CIP2C 64         3572           1476         3262         5048         6834         784CIP2C 65         3573           1477         3263         5049         6835         784CIP2C 66         3574           1478         3264         5050         6836         784CIP2C 67         3583           1479         3265         5051         6837         784CIP2C 68         3615           1480         3266         5052         6838         784CIP2C 69         3623           1481         3267         5053         6839         784CIP2C 70         3629           1482         3268         5054         6840         784CIP2C 71         3666           1483         3269         5055         6841         784CIP2C 72         3667           1484         3270         5056         6842         784CIP2C 73         3906		3258				
1474     3260     5046     6832     784CIP2C 63     3567       1475     3261     5047     6833     784CIP2C 64     3572       1476     3262     5048     6834     784CIP2C 65     3573       1477     3263     5049     6835     784CIP2C 66     3574       1478     3264     5050     6836     784CIP2C 67     3583       1479     3265     5051     6837     784CIP2C 68     3615       1480     3266     5052     6838     784CIP2C 69     3623       1481     3267     5053     6839     784CIP2C 70     3629       1482     3268     5054     6840     784CIP2C 71     3666       1483     3269     5055     6841     784CIP2C 72     3667       1484     3270     5056     6842     784CIP2C 73     3906		3259	5045			
1475         3261         5047         6833         784CIP2C 64         3572           1476         3262         5048         6834         784CIP2C 65         3573           1477         3263         5049         6835         784CIP2C 66         3574           1478         3264         5050         6836         784CIP2C 67         3583           1479         3265         5051         6837         784CIP2C 68         3615           1480         3266         5052         6638         784CIP2C 69         3623           1481         3267         5053         6839         784CIP2C 70         3629           1482         3268         5054         6840         784CIP2C 71         3666           1483         3269         5055         6841         784CIP2C 72         3667           1484         3270         5056         6842         784CIP2C 73         3906	<u> </u>	3260	5046			
1476         3262         5048         6834         784CIP2C 65         3573           1477         3263         5049         6835         784CIP2C 66         3574           1478         3264         5050         6836         784CIP2C 67         3583           1479         3265         5051         6837         784CIP2C 68         3615           1480         3266         5052         6838         784CIP2C 69         3623           1481         3267         5053         6839         784CIP2C 70         3629           1482         3268         5054         6840         784CIP2C 71         3666           1483         3269         5055         6841         784CIP2C 72         3667           1484         3270         5056         6842         784CIP2C 73         3906		3261				
1477         3263         5049         6835         784CIP2C 66         3574           1478         3264         5050         6836         784CIP2C 67         3583           1479         3265         5051         6837         784CIP2C 68         3615           1480         3266         5052         6838         784CIP2C 69         3623           1481         3267         5053         6839         784CIP2C 70         3629           1482         3268         5054         6840         784CIP2C 71         3666           1483         3269         5055         6841         784CIP2C 72         3667           1484         3270         5056         6842         784CIP2C 73         3906		3262	5048			
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1479     3265     5051     6837     784CIP2C 68     3615       1480     3266     5052     6838     784CIP2C 69     3623       1481     3267     5053     6839     784CIP2C 70     3629       1482     3268     5054     6840     784CIP2C 71     3666       1483     3269     5055     6841     784CIP2C 72     3667       1484     3270     5056     6842     784CIP2C 73     3906		3264	5050			
1480     3266     5052     6838     784CIP2C_69     3623       1481     3267     5053     6839     784CIP2C_70     3629       1482     3268     5054     6840     784CIP2C_71     3666       1483     3269     5055     6841     784CIP2C_72     3667       1484     3270     5056     6842     784CIP2C_73     3906		3265				
1481     3267     5053     6839     784CIP2C 70     3629       1482     3268     5054     6840     784CIP2C 71     3666       1483     3269     5055     6841     784CIP2C 72     3667       1484     3270     5056     6842     784CIP2C 73     3906       1485     3270     5056     6842     784CIP2C 73     3906		3266				
1482     3268     5054     6840     784CIP2C 71     3666       1483     3269     5055     6841     784CIP2C 72     3667       1484     3270     5056     6842     784CIP2C 73     3906       1485     3270     5056     6842     784CIP2C 73     3906		3267				
1483     3269     5055     6841     784CIP2C_72     3667       1484     3270     5056     6842     784CIP2C_73     3906       1485     3271		3268				
1484 3270 5056 6842 784CIP2C_73 3906		3269				
1495			5056			
	1485	3271	5057	6843	784CIP2C 74	3912

Seq   10   NO   Seq   10   NO   Of full	CORO VIN NO	Table 92	1 000 70 115		· · · · · · · · · · · · · · · · · · ·	
Length   Innucleotide   Length   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence	SEQ ID NO:	SEQ ID	SEQ ID NO:	SEQ ID	Priority	SEQ ID
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1493   3279   5065   6851   784CIPZC 82   4300     1494   3280   5066   6852   784CIPZC 81   4360     1495   3281   5067   6883   784CIPZC 83   4362     1496   3282   5068   6854   784CIPZC 85   6371     1497   3283   5069   6855   784CIPZC 87   6373     1498   3284   5070   6856   784CIPZC 87   6378     1498   3284   5070   6856   784CIPZC 87   6378     1499   3285   5071   6857   784CIPZC 89   4378     1500   3286   5072   6858   784CIPZC 89   4378     1501   3287   5073   6859   784CIPZC 89   4378     1501   3287   5073   6859   784CIPZC 89   4421     1503   3289   5075   6861   784CIPZC 91   4409     1503   3289   5075   6861   784CIPZC 92   4421     1504   2390   5076   6862   784CIPZC 94   4426     1505   3291   5077   6863   784CIPZC 95   4430     1506   3329   5079   6864   784CIPZC 96   4435     1506   3329   5079   6865   784CIPZC 96   4431     1508   3294   5080   6866   784CIPZC 97   4440     1508   3294   5080   6866   784CIPZC 99   4440     1511   3297   5081   6867   784CIPZC 99   4440     1511   3297   5081   6867   784CIPZC 99   4440     1511   3298   5082   6868   784CIPZC 99   4440     1511   3299   5085   6867   784CIPZC 99   4440     1511   3299   5085   6869   784CIPZC 99   4440     1511   3299   5085   6867   784CIPZC 99   4440     1511   3299   5085   6869   784CIPZC 100   4441     1511   3299   5085   6869   784CIPZC 100   4441     1511   3300   5086   6867   784CIPZC 100   4445     1513   3301   5087   6873   784CIPZC 100   4465     1514   3300   5086   6872   784CIPZC 100   4465     1515   3301   5087   6873   784CIPZC 100   4465     1516   3302   5088   6874   784CIPZC 100   4465     1517   3303   5089   6875   784CIPZC 100   4465     1518   3304   5090   6076   784CIPZC 107   4481     1519   3305   5091   6877   784CIPZC 107   4481     1519   3305   5091   6878   784CIPZC 107   4481     1520   3314   5090   6076   784CIPZC 107   4481     1521   3307   5098   6889   784CIPZC 114   4506     1522   3308   5094   6880   784CIPZC 115   4599     1523   3314   5100   6886   784CIPZC 117				1		3989
1494 3280 5066 6852 784CIP2C 83 4360 1495 3281 5067 6853 784CIP2C 84 4362 1496 3282 5068 6854 784CIP2C 85 4371 1497 3283 5069 6855 784CIP2C 86 4373 1498 3284 5070 6856 784CIP2C 87 4376 1499 3285 5071 6857 784CIP2C 89 4378 1500 3286 5072 6858 784CIP2C 89 4378 1501 3287 5073 6859 784CIP2C 91 4409 1503 3289 5075 6860 784CIP2C 91 4409 1503 3289 5075 6860 784CIP2C 92 4421 1503 3289 5075 6861 784CIP2C 93 4421 1504 3290 5076 6862 784CIP2C 93 4421 1505 3291 5077 6863 784CIP2C 93 4430 1506 3292 5078 6864 784CIP2C 94 4426 1505 3291 5077 6863 784CIP2C 95 4430 1506 3292 5078 6866 784CIP2C 95 4430 1507 3293 5079 6865 784CIP2C 95 4430 1508 3294 5080 6866 784CIP2C 98 4436 1509 3295 5080 6866 784CIP2C 99 4440 1510 3296 5082 6866 784CIP2C 99 4440 1510 3296 5082 6866 784CIP2C 99 4440 1510 3296 5082 6866 784CIP2C 99 4440 1510 3296 5082 6866 784CIP2C 99 4440 1511 3297 5083 6867 784CIP2C 99 4440 1510 3298 5081 6867 784CIP2C 99 4440 1511 3297 5083 6866 784CIP2C 100 4441 1512 3298 5084 6870 784CIP2C 101 4442 1513 3309 5085 6871 784CIP2C 103 4462 1514 3300 5086 6872 784CIP2C 103 4462 1515 3301 5087 6873 784CIP2C 103 4462 1518 3302 5088 6874 784CIP2C 104 4466 1518 3302 5088 6874 784CIP2C 104 4466 1518 3303 5089 6875 784CIP2C 108 4483 1518 3304 5089 6875 784CIP2C 108 4483 1519 3305 5091 6877 784CIP2C 108 4483 1520 3306 5092 6878 784CIP2C 109 4484 1522 3308 5094 6880 784CIP2C 104 4466 1523 3309 5095 6881 784CIP2C 104 4466 1524 3311 5097 6883 784CIP2C 110 4486 1523 3309 5095 6881 784CIP2C 110 4486 1524 3311 5097 6883 784CIP2C 110 4486 1525 3311 5097 6883 784CIP2C 110 4486 1526 3312 5098 6886 784CIP2C 110 4486 1527 3313 5099 6886 784CIP2C 110 4486 1528 3314 5100 6886 784CIP2C 110 4486 1528 3314 5100 6886 784CIP2C 110 4486 1528 3311 5097 6883 784CIP2C 112 4499 1524 3310 5096 6889 784CIP2C 110 4486 1526 3312 5098 6889 784CIP2C 112 4537 1536 3311 5097 6883 784CIP2C 113 4506 1526 3312 5098 6886 784CIP2C 114 4506 1526 3312 5098 6889 784CIP2C 113 4506 1526 3312 5098 6896 784CIP2C 114 4506 1526 3311 5097 6889 784CIP2C 114 4506 1536 3311 5097 6889						4295
1495 3281 5067 6853 784CIP2C_84 4362 1496 3282 5068 6854 784CIP2C_86 4371 1497 3283 5069 6855 784CIP2C_86 4373 1498 3284 5070 6856 784CIP2C_87 4376 1499 3285 5071 6857 784CIP2C_87 4376 1499 3285 5071 6857 784CIP2C_89 4378 1500 3286 5072 6858 784CIP2C_99 4382 1501 3287 5073 6859 784CIP2C_91 4403 1502 3288 5074 6860 784CIP2C_91 4403 1503 3289 5074 6860 784CIP2C_91 4421 1504 3290 5076 6862 784CIP2C_94 4421 1504 3290 5076 6862 784CIP2C_94 4421 1505 3291 5077 6863 784CIP2C_94 4421 1506 3292 5078 6864 784CIP2C_95 4430 1506 3292 5078 6864 784CIP2C_95 4430 1507 3293 5079 6865 784CIP2C_96 4435 1509 3295 5080 6866 784CIP2C_98 4439 1509 3295 5081 6867 784CIP2C_99 4440 1510 3286 5082 6868 784CIP2C_99 4440 1511 3297 5083 6869 784CIP2C_104 4442 1511 3297 5083 6869 784CIP2C_104 4442 1511 3297 5083 6869 784CIP2C_104 4442 1511 3299 5085 6871 784CIP2C_104 4442 1512 3298 5084 6870 784CIP2C_104 4442 1513 3299 5085 6871 784CIP2C_109 4442 1514 3300 5086 6872 784CIP2C_109 4442 1515 3301 5087 6873 784CIP2C_109 4462 1516 3302 5088 6874 784CIP2C_109 4462 1517 3303 5089 6875 784CIP2C_109 4462 1518 3304 5090 6676 784CIP2C_109 4462 1518 3300 5086 6872 784CIP2C_109 4462 1519 3305 5081 6877 784CIP2C_109 4462 1518 3300 5088 6874 784CIP2C_109 4462 1518 3301 5087 6873 784CIP2C_109 4489 1519 3305 5081 6874 784CIP2C_109 4489 1522 3308 5094 6880 784CIP2C_108 4489 1523 3309 5095 6676 784CIP2C_108 4481 1519 3305 5098 6874 784CIP2C_109 4481 1519 3305 5098 6881 784CIP2C_108 4481 1523 3309 5095 6881 784CIP2C_111 44506 1524 3311 5097 6883 784CIP2C_111 44506 1525 3311 5097 6883 784CIP2C_118 45506 1526 3312 5098 6886 784CIP2C_118 45506 1528 3311 5097 6889 784CIP2C_119 45506 1528 3311 5097 6889 784CIP2C_119 45506 1528 3311 5097 6889 784CIP2C_119 45506 1528 3311 5097 6889 784CIP2C_119 45506 1528 3311 5097 6889 784CIP2C_119 45506 1528 3311 5097 6889 784CIP2C_119 45506 1528 3311 5097 6889 784CIP2C_119 45506 1528 3311 5097 6889 784CIP2C_119 45506 1528 3311 5097 6889 784CIP2C_119 45506 1528 3311 5097 6889 784CIP2C_119 45506 1538 3314 5100 6886 784CIP2C_119 4550			5065	6851	784CIP2C_82	4300
1496   3282   5068   6854   784CIP2C_85   4371     1497   3283   5069   6855   784CIP2C_87   4376     1498   3284   5070   6685   784CIP2C_87   4376     1499   3285   5071   6857   784CIP2C_87   4376     1500   3286   5072   6858   784CIP2C_89   4378     1501   3287   5073   6859   784CIP2C_91   4403     1502   3288   5074   6660   784CIP2C_91   4403     1503   3288   5074   6660   784CIP2C_91   4421     1504   3280   5075   6862   784CIP2C_91   4422     1505   3291   5077   6663   784CIP2C_93   4421     1506   3292   5078   6864   784CIP2C_95   4435     1507   3293   5079   6865   784CIP2C_97   4436     1508   3294   5080   6866   784CIP2C_97   4436     1509   3295   5079   6865   784CIP2C_97   4440     1510   3286   5080   6866   784CIP2C_98   4439     1509   3295   5081   6867   784CIP2C_98   4443     1510   3296   5082   6868   784CIP2C_98   4440     1511   3297   5083   6869   784CIP2C_98   4440     1511   3297   5083   6869   784CIP2C_100   4441     1512   3298   5084   6870   784CIP2C_100   4441     1513   3299   5086   6871   784CIP2C_100   4442     1514   3300   5086   6872   784CIP2C_100   4465     1515   3301   5087   6873   784CIP2C_100   4465     1518   3304   5090   6076   784CIP2C_100   4469     1519   3305   5089   6874   784CIP2C_100   4469     1518   3304   5090   6076   784CIP2C_100   4469     1519   3305   5089   6874   784CIP2C_100   4469     1519   3305   5091   6877   784CIP2C_100   4469     1520   3306   5092   6878   784CIP2C_101   4466     1521   3307   5093   6880   784CIP2C_101   4466     1522   3308   5094   6880   784CIP2C_110   4466     1523   3309   5095   6881   784CIP2C_110   4466     1524   3311   5097   6882   784CIP2C_110   4466     1526   3312   5099   6886   784CIP2C_111   4506     1526   3313   5096   6886   784CIP2C_112   4596     1526   3313   5096   6880   784CIP2C_112   4596     1527   3313   5097   6881   784CIP2C_114   4506     1528   3314   5100   6886   784CIP2C_114   4506     1528   3314   5100   6886   784CIP2C_115   4538     1536   3322   5108   6890   784CIP		3280	5066	6852	784CIP2C_83	4360
1497   3283   5069   6655   784CIP2C_86   4373     1498   3284   5070   6656   784CIP2C_87   4376     1499   3285   5071   66857   784CIP2C_89   4378     1500   3286   5072   6688   784CIP2C_90   4382     1501   3287   5073   6689   784CIP2C_91   4409     1502   3288   5074   66850   784CIP2C_91   4409     1503   3289   5075   6661   784CIP2C_91   4421     1504   3290   5076   6662   784CIP2C_94   4421     1505   3291   5077   6663   784CIP2C_94   4421     1506   3292   5078   6664   784CIP2C_95   4430     1507   3293   5079   6865   784CIP2C_95   4430     1508   3294   5080   6866   784CIP2C_96   4435     1509   3295   5081   6687   784CIP2C_99   4440     1510   3296   5082   6686   784CIP2C_99   4440     1511   3297   5083   66867   784CIP2C_100   4441     1511   3297   5083   6686   784CIP2C_101   4442     1512   3298   5084   6870   784CIP2C_102   4455     1513   3299   5085   6671   784CIP2C_102   4455     1514   3300   5086   6872   784CIP2C_104   4466     1515   3301   5087   6873   784CIP2C_104   4466     1516   3302   5088   6874   784CIP2C_105   4467     1517   3303   5089   6875   784CIP2C_106   4477     1518   3304   5090   6676   784CIP2C_107   4481     1519   3305   5091   6877   784CIP2C_107   4481     1519   3305   5091   6877   784CIP2C_107   4481     1519   3305   5091   6877   784CIP2C_107   4481     1519   3305   5091   6877   784CIP2C_107   4481     1519   3305   5091   6877   784CIP2C_107   4481     1519   3305   5091   6877   784CIP2C_107   4481     1519   3305   5091   6877   784CIP2C_107   4481     1519   3305   5091   6887   784CIP2C_107   4481     1522   3308   5094   6880   784CIP2C_110   4486     1523   3310   5096   6882   784CIP2C_111   4596     1524   3310   5096   6880   784CIP2C_111   4596     1525   3311   5007   6881   784CIP2C_111   4596     1526   3312   5098   6880   784CIP2C_114   4506     1526   3312   5098   6880   784CIP2C_114   4516     1528   3314   5100   6886   784CIP2C_114   4516     1529   3315   5101   6889   784CIP2C_121   4527     1531   3315   5101   6889	1495	3281	5067	6853	784CIP2C 84	4362
1498   3284   5070   6655   784CIP2C 87   4376     1499   3285   5071   6857   784CIP2C 89   4378     1500   3285   5072   66858   784CIP2C 90   4382     1501   3287   5073   6659   784CIP2C 91   4409     1502   3288   5074   6850   784CIP2C 91   4409     1503   3289   5075   6861   784CIP2C 93   4421     1504   3280   5076   6862   784CIP2C 93   4421     1505   3291   5077   6863   784CIP2C 94   4426     1505   3291   5077   6863   784CIP2C 94   4426     1506   3292   5078   6864   784CIP2C 95   4435     1507   3293   5079   6865   784CIP2C 96   4435     1508   3294   5080   6866   784CIP2C 98   4435     1509   3295   5081   6867   784CIP2C 98   4439     1510   3296   5082   6868   784CIP2C 99   4440     1510   3296   5082   6868   784CIP2C 99   4440     1511   3297   5083   6869   784CIP2C 100   4441     1512   3298   5084   6870   784CIP2C 101   4442     1513   3299   5085   6871   784CIP2C 103   4462     1514   3300   5086   6872   784CIP2C 103   4462     1515   3301   5087   6873   784CIP2C 104   4466     1515   3301   5087   6873   784CIP2C 108   4483     1518   3304   5090   6676   784CIP2C 108   4483     1519   3305   5091   6877   784CIP2C 108   4483     1519   3305   5091   6877   784CIP2C 108   4483     1519   3305   5091   6877   784CIP2C 108   4483     1519   3306   5092   6878   784CIP2C 108   4483     1519   3307   5093   6879   784CIP2C 108   4483     1519   3308   5094   6880   784CIP2C 108   4483     1520   3308   5095   6877   784CIP2C 108   4483     1521   3307   5093   6879   784CIP2C 108   4483     1522   3308   5094   6880   784CIP2C 108   4483     1523   3308   5095   6878   784CIP2C 108   4483     1524   3310   5096   6882   784CIP2C 108   4483     1525   3311   5097   6883   784CIP2C 114   4506     1526   3312   5098   6884   784CIP2C 115   4599     1523   3318   5100   6886   784CIP2C 116   4514     1526   3312   5098   6884   784CIP2C 116   4514     1527   3313   5100   6889   784CIP2C 120   4527     1531   3322   5110   6897   784CIP2C 123   4528     1534   3320   5106   6892   78	1496	3282	5068	6854	784CIP2C 85	4371
1498   3284   5070   6855   784CTP2C 87   4376     1499   3285   5071   6857   784CTP2C 89   4378     1500   3286   5072   6858   784CTP2C 90   4382     1501   3287   5073   6859   784CTP2C 91   4409     1502   3288   5074   6860   784CTP2C 91   4409     1503   3289   5075   6861   784CTP2C 93   4421     1504   3290   5076   6862   784CTP2C 94   4426     1505   3291   5077   6863   784CTP2C 94   4426     1506   3292   5078   6864   784CTP2C 95   4430     1506   3292   5078   6864   784CTP2C 96   4435     1507   3293   5079   6865   784CTP2C 98   4439     1508   3294   5580   6866   784CTP2C 98   4439     1509   3295   5081   6867   784CTP2C 99   4440     1510   3296   5082   6868   784CTP2C 100   4441     1511   3297   5083   6869   784CTP2C 100   4441     1512   3298   5084   6870   784CTP2C 101   4442     1513   3299   5085   6871   784CTP2C 102   4455     1514   3300   5086   6872   784CTP2C 103   4466     1515   3301   5087   6873   784CTP2C 104   4466     1516   3302   5088   6874   784CTP2C 107   4481     1519   3303   5089   6874   784CTP2C 107   4481     1519   3305   5089   6874   784CTP2C 107   4481     1519   3305   5089   6875   784CTP2C 107   4481     1519   3306   5082   6889   784CTP2C 108   4469     1516   3307   5089   6876   784CTP2C 109   4466     1516   3308   5094   6880   784CTP2C 101   4499     1520   3306   5092   6878   784CTP2C 101   4489     1521   3307   5089   6881   784CTP2C 111   4499     1522   3308   5094   6880   784CTP2C 112   4499     1523   3309   5095   6881   784CTP2C 114   4506     1524   3311   5097   6883   784CTP2C 115   4509     1526   3312   5098   6894   784CTP2C 117   4516     1527   3313   5099   6885   784CTP2C 117   4516     1528   3314   5100   6886   784CTP2C 127   4559     1534   3320   5106   6891   784CTP2C 127   4559     1535   3315   5101   6897   784CTP2C 127   4559     1536   3322   5106   6891   784CTP2C 127   4559     1539   3325   5111   6897   784CTP2C 127   4559     1539   3325   5111   6897   784CTP2C 137   4559     1534   3329   5115   6901   7	· 1497	3283	5069	6855	784CIP2C 86	4373
1499   3285   5071   6857   784CTP2C   59   4378   1500   3286   5072   6858   784CTP2C   50   4382   1501   3287   5073   6859   784CTP2C   51   4409   1502   3288   5074   6860   784CTP2C   52   4421   1503   3289   5075   6861   784CTP2C   52   4421   1504   3289   5076   6862   784CTP2C   54   4426   1505   3291   5077   6863   784CTP2C   54   4426   1505   3291   5077   6863   784CTP2C   55   4430   1506   3292   5078   6864   784CTP2C   56   4435   1507   3293   5079   6865   784CTP2C   57   4436   1507   3293   5079   6865   784CTP2C   59   4440   1508   3294   5080   6866   784CTP2C   59   4440   1510   3296   5082   6868   784CTP2C   59   4440   1511   3297   5083   6866   784CTP2C   59   4440   1511   3297   5083   6869   784CTP2C   102   4452   1513   3299   5085   6871   784CTP2C   102   4452   1513   3299   5085   6871   784CTP2C   102   4452   1513   3299   5085   6872   784CTP2C   103   4462   1514   3300   5086   6872   784CTP2C   104   4466   1515   3301   5087   6873   784CTP2C   107   4461   1517   3303   5089   6875   784CTP2C   107   4461   1518   3304   5090   6876   784CTP2C   109   4486   1520   3306   5092   6878   784CTP2C   109   4486   1520   3306   5092   6878   784CTP2C   109   4486   1521   3307   5083   6879   784CTP2C   109   4486   1521   3307   5093   6877   784CTP2C   109   4486   1521   3307   5093   6877   784CTP2C   109   4486   1521   3307   5093   6877   784CTP2C   109   4486   1521   3307   5093   6877   784CTP2C   109   4486   1521   3307   5093   6877   784CTP2C   109   4486   1521   3307   5093   6877   784CTP2C   109   4486   1521   3307   5093   6877   784CTP2C   109   4486   1521   3307   5093   6877   784CTP2C   110   4486   1521   3307   5093   6877   784CTP2C   110   4486   1521   3307   5093   6877   784CTP2C   110   4486   1521   3307   5093   6889   784CTP2C   117   4516   4514   4506   4514   4506   4514   4506   4514   4506   4514   4506   4514   4506   4514   4506   4514   4506   4514   4506   4514   4506   4514   4506   4514   4506   4514   4506   4514	1498	3284	5070	6856		
1500   3286   5072   6859   784CIP2C 50   4382   1501   3287   5073   6859   784CIP2C 51   4409   1502   3288   5074   6850   784CIP2C 92   4421   1503   3289   5075   6861   784CIP2C 93   4421   1504   3290   5076   6862   784CIP2C 94   4426   1505   3291   5077   6863   784CIP2C 94   4426   1505   3291   5077   6863   784CIP2C 95   4430   1506   3292   5078   6864   784CIP2C 96   4435   1507   3293   5079   6865   784CIP2C 96   4435   1507   3293   5079   6865   784CIP2C 97   4436   1508   3294   5080   6866   784CIP2C 98   4439   1509   3295   5081   6867   784CIP2C 99   4440   1510   3296   5082   6868   784CIP2C 99   4440   1511   3297   5083   6869   784CIP2C 100   4441   1511   3297   5083   6869   784CIP2C 100   4441   1511   3297   5083   6869   784CIP2C 100   4442   1512   3298   5084   6870   784CIP2C 103   4462   1514   3300   5086   6872   784CIP2C 103   4462   1514   3300   5086   6872   784CIP2C 104   4466   1515   3301   5087   6873   784CIP2C 105   4469   1516   3302   5088   6874   784CIP2C 105   4469   1518   3304   5090   6876   784CIP2C 107   4481   1518   3304   5090   6876   784CIP2C 107   4481   1519   3305   5081   6877   784CIP2C 107   4481   1520   3306   5092   6378   784CIP2C 107   4481   1520   3308   5094   6880   784CIP2C 110   4486   1523   3308   5094   6880   784CIP2C 111   4490   1522   3308   5095   6881   784CIP2C 113   4459   1524   3310   5086   6882   784CIP2C 113   4503   1524   3310   5096   6886   784CIP2C 114   4506   1525   3311   5097   6883   784CIP2C 115   4599   1523   3308   5094   6880   784CIP2C 114   4506   1525   3311   5097   6883   784CIP2C 117   4516   1528   3314   5100   6886   784CIP2C 117   4516   1528   3314   5100   6886   784CIP2C 117   4516   1528   3314   5100   6886   784CIP2C 117   4516   1528   3314   5100   6886   784CIP2C 117   4516   1528   3314   5100   6886   784CIP2C 117   4516   1528   3314   5100   6886   784CIP2C 121   4528   1530   3316   5102   6888   784CIP2C 121   4528   1533   3319   5105   6891   784CIP2C 122   4529   1533	1499	3285	5071	6857		
1501   3287   5073   6859   784CIP2C 31   4409     1502   3288   5074   6860   784CIP2C 32   4421     1503   3289   5075   6861   784CIP2C 32   4421     1504   3290   5076   6862   784CIP2C 34   4426     1505   3291   5077   6863   784CIP2C 34   4426     1506   3292   5078   6864   784CIP2C 36   4435     1507   3293   5079   6865   784CIP2C 36   4435     1508   3294   5080   6866   784CIP2C 39   4440     1509   3295   5081   6867   784CIP2C 39   4440     1510   3296   5082   6868   784CIP2C 39   4440     1511   3297   5083   6869   784CIP2C 30   4441     1511   3297   5083   6869   784CIP2C 30   4442     1512   3298   5084   6870   784CIP2C 30   4462     1513   3299   5085   6871   784CIP2C 30   4462     1514   3300   5086   6872   784CIP2C 30   4466     1515   3301   5087   6873   784CIP2C 30   4466     1516   3302   5088   6874   784CIP2C 30   4466     1517   3303   5089   6875   784CIP2C 30   4468     1518   3304   5090   6676   784CIP2C 30   4481     1520   3306   5092   6878   784CIP2C 30   4481     1521   3308   5091   6877   784CIP2C 30   4481     1520   3306   5092   6878   784CIP2C 30   4481     1521   3309   5095   6879   784CIP2C 30   4481     1522   3308   5094   6880   784CIP2C 31     1523   3309   5095   6881   784CIP2C 31     1524   3310   5096   6882   784CIP2C 31     1525   3311   5097   6883   784CIP2C 31     1526   3312   5098   6884   784CIP2C 31     1527   3313   5099   6885   784CIP2C 31     1528   3314   500   6886   784CIP2C 31     1529   3315   5101   6887   784CIP2C 31     1520   3316   5102   6888   784CIP2C 32     1531   3317   5103   6889   784CIP2C 32     1532   3318   5100   6886   784CIP2C 32     1533   3319   5105   6891   784CIP2C 32     1534   3320   5106   6892   784CIP2C 32     1535   3311   5097   6893   784CIP2C 32     1536   3322   5108   6894   784CIP2C 32     1536   3322   5108   6894   784CIP2C 32     1537   3333   5106   6899   784CIP2C 32   4559      1538   3324   5110   6899   784CIP2C 33   4568      1544   3330   5116   6902   784CIP2C 33   4568      1545   3331	1500	3286	1			
1502   3288   5074   6850   784CIP2C 92   4421     1503   3289   5075   6861   784CIP2C 93   4421     1504   3290   5076   6862   784CIP2C 93   4421     1505   3291   5077   6863   784CIP2C 95   4430     1506   3291   5077   6863   784CIP2C 95   4435     1507   3293   5079   6865   784CIP2C 96   4435     1508   3294   5080   6866   784CIP2C 97   4436     1508   3294   5080   6866   784CIP2C 98   4439     1509   3295   5081   6867   784CIP2C 99   4440     1510   3296   5082   6868   784CIP2C 100   4441     1511   3297   5083   6869   784CIP2C 100   4441     1511   3297   5083   6869   784CIP2C 101   4442     1512   3298   5084   6870   784CIP2C 102   4455     1513   3299   5085   6871   784CIP2C 103   4462     1514   3300   5086   6872   784CIP2C 104   4466     1515   3301   5087   6873   784CIP2C 105   4469     1516   3302   5088   6874   784CIP2C 106   4477     1517   3303   5089   6875   784CIP2C 107   4481     1518   3304   5090   6076   784CIP2C 109   4486     1518   3305   5091   6877   784CIP2C 109   4486     1520   3306   5092   6378   784CIP2C 110   4486     1521   3307   5093   6879   784CIP2C 101   4486     1522   3308   5094   6880   784CIP2C 111   4490     1523   3309   5095   6881   784CIP2C 113   4503     1524   3310   5096   6882   784CIP2C 114   4506     1525   3311   5097   6883   784CIP2C 115   4509     1528   3314   5100   6886   784CIP2C 116   4514     1528   3314   5100   6886   784CIP2C 117   4516     1528   3314   5100   6886   784CIP2C 121   4528     1530   3315   5101   6897   784CIP2C 124   4537     1531   3317   5103   6899   784CIP2C 127   4552     1533   3319   5105   6891   784CIP2C 127   4552     1534   3320   5106   6892   784CIP2C 127   4552     1536   3322   5108   6894   784CIP2C 127   4552     1537   3323   5106   6892   784CIP2C 127   4552     1538   3324   5110   6896   784CIP2C 127   4553     1539   3325   5111   6897   784CIP2C 127   4552     1530   3326   5112   6898   784CIP2C 127   4552     1531   3327   5113   6899   784CIP2C 137   4558     1544   3330   5116   6902	1501		L		I	
1503   3289   5075   6861   784CIP2C 93   4421						
1504   3250   5076   6862   784CIP2C 93   4426     1505   3291   5077   6863   784CIP2C 95   4430     1506   3292   5078   6864   784CIP2C 95   4430     1507   3293   5079   6865   784CIP2C 97   4436     1508   3294   5080   6866   784CIP2C 98   4439     1509   3295   5081   6867   784CIP2C 98   4439     1510   3296   5082   6868   784CIP2C 98   4439     1510   3296   5082   6868   784CIP2C 100   4441     1511   3297   5083   6869   784CIP2C 101   4442     1512   3298   5084   6870   784CIP2C 101   4442     1513   3299   5085   6971   784CIP2C 103   4462     1514   3300   5086   6872   784CIP2C 104   4466     1515   3301   5087   6873   784CIP2C 104   4466     1516   3302   5088   6874   784CIP2C 105   4469     1518   3304   5090   6876   784CIP2C 106   4477     1517   3303   5089   6877   784CIP2C 107   4481     1519   3305   5091   6877   784CIP2C 108   4483     1520   3306   5092   6878   784CIP2C 109   4486     1521   3307   5093   6879   784CIP2C 109   4486     1521   3307   5093   6879   784CIP2C 101   4490     1523   3308   5094   6880   784CIP2C 111   4490     1524   3310   5096   6882   784CIP2C 112   4499     1523   3308   5095   6881   784CIP2C 112   4499     1524   3311   5097   6883   784CIP2C 114   4506     1525   3311   5097   6883   784CIP2C 115   4509     1526   3312   5098   6884   784CIP2C 116   4514     1527   3313   5099   6885   784CIP2C 117   4516     1528   3314   5100   6886   784CIP2C 117   4516     1529   3315   5101   6887   784CIP2C 120   4527     1531   3317   5103   6889   784CIP2C 120   4527     1531   3317   5103   6889   784CIP2C 120   4527     1531   3327   5113   6899   784CIP2C 122   4529     1531   3321   5107   6893   784CIP2C 122   4528     1536   3322   5108   6894   784CIP2C 122   4551     1536   3322   5108   6894   784CIP2C 123   4532     1537   3331   5107   6893   784CIP2C 124   4551     1538   3324   5110   6896   784CIP2C 125   4551     1539   3325   5111   6897   784CIP2C 128   4555     1530   3326   5112   6898   784CIP2C 133   4592     1544   3330   5116   69			1_			
1505   3231   5077   6863   784CIP2C_95   4435     1506   3292   5078   6864   784CIP2C_96   4435     1507   3293   5079   6865   784CIP2C_97   4436     1508   3294   5080   6866   784CIP2C_99   4440     1510   3295   5081   6867   784CIP2C_99   4440     1510   3296   5082   6868   784CIP2C_101   4441     1511   3297   5083   6869   784CIP2C_101   4442     1512   3298   5084   6870   784CIP2C_102   4455     1513   3299   5085   6871   784CIP2C_102   4455     1514   3300   5086   6872   784CIP2C_105   4466     1515   3301   5087   6873   784CIP2C_105   4466     1515   3301   5087   6873   784CIP2C_105   4469     1516   3302   5088   6874   784CIP2C_105   4469     1518   3304   5090   6875   784CIP2C_106   4477     1518   3304   5090   6876   784CIP2C_107   4481     1519   3305   5091   6877   784CIP2C_109   4484     1520   3306   5092   6878   784CIP2C_109   4484     1521   3307   5093   6877   784CIP2C_109   4486     1521   3307   5093   6877   784CIP2C_110   4486     1522   3308   5094   6880   784CIP2C_110   4486     1524   3310   5096   6880   784CIP2C_111   4499     1523   3309   5095   6881   784CIP2C_112   4499     1524   3310   5096   6882   784CIP2C_113   4503     1525   3311   5097   6883   784CIP2C_114   4506     1526   3312   5098   6886   784CIP2C_116   4514     1529   3316   5100   6886   784CIP2C_116   4514     1529   3316   5100   6886   784CIP2C_117   4516     1528   3314   5100   6886   784CIP2C_118   4522     1530   3316   5102   6898   784CIP2C_120   4527     1531   3317   5103   6899   784CIP2C_120   4527     1531   3317   5103   6899   784CIP2C_120   4527     1531   3327   5113   6899   784CIP2C_120   4559     1534   3320   5106   6896   784CIP2C_120   4527     1531   3317   5103   6899   784CIP2C_120   4527     1531   3317   5103   6899   784CIP2C_120   4527     1531   3317   5103   6899   784CIP2C_120   4527     1531   3327   5113   6899   784CIP2C_120   4527     1534   3320   5106   6896   784CIP2C_120   4559     1534   3325   5111   6997   784CIP2C_133   4592     1544   3330   5116						
1506   3292   5078   6864   784CIP2C   56   4435     1507   3293   5079   6865   784CIP2C   97     4436   1508   3294   5080   6866   784CIP2C   98     4439   1509   3295   5081   6867   784CIP2C   99   4440     1510   3296   5082   6868   784CIP2C   99   4440     1511   3297   5083   6869   784CIP2C   100   4441     1511   3298   5084   6870   784CIP2C   101   4442     1512   3298   5084   6870   784CIP2C   102   4455     1514   3300   5086   6872   784CIP2C   103   4462     1515   3301   5087   6873   784CIP2C   104   4466     1515   3301   5087   6873   784CIP2C   105   4469     1516   3302   5088   6874   784CIP2C   105   4469     1517   3303   5089   6875   784CIP2C   107   4481     1518   3304   5090   6876   784CIP2C   108   4483     1519   3305   5091   6877   784CIP2C   109   4484     1520   3306   5092   6878   784CIP2C   101   4486     1521   3307   5093   6879   784CIP2C   110   4486     1522   3308   5094   6880   784CIP2C   111   4490     1523   3308   5094   6880   784CIP2C   111   4490     1524   3310   5096   6882   784CIP2C   114   4506     1525   3311   5097   6883   784CIP2C   114   4506     1526   3312   5098   6884   784CIP2C   116   4514     1527   3313   5099   6885   784CIP2C   117   4516     1528   3314   5100   6886   784CIP2C   117   4516     1529   3316   5102   6888   784CIP2C   117   4516     1529   3316   5102   6888   784CIP2C   117   4516     1520   3316   5102   6888   784CIP2C   127   4528     1531   3317   5103   6899   784CIP2C   129   4527     1531   3317   5103   6899   784CIP2C   129   4528     1531   3317   5103   6899   784CIP2C   129   4528     1532   3318   5104   6890   784CIP2C   127   4552     1533   3319   5105   6891   784CIP2C   127   4552     1534   3320   5106   6892   784CIP2C   127   4552     1535   3321   5107   6893   784CIP2C   129   4528     1536   3322   5108   6694   784CIP2C   129   4528     1537   3323   5109   6895   784CIP2C   129   4552     1538   3324   5110   6896   784CIP2C   130   4568     1544   3330   5116   6902   784CIP2C   135   4616						
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1508   3294   5080   6866   784CIP2C 98   4439					_	
1509   3295   5081   6867   784CIP2C 99   4440     1510   3296   5082   6868   784CIP2C 100   4441     1511   3297   5083   6869   784CIP2C 101   4442     1512   3298   5084   6870   784CIP2C 102   4455     1513   3299   5085   6971   784CIP2C 103   4466     1514   3300   5086   6872   784CIP2C 104   4466     1515   3301   5087   6873   784CIP2C 105   4469     1516   3302   5088   6974   784CIP2C 106   4477     1517   3303   5089   6875   784CIP2C 106   4477     1517   3303   5089   6875   784CIP2C 106   4477     1518   3304   5090   6876   784CIP2C 107   4481     1518   3304   5090   6876   784CIP2C 109   4484     1520   3306   5091   6877   784CIP2C 109   4484     1521   3307   5093   6879   784CIP2C 109   4486     1521   3307   5093   6879   784CIP2C 110   4486     1522   3308   5094   6880   784CIP2C 111   4490     1522   3308   5094   6880   784CIP2C 112   4499     1523   3309   5095   6881   784CIP2C 112   4499     1524   3310   5096   6882   784CIP2C 114   4506     1526   3311   5097   6883   784CIP2C 114   4506     1527   3313   5099   6885   784CIP2C 115   4509     1528   3314   5100   6886   784CIP2C 117   4516     1529   3316   5102   6888   784CIP2C 117   4526     1531   3317   5103   6889   784CIP2C 121   4528     1533   3319   5104   6889   784CIP2C 121   4528     1534   3320   5106   6892   784CIP2C 121   4528     1535   3321   5107   6893   784CIP2C 122   4527     1538   3324   5110   6896   784CIP2C 123   4532     1536   3322   5107   6893   784CIP2C 124   4537     1538   3324   5110   6896   784CIP2C 126   4551     1539   3325   5111   6897   784CIP2C 127   4552     1530   3365   5112   6898   784CIP2C 129   4567     1540   3326   5112   6898   784CIP2C 121   4528     1531   3327   5113   6899   784CIP2C 123   4585     1541   3327   5113   6899   784CIP2C 134   4609     1544   3330   5116   6890   784CIP2C 134   4609     1544   3330   5116   6890   784CIP2C 137   4568     1546   3332   5116   6890   784CIP2C 137   4568     1546   3333   5117   6903   784CIP2C 137   4618						L
1510   3296   5082   6868   784CIP2C_100   4441     1511   3297   5083   6869   784CIP2C_101   4442     1512   3298   5084   6870   784CIP2C_102   4455     1513   3299   5085   6971   784CIP2C_103   4462     1514   3300   5086   6872   784CIP2C_104   4466     1515   3301   5087   6873   784CIP2C_105   4469     1516   3302   5088   6874   784CIP2C_106   4477     1517   3303   5089   6875   784CIP2C_107   4481     1518   3304   5090   6876   784CIP2C_107   4481     1519   3305   5091   6877   784CIP2C_109   4484     1520   3306   5092   6878   784CIP2C_109   4486     1521   3307   5093   6879   784CIP2C_109   4486     1521   3307   5093   6879   784CIP2C_110   4486     1522   3308   5094   6880   784CIP2C_111   4490     1523   3309   5095   6881   784CIP2C_111   4490     1524   3310   5096   6882   784CIP2C_112   4499     1526   3311   5097   6883   784CIP2C_114   4506     1527   3313   5099   6885   784CIP2C_116   4514     1529   3316   5091   6887   784CIP2C_116   4514     1529   3315   5101   6687   784CIP2C_117   4516     1528   3314   5100   6686   784CIP2C_117   4516     1529   3315   5101   6687   784CIP2C_119   4525     1530   3316   5102   6888   784CIP2C_119   4525     1531   3317   5103   6689   784CIP2C_119   4525     1533   3319   5105   6891   784CIP2C_122   4529     1534   3320   5106   6689   784CIP2C_124   4537     1535   3321   5107   6893   784CIP2C_124   4537     1537   3323   5109   6895   784CIP2C_126   4551     1539   3325   5101   6896   784CIP2C_127   4552     1530   3316   5102   6898   784CIP2C_127   4552     1531   3317   5103   6899   784CIP2C_127   4552     1533   3321   5107   6893   784CIP2C_127   4552     1534   3320   5106   6692   784CIP2C_127   4552     1538   3324   5110   6896   784CIP2C_127   4552     1538   3324   5110   6896   784CIP2C_127   4552     1539   3325   5111   6897   784CIP2C_134   4509     1544   3330   5116   6902   784CIP2C_134   4569     1543   3329   5115   6901   784CIP2C_134   4609     1546   3332   5116   6902   786CIP2C_135   4616     1546   3332   51						
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1512   3298   5084   6870   784CTP2C_102   4455				6868	784CIP2C_100	4441
1513   3299   5085   6971   784CIP2C 103   4462     1514   3300   5086   6872   784CIP2C 104   4466     1515   3301   5087   6873   784CIP2C 105   4469     1516   3302   5088   6874   784CIP2C 106   4477     1517   3303   5089   6875   784CIP2C 107   4481     1518   3304   5090   6876   784CIP2C 108   4483     1519   3305   5091   6877   784CIP2C 108   4484     1520   3306   5092   6878   784CIP2C 109   4484     1521   3307   5093   6879   784CIP2C 110   4486     1521   3307   5093   6879   784CIP2C 111   4490     1522   3308   5094   6880   784CIP2C 112   4499     1523   3309   5095   6881   784CIP2C 113   4503     1524   3310   5096   6882   784CIP2C 114   4506     1525   3311   5097   6883   784CIP2C 115   4509     1526   3312   5099   6885   784CIP2C 116   4514     1527   3313   5099   6885   784CIP2C 117   4516     1528   3314   5100   6886   784CIP2C 117   4516     1529   3315   5101   6887   784CIP2C 121   4528     1530   3316   5102   6888   784CIP2C 120   4527     1531   3317   5103   6889   784CIP2C 121   4528     1532   3318   5104   6890   784CIP2C 121   4528     1533   3319   5105   6891   784CIP2C 122   4529     1534   3320   5106   6892   784CIP2C 122   4529     1535   3321   5107   6893   784CIP2C 124   4537     1536   3322   5108   6894   784CIP2C 124   4537     1537   3323   5109   6895   784CIP2C 124   4537     1538   3324   5110   6896   784CIP2C 124   4537     1538   3324   5110   6896   784CIP2C 126   4551     1539   3325   5111   6897   784CIP2C 128   4559     1530   3326   5112   6898   784CIP2C 129   4528     1531   3327   5113   6899   784CIP2C 120   4529     1538   3324   5110   6896   784CIP2C 123   4528     1536   3322   5108   6894   784CIP2C 124   4537     1536   3322   5108   6895   784CIP2C 127   4552     1538   3324   5110   6896   784CIP2C 128   4559     1540   3326   5112   6898   784CIP2C 130   4568     1541   3327   5113   6899   784CIP2C 130   4568     1541   3327   5113   6899   784CIP2C 131   4568     1543   3329   5115   6901   784CIP2C 134   4609     1546   3332   51			5083	6869	784CIP2C_101	4442
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1515   3301   5087   6873   784CIP2C_105   4469     1516   3302   5088   6874   784CIP2C_106   4477     1517   3303   5089   6875   784CIP2C_107   4481     1518   3304   5090   6876   784CIP2C_107   4481     1519   3305   5091   6877   784CIP2C_109   4484     1520   3306   5092   6878   784CIP2C_109   4484     1521   3307   5093   6879   784CIP2C_110   4486     1521   3308   5094   6880   784CIP2C_111   4490     1522   3308   5094   6880   784CIP2C_111   4490     1523   3309   5095   6681   784CIP2C_113   4503     1524   3310   5096   6882   784CIP2C_113   4506     1525   3311   5097   6883   784CIP2C_115   4509     1526   3312   5098   6884   784CIP2C_115   4509     1527   3313   5099   6885   784CIP2C_117   4516     1528   3314   5100   6886   784CIP2C_119   4525     1530   3316   5102   6888   784CIP2C_119   4525     1531   3317   5103   6889   784CIP2C_121   4528     1532   3318   5104   6889   784CIP2C_121   4528     1533   3319   5105   6891   784CIP2C_122   4529     1534   3320   5106   6892   784CIP2C_124   4537     1535   3321   5107   6893   784CIP2C_125   4538     1536   3322   5108   6894   784CIP2C_125   4538     1537   3323   5109   6895   784CIP2C_126   4551     1538   3324   5110   6896   784CIP2C_127   4552     1539   3325   5111   6897   784CIP2C_129   4567     1541   3327   5113   6899   784CIP2C_129   4567     1541   3327   5113   6899   784CIP2C_129   4567     1543   3328   5114   6900   784CIP2C_130   4588     1544   3327   5113   6899   784CIP2C_131   4588     1545   3331   5117   6903   784CIP2C_134   4609     1546   3332   5116   6902   784CIP2C_135   4585     1546   3332   5116   6902   784CIP2C_135   4585     1546   3333   5116   6902   784CIP2C_135   4616     1546   3333   5116   6902   784CIP2C_135   4616     1546   3333   5116   6904   784CIP2C_135   4616     1546   3333   5116   6904   784CIP2C_135   4616     1546   3333   5116   6904   784CIP2C_135   4616     1546   3333   5116   6904   784CIP2C_135   4616     1546   3333   5116   6904   784CIP2C_135   4616     1546   3333   51		3299	5085	6971	784CIP2C 103	4462
1516   3302   5088   6874   784CIP2C 105   4467		3300	5086	6872	784CIP2C 104	4466
1516	1515	3301	5087	6873	784CIP2C 105	4469
1517         3303         5089         6875         784CIP2C_107         4481           1518         3304         5090         6876         784CIP2C_108         4483           1519         3305         5091         6877         784CIP2C_110         4484           1520         3306         5092         6878         784CIP2C_111         4486           1521         3307         5093         6879         784CIP2C_111         4490           1522         3308         5094         6880         784CIP2C_113         4503           1523         3309         5095         6881         784CIP2C_113         4503           1524         3310         5096         6882         784CIP2C_114         4506           1525         3311         5097         6883         784CIP2C_115         4509           1526         3312         5098         6884         784CIP2C_116         4514           1527         3313         5099         6885         784CIP2C_117         4516           1528         3314         5100         6886         784CIP2C_118         4522           1529         3315         5101         6887         784CIP2C_120         <	1516	3302	5088	6974	784CIP2C 106	
1518         3304         5090         6876         784CIP2C_108         4483           1519         3305         5091         6877         784CIP2C_109         4484           1520         3306         5092         6878         784CIP2C_110         4486           1521         3307         5093         6879         784CIP2C_111         4490           1522         3308         5094         6880         784CIP2C_112         4499           1523         3309         5095         6861         784CIP2C_113         4503           1524         3310         5096         6882         784CIP2C_114         4506           1525         3311         5097         6883         784CIP2C_115         4509           1526         3312         5098         6884         784CIP2C_116         4514           1527         3313         5099         6885         784CIP2C_117         4516           1528         3314         5100         6886         784CIP2C_117         4516           1529         3315         5101         6887         784CIP2C_118         4525           1530         3316         5102         6888         784CIP2C_120         <	1517	3303	5089	6875	784CIP2C 107	
1519         3305         5091         6877         784CIP2C_109         4484           1520         3306         5092         6878         784CIP2C_110         4486           1521         3307         5093         6879         784CIP2C_111         4490           1522         3308         5094         6880         784CIP2C_112         4499           1523         3309         5095         6881         784CIP2C_114         4506           1524         3310         5096         6882         784CIP2C_114         4506           1525         3311         5097         6883         784CIP2C_115         4509           1526         3312         5098         6884         784CIP2C_116         4514           1527         3313         5099         6885         784CIP2C_117         4516           1528         3314         5100         6886         784CIP2C_118         4522           1529         3315         5101         6887         784CIP2C_119         4525           1530         3316         5102         6888         784CIP2C_120         4527           1531         3317         5103         6889         784CIP2C_121         <	1518	3304	5090	6876		
1520         3306         5092         6878         784CIP2C_110         4486           1521         3307         5093         6879         784CIP2C_111         4490           1522         3308         5094         6880         784CIP2C_112         4499           1523         3309         5095         6881         784CIP2C_113         4503           1524         3310         5096         6882         784CIP2C_115         4509           1525         3311         5097         6883         784CIP2C_115         4509           1526         3312         5098         6884         784CIP2C_116         4514           1527         3313         5099         6885         784CIP2C_117         4516           1528         3314         5100         6886         784CIP2C_118         4522           1529         3315         5101         6887         784CIP2C_119         4525           1530         3316         5102         6888         784CIP2C_120         4527           1531         3317         5103         6889         784CIP2C_121         4528           1532         3318         5104         6890         784CIP2C_122         <	1519	3305	5091	6877		
1521         3307         5093         6879         784CIP2C 111         4490           1522         3308         5094         6880         784CIP2C 112         4499           1523         3309         5095         6881         784CIP2C 113         4503           1524         3310         5096         6882         784CIP2C 114         4506           1525         3311         5097         6883         784CIP2C 115         4509           1526         3312         5098         6884         784CIP2C 116         4514           1527         3313         5099         6885         784CIP2C 117         4516           1528         3314         5100         6886         784CIP2C 118         4522           1529         3315         5101         6887         784CIP2C 119         4525           1530         3316         5102         6888         784CIP2C 121         4528           1531         3317         5103         6889         784CIP2C 121         4528           1532         3318         5104         6890         784CIP2C 122         4529           1533         3319         5105         6891         784CIP2C 122         <	1520	3306	5092	6878		
1522         3308         5094         6880         784CIP2C         112         4499           1523         3309         5095         6881         784CIP2C         113         4503           1524         3310         5096         6882         784CIP2C         114         4506           1525         3311         5097         6883         784CIP2C         115         4509           1526         3312         5098         6884         784CIP2C         116         4514           1527         3313         5099         6885         784CIP2C         117         4516           1528         3314         5100         6886         784CIP2C         119         4525           1529         3315         5101         6887         784CIP2C         119         4525           1530         3316         5102         6888         784CIP2C         120         4527           1531         3317         5103         6889         784CIP2C         121         4528           1532         3318         5104         6890         784CIP2C         121         4528           1533         3319         5105         6891 <td< td=""><td>1521</td><td>3307</td><td>5093</td><td></td><td></td><td></td></td<>	1521	3307	5093			
1523         3309         5095         6881         784CIP2C         113         4503           1524         3310         5096         6882         784CIP2C         114         4506           1525         3311         5097         6883         784CIP2C         115         4509           1526         3312         5098         6884         784CIP2C         116         4514           1527         3313         5099         6885         784CIP2C         117         4516           1528         3314         5100         6886         784CIP2C         118         4522           1529         3315         5101         6887         784CIP2C         119         4525           1530         3316         5102         6888         784CIP2C         120         4527           1531         3317         5103         6889         784CIP2C         121         4528           1532         3318         5104         6890         784CIP2C         122         4529           1533         3319         5105         6891         784CIP2C         122         4529           1533         3321         5106         6892 <td< td=""><td>1522</td><td>3308</td><td>5094</td><td></td><td></td><td></td></td<>	1522	3308	5094			
1524         3310         5096         6882         784CIP2C         114         4506           1525         3311         5097         6883         784CIP2C         115         4509           1526         3312         5098         6884         784CIP2C         116         4514           1527         3313         5099         6885         784CIP2C         117         4516           1528         3314         5100         6886         784CIP2C         118         4522           1529         3315         5101         6887         784CIP2C         119         4525           1530         3316         5102         6888         784CIP2C         120         4527           1531         3317         5103         6889         784CIP2C         121         4528           1532         3318         5104         6890         784CIP2C         121         4528           1533         3319         5105         6891         784CIP2C         122         4529           1534         3320         5106         6892         784CIP2C         123         4532           1535         3321         5107         6893 <td< td=""><td>1523</td><td></td><td></td><td></td><td></td><td></td></td<>	1523					
1525         3311         5097         6883         784CIP2C         115         4509           1526         3312         5098         6884         784CIP2C         116         4514           1527         3313         5099         6885         784CIP2C         117         4516           1528         3314         5100         6886         784CIP2C         119         4522           1529         3315         5101         6887         784CIP2C         119         4525           1530         3316         5102         6888         784CIP2C         120         4527           1531         3317         5103         6889         784CIP2C         121         4528           1532         3318         5104         6890         784CIP2C         121         4528           1533         3319         5105         6891         784CIP2C         123         4532           1534         3320         5106         6892         784CIP2C         124         4537           1535         3321         5107         6893         784CIP2C         125         4538           1536         3322         5108         6894 <td< td=""><td>1524</td><td></td><td></td><td></td><td></td><td></td></td<>	1524					
1526         3312         5098         6884         784CIP2C 116         4514           1527         3313         5099         6885         784CIP2C 117         4516           1528         3314         5100         6886         784CIP2C 118         4522           1529         3315         5101         6887         784CIP2C 119         4525           1530         3316         5102         6888         784CIP2C 120         4527           1531         3317         5103         6889         784CIP2C 121         4528           1532         3318         5104         6890         784CIP2C 122         4529           1533         3319         5105         6891         784CIP2C 122         4529           1533         3319         5105         6891         784CIP2C 123         4532           1534         3320         5106         6892         784CIP2C 124         4537           1535         3321         5107         6893         784CIP2C 125         4538           1536         3322         5108         6894         784CIP2C 126         4551           1537         3323         5109         6895         784CIP2C 127         <						
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1528         3314         5100         6886         784CIP2C_118         4522           1529         3315         5101         6887         784CIP2C_119         4525           1530         3316         5102         6888         784CIP2C_120         4527           1531         3317         5103         6889         784CIP2C_121         4528           1532         3318         5104         6890         784CIP2C_122         4529           1533         3319         5105         6891         784CIP2C_123         4532           1534         3320         5106         6892         784CIP2C_124         4537           1535         3321         5107         6893         784CIP2C_125         4538           1536         3322         5108         6894         784CIP2C_126         4551           1537         3323         5109         6895         784CIP2C_126         4551           1538         3324         5110         6896         784CIP2C_128         4559           1539         3325         5111         6897         784CIP2C_130         4568           1540         3326         5112         6898         784CIP2C_130         <						
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1672   3458   5244   7030   784CIPED 20   8819	sequence	peptide	1	1	}	137,133,133
1673		sequence		1		
1674   3460   5246   7032   784CTP2D   22   8846   1675   3461   5247   7033   784CTP2D   22   8846   1675   3462   5248   7034   784CTP2D   24   8918   1676   3462   5248   7035   784CTP2D   25   8918   1677   3463   5249   7035   784CTP2D   26   8941   1679   3465   5250   7035   784CTP2D   26   8941   1679   3465   5252   7038   784CTP2D   27   8941   1680   3466   5252   7038   784CTP2D   27   8941   1680   3466   5252   7038   784CTP2D   28   8951   1681   3467   5253   7039   784CTP2D   29   8951   1681   3467   5253   7039   784CTP2D   29   8951   1682   3468   5254   7040   784CTP2D   29   8951   1682   3468   5254   7040   784CTP2D   32   9037   1684   3470   5256   7042   784CTP2D   31   9032   1684   3470   5256   7042   784CTP2D   31   9032   1685   3471   5257   7043   784CTP2D   31   9035   1685   3471   5257   7043   784CTP2D   33   9035   1686   3472   5258   7044   784CTP2D   33   9035   1687   3473   5269   7046   784CTP2D   33   9035   1689   3475   5261   7047   794CTP2D   33   9034   1689   3475   5261   7047   794CTP2D   37   9113   1690   3476   5262   7048   784CTP2D   39   9152   1693   3479   5265   7049   784CTP2D   39   9152   1693   3479   5265   7051   784CTP2D   40   9152   1694   3480   5266   7052   784CTP2D   40   9152   1694   3480   5266   7052   784CTP2D   40   9152   1698   3484   5267   7053   784CTP2D   40   9231   1698   3484   5267   7053   784CTP2D   42   9233   1698   3484   5267   7053   784CTP2D   40   9152   1698   3484   5267   7053   784CTP2D   42   9231   1699   3485   5271   7057   784CTP2D   48   9231   1700   3486   5272   7058   784CTP2D   48   9231   1699   3485   5271   7057   784CTP2D   48   9231   1700   3486   5272   7058   784CTP2D   58   9309   1700   3486   5272   7058   784CTP2D   58   9309   1700   3486   5272   7058   784CTP2D   58   9309   1700   3495   5281   7067   784CTP2D   58   9309   1700   3495   5281   7067   784CTP2D   58   9309   1700   3495   5282   7068   784CTP2D   58   9309   1700   3495   5287   7065   784CTP2D   58   9365   1706	L	3458	5244	7030	784CIP2D 20	8818
1675   3461   5247   7033   784CIPZD_23   8912		3459	5245	7031	784CIP2D_21	8844
1676   3462   \$248   7034   784CIPZD_24   8918   1678   3464   5250   7035   784CIPZD_25   8918   1678   3464   5250   7035   784CIPZD_26   8931   1679   3465   \$5251   7037   784CIPZD_27   8941   1680   3466   \$5252   7038   784CIPZD_27   8941   1681   3467   \$5253   7039   784CIPZD_29   8951   1682   3468   \$5254   7040   784CIPZD_29   8951   1683   3469   \$5255   7040   784CIPZD_30   9051   1683   3469   \$5255   7041   784CIPZD_31   9012   1684   3470   \$5255   7041   784CIPZD_31   9012   1685   3471   \$5257   7043   784CIPZD_31   9012   1685   3471   \$5257   7043   784CIPZD_33   9025   1687   3473   \$5259   7044   784CIPZD_33   9025   1688   3474   \$5250   7046   784CIPZD_33   9034   1689   3475   \$5261   7047   784CIPZD_36   9054   1690   3476   \$5262   7048   784CIPZD_37   9113   1691   3477   \$5263   7049   784CIPZD_38   9154   1692   3478   \$5264   7050   784CIPZD_39   9152   1693   3479   \$5265   7061   784CIPZD_30   9152   1694   3480   \$5266   7052   784CIPZD_40   9152   1695   3480   \$5266   7052   784CIPZD_41   9223   1696   3480   \$5266   7052   784CIPZD_41   9223   1697   3483   \$5268   7055   784CIPZD_44   9223   1698   3484   \$5270   7056   784CIPZD_44   9223   1699   3485   \$5271   7057   784CIPZD_44   9223   1699   3485   \$5272   7058   784CIPZD_54   9223   1699   3485   \$5272   7058   784CIPZD_54   9223   1699   3485   \$5271   7057   784CIPZD_54   9336   1700   3486   \$5272   7058   784CIPZD_55   9346   1701   3489   \$5275   7061   784CIPZD_56   9314   1702   3498   \$5274   7060   784CIPZD_56   9314   1703   3489   \$5275   7061   784CIPZD_56   9314   1704   3490   \$528   7059   784CIPZD_56   9314   1705   3491   \$5277   7063   784CIPZD_56   9314   1706   3494   \$5280   7056   784CIPZD_56   9314   1707   3493   \$5275   7061   784CIPZD_56   9314   1708   3494   \$5280   7066   784CIPZD_56   9314   1709   3495   \$5281   7067   784CIPZD_56   9314   1700   3496   \$5282   7068   784CIPZD_56   9369   1710   3496   \$5282   7068   784CIPZD_56   9356   1711   3501   \$5295   7078   784CIPZD_56   9556			5246	7032	784CIP2D_22	8846
1677 3463 5249 7035 784CIP2D 25 8918 1679 3464 5250 7036 784CIP2D 26 8941 1679 3465 5251 7037 784CIP2D 27 8941 1680 3466 5252 7038 784CIP2D 28 8951 1680 3466 5252 7038 784CIP2D 28 8951 1681 3467 5253 7039 784CIP2D 28 8951 1682 3468 5254 7040 784CIP2D 30 9007 1683 3469 5255 7041 784CIP2D 30 9007 1683 3469 5255 7041 784CIP2D 31 9012 1684 3470 5256 7042 784CIP2D 32 9013 1685 3471 5257 7043 784CIP2D 32 9013 1686 3472 5259 7044 784CIP2D 34 9035 1686 3472 5259 7044 784CIP2D 34 9035 1687 3473 5259 7044 784CIP2D 34 9035 1688 3474 5260 7046 784CIP2D 34 9035 1689 3476 5262 7048 784CIP2D 38 9034 1689 3476 5262 7048 784CIP2D 38 9134 1690 3476 5262 7048 784CIP2D 38 9134 1691 3477 5263 7049 784CIP2D 39 9152 1692 3478 5264 7050 784CIP2D 39 9152 1693 3478 5264 7050 784CIP2D 40 9152 1693 3479 5265 7051 784CIP2D 41 9211 1694 3480 5266 7052 784CIP2D 41 9211 1694 3480 5266 7052 784CIP2D 43 9233 1695 3481 5267 7053 784CIP2D 43 9233 1696 3482 5268 7054 784CIP2D 43 9231 1697 3483 5259 7055 784CIP2D 43 9231 1698 3486 5270 7056 784CIP2D 43 9231 1699 3485 5271 7057 784CIP2D 49 9314 1700 3486 5272 7058 784CIP2D 49 9314 1700 3488 5274 7060 784CIP2D 49 9314 1700 3488 5271 7057 784CIP2D 59 9326 1700 3488 5275 7061 784CIP2D 59 9326 1701 3489 5275 7061 784CIP2D 59 9326 1700 3486 5272 7058 784CIP2D 59 9326 1700 3488 5271 7057 784CIP2D 59 9326 1700 3488 5271 7057 784CIP2D 59 9326 1700 3488 5271 7057 784CIP2D 59 9326 1700 3488 5275 7061 784CIP2D 59 9326 1700 3488 5275 7061 784CIP2D 59 9326 1700 3488 5275 7061 784CIP2D 59 9326 1700 3488 5270 7056 784CIP2D 59 9326 1700 3488 5270 7056 784CIP2D 59 9326 1700 3489 5275 7061 784CIP2D 59 9326 1700 3489 5275 7061 784CIP2D 59 9326 1700 3488 5271 7057 784CIP2D 59 9326 1700 3488 5271 7057 784CIP2D 59 9326 1700 3488 5270 7060 784CIP2D 59 9326 1700 3489 5275 7061 784CIP2D 59 9351 1701 3489 5289 7065 784CIP2D 59 9351 1702 3488 5289 7068 784CIP2D 59 9351 1704 3490 5276 7060 784CIP2D 59 9365 1704 3490 5276 7076 784CIP2D 59 9365 1704 3490 5286 7072 784CIP2D 59 9365 1704 3490 5286 7072 784CIP2D 59 9365 1704 3490 5			5247	7033	784CIP2D_23	8912
1678	L		5248	7034	784CIP2D_24	8918
1679   3465   5251   7037   784CIP2D_27   8941     1680   3466   5252   7038   784CIP2D_27   8941     1681   3467   5253   7039   784CIP2D_29   8951     1681   3467   5253   7039   784CIP2D_29   8951     1682   3468   5254   7040   784CIP2D_30   9007     1683   3469   5255   7041   784CIP2D_31   9012     1684   3470   5256   7042   784CIP2D_32   9013     1685   3471   5257   7043   784CIP2D_33   9025     1686   3472   5258   7043   784CIP2D_33   9025     1687   3473   5259   7045   784CIP2D_34   9053     1688   3474   5260   7046   784CIP2D_35   9054     1689   3474   5260   7046   784CIP2D_35   9054     1689   3475   5261   7047   784CIP2D_36   9054     1689   3476   5262   7048   784CIP2D_38   9134     1691   3477   5263   7049   784CIP2D_38   9134     1692   3478   5264   7050   784CIP2D_39   9152     1693   3479   5265   7051   784CIP2D_40   9152     1694   3480   5266   7052   784CIP2D_40   9152     1695   3481   5267   7053   784CIP2D_43   9223     1695   3481   5267   7053   784CIP2D_44   9231     1697   3483   5286   7054   784CIP2D_44   9231     1698   3484   5270   7056   784CIP2D_49   9236     1699   3485   5271   7057   784CIP2D_49   9314     1700   3486   5272   7058   784CIP2D_59   9314     1700   3486   5272   7058   784CIP2D_59   9314     1700   3486   5272   7058   784CIP2D_59   9314     1701   3489   5276   7062   784CIP2D_59   9314     1702   3498   5276   7062   784CIP2D_59   9314     1703   3499   5276   7062   784CIP2D_59   9318     1704   3490   5276   7062   784CIP2D_59   9319     1701   3493   5279   7065   784CIP2D_59   9319     1701   3493   5279   7065   784CIP2D_59   9319     1701   3493   5279   7066   784CIP2D_59   9319     1702   3498   5278   7066   784CIP2D_59   9319     1703   3499   5288   7074   784CIP2D_59   9319     1704   3490   5276   7062   784CIP2D_59   9319     1705   3491   5277   7063   784CIP2D_59   9319     1706   3492   5288   7074   784CIP2D_59   9319     1707   3493   5289   7066   784CIP2D_59   9319     1708   3499   5288   7074   784CIP2D_59   9319     1711		1	5249		784CIP2D_25	8918
1680   3466   5252   7038   784CIP2D_28   8951     1681   3467   5253   7039   784CIP2D_29   8951     1682   3468   5254   7040   784CIP2D_30   9007     1683   3469   5255   7041   784CIP2D_31   9012     1684   3470   5255   7041   784CIP2D_31   9012     1685   3471   5257   7043   784CIP2D_31   9013     1686   3472   5258   7044   784CIP2D_34   9053     1686   3472   5258   7044   784CIP2D_34   9053     1687   3473   5259   7045   784CIP2D_34   9053     1688   3474   5257   7043   784CIP2D_35   9054     1689   3475   5261   7047   784CIP2D_37   9113     1690   3476   5262   7048   784CIP2D_37   9113     1691   3477   5263   7049   784CIP2D_39   9152     1692   3478   5264   7050   784CIP2D_39   9152     1693   3479   5265   7051   784CIP2D_44   9211     1694   3480   5266   7052   784CIP2D_44   9221     1695   3481   5267   7053   784CIP2D_44   9223     1695   3481   5267   7053   784CIP2D_44   9223     1696   3462   5268   7056   784CIP2D_42   9223     1697   3463   5225   7056   784CIP2D_44   9231     1698   3484   5270   7056   784CIP2D_46   9236     1699   3486   5272   7058   784CIP2D_48   9309     1701   3487   5273   7059   784CIP2D_59   9314     1702   3488   5274   7060   784CIP2D_55   9326     1703   3489   5275   7061   784CIP2D_55   9326     1704   3490   5276   7065   784CIP2D_55   9326     1705   3491   5277   7063   784CIP2D_55   9318     1706   3492   5278   7065   784CIP2D_55   9318     1707   3493   5279   7065   784CIP2D_55   9318     1708   3494   5270   7056   784CIP2D_55   9319     1709   3495   5281   7067   784CIP2D_55   9316     1701   3487   5273   7059   784CIP2D_55   9318     1702   3498   5274   7060   784CIP2D_55   9318     1703   3493   5275   7061   784CIP2D_55   9318     1704   3490   5276   7065   784CIP2D_55   9318     1705   3491   5277   7063   784CIP2D_55   9318     1706   3493   5280   7066   784CIP2D_55   9318     1707   3493   5280   7066   784CIP2D_55   9367     1708   3494   5280   7066   784CIP2D_55   9367     1718   3500   5296   7077   784CIP2D_55   9367     1719		3464	5250	7036	784CIP2D_26	8941
1681   3467   5253   7039   784CIP2D_29   8951   1682   3468   5254   7040   784CIP2D_30   9007   1683   3469   5255   7041   784CIP2D_31   9012   1684   3470   5256   7042   784CIP2D_32   9013   1685   3471   5257   7043   784CIP2D_32   9013   1686   3472   5258   7044   784CIP2D_33   9025   1686   3472   5258   7044   784CIP2D_34   9053   1687   3473   5259   7045   784CIP2D_35   9054   1688   3474   5260   7046   784CIP2D_35   9054   1689   3475   5261   7047   784CIP2D_36   9054   1689   3476   5262   7048   784CIP2D_39   9154   1690   3476   5262   7048   784CIP2D_39   9152   1691   3477   5263   7049   784CIP2D_39   9152   1692   3478   5264   7050   784CIP2D_40   9152   1693   3479   5265   7051   784CIP2D_40   9152   1694   3480   5266   7052   784CIP2D_40   9213   1695   3481   5267   7053   784CIP2D_40   9213   1695   3481   5267   7053   784CIP2D_40   9223   1695   3481   5267   7053   784CIP2D_40   9223   1699   3488   5270   7056   784CIP2D_40   9236   1699   3488   5270   7056   784CIP2D_40   9236   1699   3488   5271   7057   784CIP2D_40   9236   1699   3488   5272   7058   784CIP2D_40   9236   1690   3486   5272   7058   784CIP2D_50   9314   1700   3486   5272   7058   784CIP2D_50   9314   1701   3497   5277   7057   784CIP2D_50   9314   1702   3488   5274   7060   784CIP2D_50   9314   1703   3489   5275   7061   784CIP2D_50   9314   1704   3490   5276   7062   784CIP2D_50   9314   1706   3494   5280   7066   784CIP2D_50   9314   1707   3493   5279   7065   784CIP2D_50   9314   1708   3494   5280   7066   784CIP2D_50   9314   1709   3495   5281   7067   784CIP2D_50   9356   1700   3495   5280   7076   784CIP2D_50   9356   1701   3495   5280   7066   784CIP2D_50   9356   1703   3493   5276   7062   784CIP2D_50   9356   1704   3493   5276   7062   784CIP2D_50   9356   1705   3491   5280   7066   784CIP2D_50   9356   1706   3492   5286   7070   784CIP2D_50   9356   1707   3493   5285   7066   784CIP2D_50   9356   1708   3494   5280   7066   784CIP2D_50   9356   1714   3500   5286   7070   784CIP2		1	5251	7037	784CIP2D_27	8941
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1683   3469   5255   7041   784CIP2D_31   9012			L		784CIP2D_29	8951
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1685   3471   5257   7043   784CIP2D 33   9025     1686   3472   5258   7044   784CIP2D 34   9053     1687   3473   5259   7044   784CIP2D 34   9053     1688   3474   5260   7046   784CIP2D 35   9054     1688   3474   5260   7046   784CIP2D 36   9054     1689   3475   5261   7047   784CIP2D 37   9113     1690   3476   5262   7048   784CIP2D 38   9134     1691   3477   5263   7049   784CIP2D 39   9152     1692   3478   5264   7050   784CIP2D 40   9152     1693   3479   5265   7051   784CIP2D 40   9152     1694   3480   5266   7052   784CIP2D 42   9223     1695   3481   5267   7053   784CIP2D 42   9223     1695   3481   5267   7053   784CIP2D 44   9231     1697   3483   5268   7054   784CIP2D 44   9231     1698   3484   5270   7056   784CIP2D 46   9236     1699   3485   5271   7057   784CIP2D 47   9303     1700   3486   5272   7058   784CIP2D 49   9314     1702   3488   5274   7060   784CIP2D 50   9326     1703   3489   5275   7061   784CIP2D 50   9326     1704   3490   5276   7062   784CIP2D 50   9326     1705   3491   5277   7063   784CIP2D 50   9326     1706   3492   5278   7066   784CIP2D 50   9326     1707   3493   5276   7062   784CIP2D 50   9326     1708   3494   5270   7063   784CIP2D 50   9326     1709   3495   5275   7061   784CIP2D 50   9326     1701   3497   5287   7063   784CIP2D 50   9326     1702   3498   5276   7062   784CIP2D 50   9326     1703   3499   5275   7065   784CIP2D 50   9326     1704   3493   5276   7062   784CIP2D 50   9326     1705   3491   5277   7063   784CIP2D 50   9326     1706   3492   5278   7065   784CIP2D 50   9348     1707   3493   5280   7066   784CIP2D 50   9419     1709   3495   5281   7067   784CIP2D 50   9419     1710   3496   5282   7068   784CIP2D 50   9419     1711   3496   5282   7068   784CIP2D 50   9419     1712   3498   5280   7066   784CIP2D 50   9419     1713   3499   5285   7071   784CIP2D 60   9501     1714   3500   5286   7072   784CIP2D 60   9501     1715   3501   5287   7073   784CIP2D 60     9504   9506   5292   7078   784CIP2D 60     9506   5292   7078				1	· · · · · · - ·	9012
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1690						
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1694   3480   5266   7052   784CIP2D 42   9223   1695   3481   5267   7053   784CIP2D 43   9223   1696   3482   5268   7055   784CIP2D 44   9231   1697   3483   5269   7055   784CIP2D 45   9236   1698   3484   5270   7056   784CIP2D 46   9236   1699   3485   5271   7057   784CIP2D 46   9236   1699   3485   5271   7057   784CIP2D 48   9309   1700   3486   5272   7058   784CIP2D 48   9309   1701   3487   5273   7059   784CIP2D 49   9314   1702   3488   5274   7060   784CIP2D 49   9314   1703   3489   5275   7061   784CIP2D 50   9326   1704   3490   5276   7062   784CIP2D 51   9339   1705   3491   5277   7063   784CIP2D 52   9348   1706   3492   5278   7064   784CIP2D 54   9382   1707   3493   5279   7065   784CIP2D 55   9407   1708   3494   5280   7066   784CIP2D 55   9407   1709   3495   5281   7067   784CIP2D 57   9439   1710   3496   5282   7068   784CIP2D 59   9493   1711   3497   5283   7069   784CIP2D 59   9493   1712   3498   5284   7070   784CIP2D 60   9501   1713   3499   5285   7071   784CIP2D 60   9501   1714   3500   5286   7072   784CIP2D 63   9551   1716   3502   5288   7074   784CIP2D 63   9551   1716   3502   5288   7077   784CIP2D 63   9551   1716   3503   5289   7075   784CIP2D 64   9588   1719   3505   5291   7077   784CIP2D 64   9557   1719   3503   5289   7075   784CIP2D 65   9568   1719   3505   5291   7077   784CIP2D 66   9558   1719   3505   5291   7077   784CIP2D 66   9568   1719   3505   5291   7077   784CIP2D 66   9568   1719   3505   5291   7077   784CIP2D 66   9568   1719   3505   5291   7077   784CIP2D 67   9660   1722   3508   5294   7080   784CIP2D 67   9660   1723   3509   5295   7081   784CIP2D 67   9660   1724   3510   5296   7082   784CIP2D 79   9660   1725   3511   5297   7083   784CIP2D 79   9661   1726   3514   5300   7086   784CIP2D 79   9662   1726   3515   5301   7087   784CIP2D 75   9746   1729   3515   5301   7087   784CIP2D 79   9662   1721   3513   5299   7008   784CIP2D 79   9662   1722   3516   5302   7088   784CIP2D 79   9662   1723   3516   5302   7088   784CIP2					1	
1695   3481   5267   7053   784CIP2D_43   9223     1696   3482   5268   7054   784CIP2D_44   9231     1697   3483   5269   7055   784CIP2D_45   9236     1698   3484   5270   7056   784CIP2D_46   9236     1699   3485   5271   7057   784CIP2D_46   9236     1699   3485   5271   7057   784CIP2D_47   9303     1700   3486   5272   7058   784CIP2D_48   9309     1701   3487   5273   7059   784CIP2D_49   9314     1702   3488   5274   7060   784CIP2D_50   9326     1703   3489   5275   7061   784CIP2D_50   9326     1704   3490   5276   7062   784CIP2D_52   9348     1705   3491   5277   7063   784CIP2D_52   9348     1706   3492   5278   7064   784CIP2D_52   9348     1707   3493   5279   7065   784CIP2D_55   9407     1708   3494   5280   7066   784CIP2D_55   9407     1708   3494   5280   7066   784CIP2D_55   9407     1708   3494   5280   7066   784CIP2D_56   9414     1709   3495   5281   7067   784CIP2D_58   9485     1710   3498   5282   7068   784CIP2D_58   9485     1711   3497   5283   7069   784CIP2D_58   9493     1712   3498   5284   7070   784CIP2D_61   9526     1713   3499   5285   7071   784CIP2D_61   9526     1714   3500   5286   7072   784CIP2D_62   9526     1715   3501   5287   7073   784CIP2D_62   9526     1716   3502   5288   7074   784CIP2D_64   9557     1717   3503   5289   7075   784CIP2D_65   9588     1719   3505   5291   7077   784CIP2D_65   9588     1719   3505   5291   7077   784CIP2D_66   9588     1719   3506   5292   7078   784CIP2D_66   9588     1719   3506   5292   7078   784CIP2D_66   9589     1721   3507   5293   7079   784CIP2D_67   9557     1722   3508   5296   7081   784CIP2D_79   9649     1723   3509   5296   7081   784CIP2D_79   9649     1724   3510   5295   7081   784CIP2D_79   9649     1725   3511   5297   7083   784CIP2D_79   9649     1726   3512   5298   7086   784CIP2D_79   9649     1721   3507   5293   7079   784CIP2D_79   9649     1723   3516   5301   7087   784CIP2D_79   9649     1724   3510   5296   7081   784CIP2D_79   9649     1725   3511   5297   7083   784CIP2D_79   9787     1726						
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1700   3486   5272   7058   784CIP2D_48   9309     1701   3487   5273   7059   784CIP2D_49   9314     1702   3488   5274   7060   784CIP2D_50   9326     1703   3489   5275   7061   784CIP2D_50   9326     1704   3490   5276   7062   784CIP2D_52   9348     1705   3491   5277   7063   784CIP2D_52   9348     1706   3492   5278   7064   784CIP2D_53   9376     1707   3493   5279   7065   784CIP2D_55   9382     1707   3493   5279   7065   784CIP2D_55   9407     1708   3494   5280   7066   784CIP2D_55   9407     1709   3495   5281   7067   784CIP2D_56   9414     1709   3495   5282   7068   784CIP2D_57   9439     1710   3496   5282   7068   784CIP2D_59   9493     1711   3497   5283   7069   784CIP2D_59   9493     1712   3498   5284   7070   784CIP2D_60   9501     1713   3499   5285   7071   784CIP2D_60   9501     1714   3500   5286   7072   784CIP2D_62   9526     1714   3501   5287   7073   784CIP2D_63   9551     1716   3502   5288   7074   784CIP2D_63   9551     1718   3504   5290   7076   784CIP2D_63   9551     1719   3503   5289   7075   784CIP2D_66   9588     1719   3505   5291   7077   784CIP2D_66   9588     1719   3506   5290   7076   784CIP2D_66   9588     1720   3506   5292   7078   784CIP2D_68   9615     1721   3501   5287   7073   784CIP2D_66   9588     1719   3505   5291   7077   784CIP2D_66   9588     1719   3505   5291   7077   784CIP2D_66   9588     1719   3506   5292   7078   784CIP2D_68   9615     1721   3507   5293   7079   784CIP2D_70   9649     1722   3508   5294   7080   784CIP2D_71   9652     1724   3510   5295   7081   784CIP2D_73   9662     1725   3511   5297   7083   784CIP2D_73   9662     1726   3512   5298   7084   784CIP2D_73   9662     1727   3513   5299   7085   784CIP2D_77   9787     1728   3514   5300   7086   784CIP2D_77   9787     1729   3515   5301   7087   784CIP2D_77   9787     1728   3514   5300   7086   784CIP2D_77   9787     1730   3516   5302   7088   784CIP2D_77   9787     1731   3517   5303   7099   784CIP2D_78   9790     1731   3517   5303   7099   784CIP2D_78   9790     1731				1		
1701   3487   5273   7059   784CIP2D 49   9314     1702   3488   5274   7060   784CIP2D 50   9326     1703   3489   5275   7061   784CIP2D 51   9339     1704   3490   5276   7062   784CIP2D 51   9339     1705   3491   5277   7063   784CIP2D 53   9376     1706   3492   5278   7064   784CIP2D 53   9376     1706   3492   5278   7064   784CIP2D 54   9382     1707   3493   5279   7065   784CIP2D 55   9407     1708   3494   5280   7066   784CIP2D 56   9414     1709   3495   5281   7067   784CIP2D 57   9439     1710   3496   5282   7068   784CIP2D 59   9485     1711   3497   5283   7069   784CIP2D 59   9485     1712   3498   5284   7070   784CIP2D 60   9501     1713   3499   5285   7071   784CIP2D 61   9526     1714   3500   5286   7072   784CIP2D 62   9526     1715   3501   5287   7073   784CIP2D 62   9526     1716   3502   5288   7074   784CIP2D 63   9557     1717   3503   5289   7075   784CIP2D 65   9568     1719   3505   5291   7077   784CIP2D 65   9588     1719   3505   5291   7077   784CIP2D 65   9588     1719   3505   5291   7077   784CIP2D 69   9628     1720   3506   5292   7078   784CIP2D 69   9628     1721   3507   5293   7079   784CIP2D 69   9628     1722   3508   5294   7080   784CIP2D 70   9649     1723   3509   5295   7081   784CIP2D 70   9649     1724   3510   5296   7082   784CIP2D 72   9660     1725   3511   5297   7083   784CIP2D 73   9652     1726   3512   5298   7084   784CIP2D 73   9652     1728   3514   5300   7086   784CIP2D 74   9725     1728   3514   5300   7086   784CIP2D 75   9746     1728   3514   5300   7086   784CIP2D 76   9777     1729   3515   5301   7087   784CIP2D 76   9777     1728   3516   5302   7088   784CIP2D 78   9790     1731   3517   5303   7089   784CIP2D 78   9790     1731   3518   5304   7090   784CIP2D 78   9790     1731   3518   5304   7090   784CIP2D 78   9790     1731   3518   5304   7090   784CIP2D 78   9790     1731   3518   5304   7090   784CIP2D 78   9790     1731   3518   5304   7090   784CIP2D 78   9790     1731   3518   5304   7090   784CIP2D 78   9790     1731						
1702   3498   5274   7060   784CIP2D   50   9326     1703   3489   5275   7061   784CIP2D   51   9339     1704   3490   5276   7062   784CIP2D   52   9348     1705   3491   5277   7063   784CIP2D   52   9348     1706   3492   5278   7064   784CIP2D   54   9382     1707   3493   5279   7065   784CIP2D   55   9407     1708   3494   5280   7066   784CIP2D   56   9414     1709   3495   5281   7067   784CIP2D   58   9485     1710   3496   5282   7068   784CIP2D   58   9485     1711   3497   5283   7069   784CIP2D   59   9493     1712   3498   5284   7070   784CIP2D   60   9501     1713   3499   5285   7071   784CIP2D   60   9501     1714   3500   5286   7072   784CIP2D   62   9526     1715   3501   5287   7073   784CIP2D   62   9526     1716   3502   5288   7074   784CIP2D   63   9557     1717   3503   5289   7075   784CIP2D   63   9557     1718   3504   5290   7076   784CIP2D   66   9588     1719   3505   5291   7077   784CIP2D   66   9588     1719   3505   5291   7077   784CIP2D   66   9588     1719   3506   5292   7078   784CIP2D   66   9588     1719   3505   5291   7077   784CIP2D   67   9597     1720   3506   5292   7078   784CIP2D   67   9597     1721   3501   5287   7073   784CIP2D   67   9597     1722   3508   5294   7080   784CIP2D   67   9597     1723   3506   5292   7078   784CIP2D   69   9628     1724   3510   5295   7081   784CIP2D   70   9649     1723   3509   5295   7081   784CIP2D   70   9649     1724   3510   5296   7082   784CIP2D   70   9660     1725   3511   5297   7083   784CIP2D   73   9660     1726   3512   5298   7084   784CIP2D   74   9725     1727   3513   5299   7085   784CIP2D   75   9746     1728   3514   5300   7086   784CIP2D   77   9787     1730   3516   5302   7088   784CIP2D   79   9746     1731   3517   5303   7089   784CIP2D   79   9746     1732   3518   5304   7090   784CIP2D   79   9746     1733   3516   5302   7088   784CIP2D   79   9746     1731   3517   5303   7089   784CIP2D   79   9746     1731   3517   5303   7089   784CIP2D   79   9746     1731   3517   5303   7089   78						
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1704						
1705   3491   5277   7063   784CIP2D 53   9376     1706   3492   5278   7064   784CIP2D 54   9382     1707   3493   5279   7065   784CIP2D 55   9407     1708   3494   5280   7066   784CIP2D 56   9414     1709   3495   5281   7067   784CIP2D 57   9439     1710   3496   5282   7068   784CIP2D 58   9485     1711   3497   5283   7069   784CIP2D 59   9493     1712   3498   5284   7070   784CIP2D 59   9493     1713   3499   5285   7071   784CIP2D 60   9501     1714   3500   5286   7072   784CIP2D 61   9526     1715   3501   5287   7073   784CIP2D 62   9526     1716   3502   5288   7074   784CIP2D 63   9551     1716   3502   5288   7074   784CIP2D 64   9557     1717   3503   5289   7075   784CIP2D 65   9568     1718   3504   5290   7076   784CIP2D 66   9588     1719   3505   5291   7077   784CIP2D 66   9588     1719   3505   5291   7077   784CIP2D 68   9615     1720   3506   5292   7078   784CIP2D 68   9615     1721   3507   5293   7079   784CIP2D 69   9628     1722   3508   5294   7080   784CIP2D 69   9628     1723   3509   5295   7081   784CIP2D 70   9649     1723   3509   5295   7081   784CIP2D 70   9649     1724   3510   5296   7082   784CIP2D 70   9649     1725   3511   5297   7083   784CIP2D 71   9652     1726   3512   5298   7084   784CIP2D 72   9660     1727   3513   5299   7085   784CIP2D 75   9746     1728   3514   5300   7086   784CIP2D 75   9746     1729   3515   5301   7087   784CIP2D 78   9790     1731   3517   5303   7089   784CIP2D 78   9790     1731   3517   5303   7089   784CIP2D 79   9642     1732   3518   5304   7090   784CIP2D 79   9642     1731   3518   5304   7090   784CIP2D 79   9642     1732   3518   5304   7090   784CIP2D 79   9642     1733   3516   5304   7090   784CIP2D 79   9642     1731   3517   5303   7089   784CIP2D 79   9642     1732   3518   5304   7090   784CIP2D 80   9842     1733   3516   5304   7090   784CIP2D 80   9842     1731   3517   5303   7089   784CIP2D 80   9842     1731   3517   5303   7089   784CIP2D 80	I					
1706         3492         5278         7064         784CIP2D 54         9382           1707         3493         5279         7065         784CIP2D 55         9407           1708         3494         5280         7066         784CIP2D 56         9414           1709         3495         5281         7067         784CIP2D 57         9439           1710         3496         5282         7068         784CIP2D 59         9493           1711         3497         5283         7069         784CIP2D 59         9493           1712         3498         5284         7070         784CIP2D 60         9501           1713         3499         5285         7071         784CIP2D 61         9526           1714         3500         5286         7072         784CIP2D 62         9526           1715         3501         5287         7073         784CIP2D 63         9551           1716         3502         5288         7074         784CIP2D 64         9557           1717         3503         5289         7075         784CIP2D 64         9557           1718         3504         5290         7076         784CIP2D 65         9588						
1707   3493   5279   7065   784CIP2D   55   9407	1706					
1708	1707	1				
1709         3495         5281         7067         784CIP2D 57         9439           1710         3496         5282         7068         784CIP2D 58         9485           1711         3497         5283         7069         784CIP2D 59         9493           1712         3498         5284         7070         784CIP2D 60         9501           1713         3499         5285         7071         784CIP2D 61         9526           1714         3500         5286         7072         784CIP2D 62         9526           1715         3501         5287         7073         784CIP2D 63         9551           1716         3502         5288         7074         784CIP2D 63         9551           1717         3503         5289         7075         784CIP2D 65         9568           1718         3504         5290         7076         784CIP2D 66         9588           1719         3505         5291         7077         784CIP2D 67         9597           1720         3506         5292         7078         784CIP2D 69         9628           1721         3507         5293         7079         784CIP2D 69         9628	1708					
1710         3496         5282         7068         784CIP2D 58         9485           1711         3497         5283         7069         784CIP2D 59         9493           1712         3498         5284         7070         784CIP2D 60         9501           1713         3499         5285         7071         784CIP2D 61         9526           1714         3500         5286         7072         784CIP2D 62         9526           1715         3501         5287         7073         784CIP2D 63         9551           1716         3502         5288         7074         784CIP2D 63         9551           1717         3503         5289         7075         784CIP2D 63         9557           1717         3503         5289         7075         784CIP2D 65         9568           1718         3504         5290         7076         784CIP2D 65         9588           1719         3505         5291         7077         784CIP2D 67         9597           1720         3506         5292         7078         784CIP2D 69         9628           1721         3507         5293         7079         784CIP2D 69         9628	1709	3495				
1711         3497         5283         7069         784CIP2D 59         9493           1712         3498         5284         7070         784CIP2D 60         9501           1713         3499         5285         7071         784CIP2D 61         9526           1714         3500         5286         7072         784CIP2D 62         9526           1715         3501         5287         7073         784CIP2D 63         9551           1716         3502         5288         7074         784CIP2D 63         9557           1717         3503         5289         7075         784CIP2D 64         9557           1717         3503         5289         7075         784CIP2D 65         9568           1718         3504         5290         7076         784CIP2D 65         9588           1719         3505         5291         7077         784CIP2D 67         9597           1720         3506         5292         7078         784CIP2D 69         9628           1721         3507         5293         7079         784CIP2D 70         9649           1723         3508         5294         7080         784CIP2D 70         9649	1710	3496	5282			
1712         3498         5284         7070         784CIP2D_60         9501           1713         3499         5285         7071         784CIP2D_61         9526           1714         3500         5286         7072         784CIP2D_62         9526           1715         3501         5287         7073         784CIP2D_63         9551           1716         3502         5288         7074         784CIP2D_65         958           1717         3503         5289         7075         784CIP2D_65         958           1718         3504         5290         7076         784CIP2D_66         9588           1719         3505         5291         7077         784CIP2D_66         9588           1719         3506         5292         7078         784CIP2D_67         9597           1720         3506         5292         7078         784CIP2D_69         9628           1721         3507         5293         7079         784CIP2D_70         9649           1723         3508         5294         7080         784CIP2D_70         9649           1723         3509         5295         7081         784CIP2D_71         9652	1711	3497	5283	7069	784CIP2D 59	
1713         3499         5285         7071         784CIP2D_61         9526           1714         3500         5286         7072         784CIP2D_62         9526           1715         3501         5287         7073         784CIP2D_63         9551           1716         3502         5288         7074         784CIP2D_64         9557           1717         3503         5289         7075         784CIP2D_65         9568           1718         3504         5290         7076         784CIP2D_66         9588           1719         3505         5291         7077         784CIP2D_67         9597           1720         3506         5292         7078         784CIP2D_68         9615           1721         3507         5293         7079         784CIP2D_68         9615           1721         3507         5293         7079         784CIP2D_68         9615           1722         3508         5294         7080         784CIP2D_70         9649           1723         3509         5295         7061         784CIP2D_71         9652           1724         3510         5296         7082         784CIP2D_72         9660	1712	3498	5284	7070		
1714         3500         5286         7072         784CIP2D 62         9526           1715         3501         5287         7073         784CIP2D 63         9551           1716         3502         5288         7074         784CIP2D 64         9557           1717         3503         5289         7075         784CIP2D 65         9568           1718         3504         5290         7076         784CIP2D 66         9588           1719         3505         5291         7077         784CIP2D 67         9597           1720         3506         5292         7078         784CIP2D 68         9615           1721         3507         5293         7079         784CIP2D 68         9615           1721         3507         5293         7079         784CIP2D 68         9615           1722         3508         5294         7080         784CIP2D 70         9649           1723         3509         5295         7081         784CIP2D 71         9652           1724         3510         5296         7082         784CIP2D 71         9652           1725         3511         5297         7083         784CIP2D 73         9662		3499	5285	7071		
1715     3501     5287     7073     784CIP2D_63     9551       1716     3502     5288     7074     784CIP2D_64     9557       1717     3503     5289     7075     784CIP2D_65     9568       1718     3504     5290     7076     784CIP2D_66     9588       1719     3505     5291     7077     784CIP2D_67     9597       1720     3506     5292     7078     784CIP2D_68     9615       1721     3507     5293     7079     784CIP2D_69     9628       1722     3508     5294     7080     784CIP2D_70     9649       1723     3509     5295     7081     784CIP2D_71     9652       1724     3510     5296     7082     784CIP2D_72     9660       1725     3511     5297     7083     784CIP2D_73     9662       1726     3512     5298     7084     784CIP2D_74     9725       1727     3513     5299     7085     784CIP2D_76     9777       1728     3514     5300     7086     784CIP2D_76     9777       1729     3515     5301     7087     784CIP2D_76     9777       1730     3516     5302     7088     784CIP2			5286	7072		
1716         3502         5288         7074         784CIP2D_64         9557           1717         3503         5289         7075         784CIP2D_65         9568           1718         3504         5290         7076         784CIP2D_66         9588           1719         3505         5291         7077         784CIP2D_67         9597           1720         3506         5292         7078         784CIP2D_68         9615           1721         3507         5293         7079         784CIP2D_69         9628           1722         3508         5294         7080         784CIP2D_70         9649           1723         3509         5295         7081         784CIP2D_71         9652           1724         3510         5296         7082         784CIP2D_72         9660           1725         3511         5297         7083         784CIP2D_73         9662           1726         3512         5298         7084         784CIP2D_74         9725           1727         3513         5299         7085         784CIP2D_75         9746           1728         3514         5300         7086         784CIP2D_76         9777			5287	7073	784CIP2D 63	
1717     3503     5289     7075     784CIP2D_65     9568       1718     3504     5290     7076     784CIP2D_66     9588       1719     3505     5291     7077     784CIP2D_67     9597       1720     3506     5292     7078     784CIP2D_68     9615       1721     3507     5293     7079     784CIP2D_69     9628       1722     3508     5294     7080     784CIP2D_70     9649       1723     3509     5295     7081     784CIP2D_70     9649       1724     3510     5296     7082     784CIP2D_72     9660       1725     3511     5297     7083     784CIP2D_73     9662       1726     3512     5298     7084     784CIP2D_74     9725       1727     3513     5299     7085     784CIP2D_75     9746       1728     3514     5300     7086     784CIP2D_76     9777       1729     3515     5301     7087     784CIP2D_77     9787       1730     3516     5302     7088     784CIP2D_79     9842       1731     3518     5304     7090     784CIP2D_80     9842			5288	7074	784CIP2D 64	
1718     3504     5290     7076     784CIP2D_66     9588       1719     3505     5291     7077     784CIP2D_67     9597       1720     3506     5292     7078     784CIP2D_68     9615       1721     3507     5293     7079     784CIP2D_69     9628       1722     3508     5294     7080     784CIP2D_70     9649       1723     3509     5295     7081     784CIP2D_71     9652       1724     3510     5296     7082     784CIP2D_72     9660       1725     3511     5297     7083     784CIP2D_73     9662       1726     3512     5298     7084     784CIP2D_74     9725       1727     3513     5299     7085     784CIP2D_75     9746       1728     3514     5300     7086     784CIP2D_76     9777       1729     3515     5301     7087     784CIP2D_77     9787       1730     3516     5302     7088     784CIP2D_79     9842       1731     3517     5303     7089     784CIP2D_79     9842       1732     3518     5304     7090     784CIP2D_80     9842				7075	784CIP2D_65	
1720         3506         5292         7078         784CIP2D_68         9615           1721         3507         5293         7079         784CIP2D_69         9628           1722         3508         5294         7080         784CIP2D_70         9649           1723         3509         5295         7081         784CIP2D_71         9652           1724         3510         5296         7082         784CIP2D_72         9660           1725         3511         5297         7083         784CIP2D_73         9662           1726         3512         5298         7084         784CIP2D_74         9725           1727         3513         5299         7085         784CIP2D_75         9746           1728         3514         5300         7086         784CIP2D_76         9777           1729         3515         5301         7087         784CIP2D_77         9787           1730         3516         5302         7088         784CIP2D_79         9842           1731         3518         5304         7090         784CIP2D_80         9842			5290	7076	784CIP2D_66	
1721         3507         5293         7079         784CIP2D_69         9628           1722         3508         5294         7080         784CIP2D_70         9649           1723         3509         5295         7081         784CIP2D_71         9652           1724         3510         5296         7082         784CIP2D_72         9660           1725         3511         5297         7083         784CIP2D_73         9662           1726         3512         5298         7084         784CIP2D_74         9725           1727         3513         5299         7085         784CIP2D_75         9746           1728         3514         5300         7086         784CIP2D_76         9777           1729         3515         5301         7087         784CIP2D_77         9787           1730         3516         5302         7088         784CIP2D_78         9790           1731         3518         5304         7090         784CIP2D_80         9842			5291	7077	784CIP2D_67	9597
1721         3507         5293         7079         784CIP2D 69         9628           1722         3508         5294         7080         784CIP2D 70         9649           1723         3509         5295         7081         784CIP2D 71         9652           1724         3510         5296         7082         784CIP2D 72         9660           1725         3511         5297         7083         784CIP2D 73         9662           1726         3512         5298         7084         784CIP2D 74         9725           1727         3513         5299         7085         784CIP2D 75         9746           1728         3514         5300         7086         784CIP2D 76         9777           1729         3515         5301         7087         784CIP2D 77         9787           1730         3516         5302         7088         784CIP2D 78         9790           1731         3517         5303         7089         784CIP2D 79         9842           1732         3518         5304         7090         784CIP2D 80         9842			5292	7078	784CIP2D_68	
1723         3509         5295         7081         784CIP2D_71         9652           1724         3510         5296         7082         784CIP2D_72         9660           1725         3511         5297         7083         784CIP2D_73         9662           1726         3512         5298         7084         784CIP2D_74         9725           1727         3513         5299         7085         784CIP2D_75         9746           1728         3514         5300         7086         784CIP2D_76         9777           1729         3515         5301         7087         784CIP2D_77         9787           1730         3516         5302         7088         784CIP2D_78         9790           1731         3517         5303         7089         784CIP2D_79         9842           1732         3518         5304         7090         784CIP2D_80         9842				7079	784CIP2D_69	9628
1724         3510         5295         7082         784CIP2D_72         9660           1725         3511         5297         7083         784CIP2D_73         9662           1726         3512         5298         7084         784CIP2D_74         9725           1727         3513         5299         7085         784CIP2D_75         9746           1728         3514         5300         7086         784CIP2D_76         9777           1729         3515         5301         7087         784CIP2D_77         9787           1730         3516         5302         7088         784CIP2D_78         9790           1731         3517         5303         7089         784CIP2D_79         9842           1732         3518         5304         7090         784CIP2D_80         9842				7080	784CIP2D_70	9649
1725         3511         5297         7083         784CIP2D_73         9662           1726         3512         5298         7084         784CIP2D_74         9725           1727         3513         5299         7085         784CIP2D_75         9746           1728         3514         5300         7086         784CIP2D_76         9777           1729         3515         5301         7087         784CIP2D_77         9787           1730         3516         5302         7088         784CIP2D_78         9790           1731         3517         5303         7089         784CIP2D_79         9842           1732         3518         5304         7090         784CIP2D_80         9842				7081	784CIP2D_71	
1726         3512         5298         7084         784CIP2D_74         9725           1727         3513         5299         7085         784CIP2D_75         9746           1728         3514         5300         7086         784CIP2D_76         9777           1729         3515         5301         7087         784CIP2D_77         9787           1730         3516         5302         7088         784CIP2D_78         9790           1731         3517         5303         7089         784CIP2D_79         9842           1732         3518         5304         7090         784CIP2D_80         9842				7082	784CIP2D_72	9660
1727         3513         5299         7085         784CIP2D_75         9746           1728         3514         5300         7086         784CIP2D_76         9777           1729         3515         5301         7087         784CIP2D_77         9787           1730         3516         5302         7088         784CIP2D_78         9790           1731         3517         5303         7089         784CIP2D_79         9842           1732         3518         5304         7090         784CIP2D_80         9842				7083	784CIP2D_73	9662
1728         3514         5300         7086         784CIP2D_76         9777           1729         3515         5301         7087         784CIP2D_76         9777           1730         3516         5302         7088         784CIP2D_78         9790           1731         3517         5303         7089         784CIP2D_79         9842           1732         3518         5304         7090         784CIP2D_80         9842				7084	784CIP2D_74	9725
1729 3515 5301 7087 784CIP2D 77 9787 1730 3516 5302 7088 784CIP2D 78 9790 1731 3517 5303 7089 784CIP2D 79 9842 1732 3518 5304 7090 784CIP2D 80 9842			<del></del>	7085	784CIP2D 75	
1730 3516 5302 7088 784CIP2D 78 9790 1731 3517 5303 7089 784CIP2D 79 9842 1732 3518 5304 7090 784CIP2D 80 9842				7086	784CIP2D_76	9777
1731 3517 5303 7089 784CIP2D 79 9842 1732 3518 5304 7090 784CIP2D 80 9842					784CIP2D_77	9787
1732 3518 5304 7090 784CIP2D_80 9842				I	784CIP2D_78	9790
1722 7642 7642 7642 7642 7642 7642 7642 7					784CIP2D_79	9842
1/33   3519   5305   7091   784CIP2D_81   9848						
	1/33	3519	5305	7091	784CIP2D_81	9848

SEQ ID NO:	SEO ID	[ AHA YA 33A			
of full-	NO: OF	SEQ ID NO:	SEQ ID	Priority	SEQ ID
length	full-	of contig	NO:	docket number_	NO:in
nucleotide	length	nucleotide	of contig	corresponding	U.S.S.N.
sequence	peptide	sequence	peptide	SEO ID NO: in	09/488,725
begaence	sequence	}	sequence	priority	j
1734	3520			application	
1735	<b>_</b>	5306	7092	784CIP2D_82	9867
	3521	5307	7093	784CIP2D_83	. 10010
1736	3522	5308	7094	784CIP2D_84	10011
1737	3523	5309	7095	784CIP2D_85	10052
1738	3524	5310	7096	784CIP2D_86	10057
1739	3525	5311	7097	784CIP2D_87	10085
1740	3526	5312	7098	784CIP2D 89	10139
1741	3527	5313	7099	784CIP2D 90	10142
1742	3528	5314	7100	784CIP2D 92	10165
1743	3529	5315	7101	784CIP2D 93	10173
1744	3530	5316	7102	784CIP2D 94	10173
1745	3531	5317	7103	784CIP2D 95	10273
1746	3532	5318	7104	784CIP2E 1	3121
1747	3533	5319	7105	784CIP2E 2	3628
1748	3534	5320	7106	784CIP2E 4	3673
1749	3535	5321	7107	784CIP2E 5	4018
1750	3536	5322	7108	784CIPZE 6	4467
1751	3537	5323	7109	784CIP2E 7	
1752	3538	5324	7110	784CIP2E 8	4865
1753	3539	5325	7111	784CIP2E 9	4916
1754	3540	5326	7112		4923
1755	3541	5327	7112	784CIP2E_10	4926
1756	3542	5328	7113	784CIP2E_11	4962
1757	3543	5329	7114	784CIP2E_12	4963
1758	3544	5330		784CIP2E_13	4964
1759	3545	5331	7116 7117	784CIP2E_14	4988
1760	3546	5332		784CIP2E_15	5835
1761	3547	5333	7118	784CIP2E_16	7682
1762	3548	5334	7119	784CIP2E_17	7682
1763	3549		7120	784CIP2E_18	7699
1764	3550	5335	7121	784CIP2E_19	7707
1765	3551	5336	7122	784CIP2E_20	7707
1766	3552	5337	7123	784CIP2E_21	7752
1767		5338	7124	784CIP2E_22	8357
1768	3553	5339	7125	784CIP2E_23	9065
1769	3554	5340	7126	784CIP2E_24	9324
1770	3555	5341	7127	784CIP2F_1	2976
	3556	5342	7128	784CIP2F_2	3559
1771	3557	5343	7129	784CIP2F_3	4021
1772 1773	3558	5344	7130	784CIP2F_4	4474
	3559	5345	7131	784CIP2F_5	4566
1774	3560	5346	7132	784CIP2F_6	4705
1775	3561	5347	7133	784CIP2F_7	4707
1776	3562	5348	7134	784CIP2F_8	4712
1777	3563	5349	7135	784CIP2F_9	5008
1778	3564	5350	7136	784CIP2F 10	5009
1779	3565	5351	7137	784CIP2F 11	5015
1780	3566	5352	7138	784CIP2F 12	5015
1781	3567	5353	7139	784CIP2F 13	7724
1782	3568	5354	7140	784CIP2F 14	7725
1783	3569	5355	7141	784CIP2F 15	8828
1784	3570	5356	7142	784CIP2F 16	8830
1785	3571	5357	7143	784CIP2F 17	9739
1786	3572	5358	7144	784CIP2F 18	9896
					2020

TRADOCS:1416247.1(%CS7011.DOC)

TABLE 7

	BLE /		
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location .	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Lcucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ļ	amino acid	sequence	Codon, /=possible nucleotide deletion.
	sequence	Dodaoneo	\=possible nucleotide insertion)
5359	337	1123	
3333	337	1131	AHLSARLSALILDEVAILPAPQNLSVLSTNMKHLLMWSPVIAPG
J			ETVYYSVEYQGEYESLYTSHIWIPSSNCSLTEGPECDVTDDITA
	ŀ	ł	TVPYNLRVRATLGSQTS/CLEHP/VSIPLIETQPSLPDL/RMEI
	1		TKDGFHLVIBLEDLGPQFEFLVAYWRREPGAEEHVKMVRSGGIP
Į	ł	j	VHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVEVQGEAIPL
	ļ		VLALFAFVGFMLILVVVPLFVWKMGRLLQ/YLLLPRGGSSOTPW
	•		KITQF
5360	2	1115	PRVRSSGGQBDPASQQWARPRFTQPSKMRRRVIARPVGSSVRLK
1	<b>)</b>		CVASGHPRPDITWMKDDQALTRPEAAEPRKKKWTLSLKNLRPED
ļ			SGKYTCRVSNRAGAINATYKVDVIQRTRSKPVLTGTHPVNTTVD
	<b> </b>	,	FGGTTSFQCKVRSDVKPVIQWLKRVEYGAEGRHNSTIDVGGQKF
			VVLPTGDVWSRPDGSYLNKLLITRARQDDAGMYICLGANTMGYS
1			FRSAFLTVLPDPKPPGPPVASSSSATSLPWPVVIGIPAGAVFIL
			GTLLLWLCQAQKKPCTPAPAPPLPGHR>PGTARDRSGDKDLPSL
			AALSAGPGVGLCEEHGSPAAPQHLLGPGPVAGPKLYPKLYTGHS
<u> </u>			TPHTYTHPPPSCQLNSSHS
5361	3	925	HEGSISSANILLDDQFQPKLTDFAMAHFRSHLEHQSCTINMTSS
		•1	SSKHLWYMPEEYIRQGKLSIKTDVYSFGIVIMEVLTGCRVVLDD
			PKHIQLRDLLRELMEKRGLDSCLSFLDKKVPPCPRNFSAKLFCL
ł			AGRCAATRAKLRPSMDEVLNTLESTQASLYFAEDPPTSLKSFRC
			PSPLFLENVPSIPVEDDESQNNNLLPSDEGLRIDRMTQKTPFEC
	÷		SQSEVMFLSLDKKPESKRNEEACNMPSSSCEESWFPKYIVPSQD
1			LRPYKVNIDPSSEAPGHSCRSRPVESSCSSKFSWDEYEOYKKE
5362	2	4879	SCQVEGCTRTYNSSQSIGKHMKTAHPDQYAAFKMQRKSKKGQXA
			NNLNTPNNGKFVYFLPSPVNSSNPFFTSQTKANGNPACSAQLQH
			VSPPIFPAHLASVSTPLLSSMESVINPNITSQDKNEQGGMLCSO
f I	·		
1 1	l l		MENLPSTALPAQMEDLTKTVLPLNIDRGSDPFLSLPAESSSIDL
1			FPSPADSGTNSVFSQLENNTNHYSSQLEGNTNSSFLKGGNGENA
1 .			VFPSQVNVANNFSSTNAQQSAPEKVKKDRGRGQTGKERKPKHNK
1 1			RAKWPAIIRDGKFICSRCYRAFTNPRSLGGHLSKRSYCKPLDGA
1 1	· .		EIAQELLQSNGQPSLLASMILSTNAVNLQQPQQSTFNPEACFKD
1 1			PSFLQLLAENRSPAFLPNTFPRSGVTNFNTSVSQEGSEIIIQAL
			ETAGIPSTFEGAEMLSHVSTGCVSDASQVNATVMPNPTVPPLLH
! [			TVCHPNTLLTNQNRTSNSKTSSIEECSSLPVFPTNDLLLKTVEN
1			GLCSSSFPNSGGPSQNFTSNSSRVSVISGPQNTRSSHLNKKGNS
			ASKRRKKVAPPLIAPNASQNLVTSDLTTMGLIAKSVEIPTTNLH
] [		•	SNVIPTCEPQSLVENLTQKLNNVNNQLFMTDVKENFKTSLESHT
] (			VLAPLTLKTENGDSQMMALNSCTTSVNSDLQISEDNVIQNFEKT
1 1			LEIIKTAMNSQILEVKSGSQGAGETSQNAQINYNIQLPSVNTVQ
] [			NNKLPDSSP\FSSFISVMPTESNIPQSE\VSHKEDQIQEILEGL
, ,	]		QKLKLENDLSTPASQCVLINTSVTLTPTPVKSTADITVIQPVSE
1	j		MINIQFNDKVNKPFVCQNQGCNYSAMTKDALFKHYGKIHOYTDR
Į I	. [		MILEIKKNQLKFAPFKCVVPTCTKTFTRNSNLRAHCQLVHHFTT
1	}		EEMVKLKIKRPYGRKSQSENVPASRSTQVKKQLAMTEENKKESQ
] [	i		PALELRAETONTHSNVAVIPEKQLIEKKSPDKTESSLQVITVTS
, I	ļ		EQCNTNALTNTQTKGRKIRRHKKEKEEKKRKKPVSQSLEFPTRY
1	j		SDADDADCAMOCCEN VELLOOM STANDS BY BELLOOM STANDS BY BELLOOM STANDS BY BELLOOM STANDS BY BELLOOM STANDS BY BELLOOM STANDS BY BELLOOM STANDS BY BELLOOM STANDS BY BELLOOM STANDS BY BELLOOM STANDS BY BELLOOM STANDS BY BELLOOM STANDS BY BELLOOM STANDS BY BELLOOM STANDS BY BELLOOM STANDS BY BELLOOM STANDS BY BELLOOM STANDS BY BELLOOM STANDS BY BELLOOM STANDS BY BELLOOM STANDS BY BELLOOM STANDS BY BELLOOM STANDS BY BELLOOM STANDS BY BELLOOM STANDS BY BELLOOM STANDS BY BELLOOM STANDS BY BELLOOM STANDS BY BELLOOM STANDS BY BELLOOM STANDS BY BELLOOM STANDS BY BELLOOM STANDS BY BELLOOM STANDS BY BELLOOM STANDS BY BELLOOM STANDS BY BELLOOM STANDS BY BELLOOM STANDS BY BELLOOM STANDS BY BELLOOM STANDS BY BELLOOM STANDS BY BELLOOM STANDS BY BELLOOM STANDS BY BELLOOM STANDS BY BELLOOM STANDS BY BELLOOM STANDS BY BELLOOM STANDS BY BELLOOM STANDS BY BELLOOM STANDS BY BELLOOM STANDS BY BELLOOM STANDS BY BELLOOM STANDS BY BELLOOM STANDS BY BELLOOM STANDS BY BELLOOM STANDS BY BELLOOM STANDS BY BELLOOM STANDS BY BELLOOM STANDS BY BELLOOM STANDS BY BELLOOM STANDS BY BELLOOM STANDS BY BELLOOM STANDS BY BY BELLOOM STANDS BY BY BELLOOM STANDS BY BY BY BY BY BY BY BY BY BY BY BY BY
Į l		İ	SPYRPYRCVHQGCFAAFTIQQNLILHYQAVHKSDLPAFSAEVEE
1	]	ļ	ESEAGKESEETETKQTLKEFRCQVSDCSRIFQAITGLIQHYMKL
, ,	}	l	HEMTPEEIESMTASVDVGKPPCDQLECKSSFTTYLNYVVHLEAD
, ,			HGIGLRASKTEEDGVYKCDCEGCDRIYATRSNLLRHIFNKHNDK
	ļ		HKAHLIRPRRLTPGQENMSSKANQEKSKSKHRGTKHSRCGKEGI
; [		Í	KMPKTKRKKKNNLENKNAKIVQIEENKPYSLKRGKHVYSIKARN
1 1			DALSECTSRFVTQYPCMIKGCTSVVTSESNIIRHYKCHKLSKAF
, ,			TSQHRNLLIVFKRCCNSQVKETSEQEGAKNDVKDSDTCVSESND
į į	1		NSRTTATVSQKEVEKNE*DEMDELTELFITKLINEDSTSVETQA
			NTSSNVSNDFQEDNLCQSERQKASNLKRVNKEKNVSQNKKRKVE
j l		•	KAEPASAAELSSVRKEEETAVAIQTIEEHPASFDWSSFKPMGFE
		}	VSFLKFLEESAVKQKKNTDKDHPNTGNKKGSHSNSRKNIDKTAV
1 !	1		TSGNHVCPCKESETFVQFANPSQLQCSDNVKIVLDKNLKDCTEL
<u> </u>			

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A-Alanine, C-Cysteine, D-Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F-Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
}	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
į.	residue of	amino acid .	W=Tryptophan, Y=Tyrcsine, X=Unknown, *=Stop
i	amino acid	sequence	Codon, /=possible nucleotide deletion,
ł	Bequence	· -	\=possible nucleotide insertion)
			VLKQLQEMKPTVSLKKLEVHSNDPDMSVMKDISIGKATGRGQY
5363	8066	703	RLCCTGGGEGTPGASGKRGPAATTSLVLCIPSVPPPVPFPTLWP
1			PPSWRRQPPGGIRRDFSRRLRREANLVATCLPVRASLPHRLNML
			RGPGPGLLLLAVLCLGTAVPSTGASKSKRQAQQMVQPQSPVAVS
1	1		QSKPGCYDNGKHYQINQQWERTYLGNALVCTCYGGSRGFNCESK
1'			PEAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS
1	]		CTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEWT
ì	Ì		CKPIAEKCFDHAAGTSYVVGETWEKPYQGWMMVDCTCLGEGSGR
ł			ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRG
1	1		EWKCERHTSVQTTSSGSGPFTDVRAAVYQPQPHPQPPPYGHCVT
1	1		DSGVVYSVGMQLA*KTQGNKQML\CTCLGNGVSCQETAVTQTYG
1	İ		GNSNGEPCVLPFTYNGRTFYSCTTEGRQDGHLWCSTTSNYECDO
1			KYSFCTDHTVLVQTRGGNSNGALCHFPFLYNNHNYTDCTSEGRR
			DNMKWCGTTQNYDADQKFGFCPMAAHEEICTTNEGVMYRIGDQW
1	ļ		DKQHDMGHMMRCTCVGNGRGEWTCIAYSQLRDQCIVDDITYNVN
1	ł		DTFHKRHEEGHMLNCTCFGQGRGRWKCDPVDQCQDSETGTFYQI
1			GDSWEKYVHGVRYQCYCYGRGIGEWHCQPLQTYPSSSGPVEVPI
	1		TETPSQPNSHPIQWNAPQPSHISKYILRWRPKNSVGRWKEATIP
ļ	ł		GHLNSYTIKGLKPGVVYEGQLISIQQYGHQEVTRFDFTTTSTST
			PVTSNT\VTGETTPFSPLVATSESVTEITASSFVVSWVSASDTV
1			SGFRVEYELSEEGDEPQYLVLPSTATSV\NIP\DLLPGRKYIVN
· ·	i		VYQISEDGEQSLILSTSQTTAPDAPPDPTVDQVDDTSIVVRWSR
			PQAPITGYRIVYSPSVEGSSTELNLPETANSVTLSDLQPGVQYN
			ITIYAVEENQESTPVVIQQETTGTPRSDTVPSPRDLQFVEVTDV
}			KVTIMWTPPESAVTGYRVDVIPVNLPGEHGQRLPLSRNTF\AEN
1			TGLSPGVTYYFKVFAVSHGRESKPLTAQQTTKL\DAPTNLQFVN
i			ETDSTVLVRWTPPRAQITGYRLTVGLTRRGQPRQYNVGPSVSKY
1			PLRNLQPASEYTVSLVAIKGNQESPKATGVFTTLOPGSSIPPYN
1 :			TEVTETTIVITWTPAPRIGFKLGVRPSQGGEAPREVTSDSGSIV
[			VSGLTPGVEYVYTIQVLRDGQERDAP\IVNK\VVTFLSPPTNLH
1			LEANPDTGVLTVSWERSTTPDITGYRITTTPTNGQQGNSLEEVV
	[		HADQSSCTF\DNLEVPGLEYNVSVYTVKDDKESVPISDTIIPAV
1			PPPTDLRFTN/ILGPDTMRVTW\APPPSIDLTNFLVRYSPVKNE
1			GRMLQSLSIFFLSDN\AVVLTNLLPGTEYVVSVSSVYEOHESTP
1 1			\LRGRQKTGLDSP\TGIDFS\DITA\NSFT\VHW\IAPRA/TPI
			TGYRIR\HHPEHF\SGRPREDR\VPHSRNSITLTNLTPGTEYVV
[			SIVALNGREESPLLIGQQSTVSDVPRDLEVVAATPTSLLI\SWD
[			APAVTVRYYRITYGETGGNSPVOEFTVPGSKSTATISGLKPGVD
1			YTITVYAVTGRGDSPASSKPISINYRTEIDKPSQMQVTDVQDNS
1			ISVKWLPSSSPVIGYRVTTT\PKNGPG\PTKTKTAGPDQTEMTI
{			EGLQPTVEYVVSVYAQNPSGESQPLVQTAVTNIDRPKGLAFTDV
<b> </b> .	,		DVDSIKIAWESPQGQVSRYRVTYSSPEDGIHELFPAPDGEEDTA
			ELQGLRPGSEYTVSVVALHDDMESQPLIGTQSTAIPAPTDLKFT
1			QVTPTSLSAQWTPPNVQLTGYRVRVTPKEKTGPMKEINLAPDSS
			SVVVSGLMVATKYEVSVYALKDTLTSRPAQGVVTTLENVSPPRR
1 1			ARVTDATETTITISWRTKTETITGFQVDAVPANGQTPIQRTIKP
1	1		DVRSYTITGLQPGTDYKIYLYTLNDNARSSPVVIDASTAIDAPS
1	İ		NLRFLATTPNSLLVSWQPPRARITGYIIKYEKPGSPPREVVPRP
	Į.	İ	RPGVTEATITGLEPGTEYTIYVIALKNNQKSEPLIGRKKTDELP
1 1	Ī		
1 1	İ		QLVTLPHPNLHGPEILDVPSTVQKTPFVTHPGYDTGNGIQLPGT SGQQPSVGQQMIFEEHGFRRTTPPTTATPIRHRPRPYPPNVGQE
1 1	1	ļ	ALSQTTISWAPFQDTSEYIISCHPVGTDEEPLOFRVPGTSTSAT
}	ļ		
1	ł		LTGLTRGATYNIIVEALKDQQRHKVREEVVTVGNSVNEGLNQPT
	į	ļ	DDSCFDPYTVSHYAVGDEWERMSESGFKLLCQCLGFGSGHFRCD
( /	(		SSRWCHDNGVNYKIGEKWDRQGENGQMMSCTCLGNGKGEFKCDP
	1		HEATCYDDGKTYHVGEQWQKEYLGAICSCTCFGGQRGWRCDNCR
	ļ	j	RPGGEPSPEGTTGQSYNQYSQRYHQRTNTNVNCPIECFMPLDVQ ADREDSRE
5364	8066	703	
}		,03	RLCCTGGGGTPGASGKRGPAATTSLVLCIPSVPPPVPFPTLWP
		!	PPSWRRQPPGGIRRDFSRRLRREANLVATCLPVRASLPHRLNML RGPGPGLIJJAVI.CLGTAVPSTGASVSPRAACOMVODOS RVAVS
			RGPGPGLLLLAVLCLGTAVPSTGASKSKRQAQQMVQPQSPVAVS

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine.
l	corresponding	to first	
	to first	amino acid	L-Leucine, M-Methionine, N-Asparagine,
- {	amino acid	residue of	P-Proline, Q-Glutamine, R-Arginine,
1	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
1	amino acid	1	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
		sequence	Codon, /=possible nucleotide deletion,
<b> </b>	sequence		\=possible nucleotide insertion)
į			QSKPGCYDNGKHYQINQQWERTYLGNALVCTCYGGSRGFNCESK
1	1		PEAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS
ŀ			CTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEWT
			CKPIAEKCFDHAAGTSYVVGETWEKPYQGWMMVDCTCLGEGSGR
Į.	ļ	1	ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRG
ļ	1		EWKCERHTSVQTTSSGSGPFTDVRAAVYQPQPHPQPPPYGHCVT
			DSGVVYSVGMQLA*KTQGNKQML\CTCLGNGVSCQETAVTQTYG
į	1		GNSNGEPCVLPFTYNGRTFYSCTTEGRQDGHLWCSTTSNYEODO
i	1		KYSFCTDHTVLVQTRGGNSNGALCHFPFLYNNHNYTDCTSEGRR
	]		DNMKWCGTTQNYDADQKFGFCPMAAHEEICTTNEGVMYRIGDQW
1	}		DKQHDMGHMMRCTCVGNGRGEWTCIAYSQLRDQCIVDDITYNVN
Ĭ	i i		DTFHKRHEEGHMLNCTCFGQGRGRWKCDPVDQCQDSETGTFYQI
	1 . 1		GDSWEKYVHGVRYQCYCYGRGIGEWHCQPLQTYPSSSGPVEVFI
J			TETPSQPNSHPIQWNAPQPSHISKYILRWRPKNSVGRWKEATIP.
1			GHLNSYTIKGLXPGVVYEGQLISIQQYGHQEVTRFDFTTTSTST
	[		PVTSNT\VTGETTPFSPLVATSESVTEITASSFVVSWVSASDTV
1		1	SGFRVEYELSEEGDEPQYLVLPSTATSV\NIP\DLLPGRKYIVN
1		•	VYQISEDGEQSLILSTSQTTAPDAPPDPTVDQVDDTSIVVRWSR
	ļ l		PQAPITGYRIVYSPSVEGSSTELNLPETANSVTLSDLQPGVOYN
1	1		ITIYAVEENQESTPVVIQQETTGTPRSDTVPSPRDLQFVEVTDV
1	1		KVTIMWTPPESAVTGYRVDVIPVNLPGEHGQRLPLSRNTF\AEN
	]		TGLSPGVTYYFKVFAVSHGRESKPLTAQQTTKL\DAPTNLQFVN
.			ETDSTVLVRWTPPRAQITGYRLTVGLTRRGQPRQYNVGPSVSKY
1			PLRNLQPASEYTVSLVAIKGNQESPKATGVFTTLQPGSSIPPYN
1 .	ļ		TEVTETTIVITWTPAPRIGFKLGVRPSQGGEAPREVTSDSGSIV
]			VSGLTPGVEYVYTIQVLRDGQERDAP\IVNK\VVTPLSPPTNLH
}			LEANPDTGVLTVSWERSTTPDITGYRITTPTNGQQGNSLEEVV
			HADQSSCTF\DNLEVPGLEYNVSVYTVKDDKESVPISDTIIPAV
1 1			PPPTDLRFTN/ILGPDTMRVTW\APPPSIDLTNFLVRYSPVKNE
] ]	]		GRMLQSLSIFFLSDN\AVVLTNLLPGTEYVVSVSSVYEQHESTP
			\LRGRQKTGLDSP\TGIDFS\DITA\NSFT\VHW\IAPRA/TPI
1 1		ĺ	TGYRIR\HHPEHF\SGRPREDR\VPHSRNSITLTNLTPGTEYVV
1 1		}	SIVALNGREESPLLIGQQSTVSDVPRDLEVVAATPTSLLI\SWD
}		j	
] [			APAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATISGLKPGVD YTITVYAVTGRGDSPASSKPISINYRTEIDKPSQMQVTDVQDNS
			ISVKWLPSSSPVTGYRVTTT\PKNGPG\PTKTKTAGPDQTEMTI
1 1	1		EGLQPTVEYVVSVYAQNPSGESQPLVQTAVTNIDRPKGLAFTDV
1 1	1		DVDSIKIAWESPQGQVSRYRVTYSSPEDGIHELFPAPDGEEDTA
1 1			ELQGLRPGSEYTVSVVALHDDMESQPLIGTQSTAIPAPTDLKFT
] [	ſ		
1	Ì	1	QVTPTSLSAQWTPPNVQLTGYRVRVTPKEKTGPMKEINLAPDSS
1			SVVVSGLMVATKYEVSVYALKDTLTSRPAQGVVTTLENVSPPRR
1 1		1	ARVTDATETTITISWRTKTETITGFQVDAVPANGQTPIQRTIKP DVRSYTITGLQPGTDYKIYLYTLNDNARSSPVVIDASTATDAPS
1			NLRFLATTPNSLLVSWQPPRARITGYIIKYEKPGSPPREVVPRP
4 1		i	
1		j	RPGVTEATITGLEPGTEYTIYVIALKNNQKSEPLIGRKKTDELP
			QLVTLPHPNLHGPEILDVPSTVQKTPFVTHPGYDTGNGIQLPGT
1 1			SGQQPSVGQQMIFEEHGFRRTTPPTTATPIRHRPRPYPPNVGQE
1		ì	ALSQTTISWAPFQDTSEYIISCHPVGTDEEPLQFRVPGTSTSAT
1 1		į	LTGLTRGATYNIIVEALKDQQRHKVRBEVVTVGNSVNEGLNQPT
1		j	DDSCFDPYTVSHYAVGDEWERMSESGFKLLCQCLGFGSGHFRCD
.			SSRWCHDNGVNYKIGEKWDRQGENGQMMSCTCLGNGKGEFKCDP
1 1			HEATCYDDGKTYHVGEQWQKEYLGAICSCTCFGGQRGWRCDNCR
1 1	1	ļ	RPGGEPSPEGTTGQSYNQYSQRYHQRTNTNVNCPIECFMPLDVQ
5365	POCC		ADREDSRE
2305	B066	703	RLCCTGGGEGTPGASGKRGPAATTSLVLCIPSVPPPVPFPTLWP
1	İ	ľ	PPSWRRQPPGGIRRDFSRRLRREANLVATCLPVRASLPHRLNML
1 1	į.		RGPGPGLLLLAVLCLGTAVPSTGASKSKRQAQQMVQPQSPVAVS
			QSKPGCYDNGKHYQINQQWBRTYLGNALVCTCYGGSRGFNCBSK
j ļ			PEAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS
ĺ	1	ľ	CTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEWT
L	<u></u>		CKPLAEKCFDHAAGTSYVVGETWEKPYQGWMMVDCTCLGEGSGR
			· · · · · · · · · · · · · · · · · · ·

SEQ	Predicted	Predicted end	Amino acid segment activity
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
[	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ı	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ł	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
)	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ĺ	amino acid	sequence	Codon, /=possible nucleotide deletion,
	acdreuce	] -	\=possible nucleotide insertion)
			ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRG
1	1	į	EWKCERHTSVQTTSSGSGPFTDVRAAVYQPQPHPQPPPYGHCVT
		1	DSGVVYSVGMQLA*KTQGNKQML\CTCLGNGVSCQETAVTQTYG
1	[		GNSNGEPCVLPFTYNGRTFYSCTTEGRQDGHLWCSTTSNYEQDQ
i	1		KYSFCTDHTVLVQTRGGNSNGALCHFPFLYNNHNYTDCTSEGRR
1	j	J	DNMKWCGTTQNYDADQKFGFCPMAAHEEICTTNEGVMYRIGDQW
-			DKQHDMGHMMRCTCVGNGRGEWTCIAYSQLRDQCIVDDITYNVN
1	İ	1	DTFHKRHEEGHMLNCTCFGQGRGRWKCDPVDQCODSETGTFYOI
ł	}	1	GDSWEKYVHGVRYQCYCYGRGIGEWHCQPLQTYPSSSGPVEVFI
- }			TETPSQPNSHPIQWNAPQPSHISKYILRWRPKNSVGRWKEATIP
			GHLNSYTIKGLKPGVVYEGQLISIQQYGHOEVTRFDFTTTSTST
ſ		ľ	PVTSNT\VTGETTPFSPLVATSESVTEITASSFVVSWVSASDTV
	1	f	SGFRVEYELSEEGDEPQYLVLPSTATSV\NIP\DLLPGRKYIVN
			VYQISEDGEQSLILSTSQTTAPDAPPDPTVDQVDDTSIVVRWSR
		i	PQAPITGYRIVYSPSVEGSSTELNLPETANSVTLSDLQPGVQYN
			ITIYAVEENQESTPVVIQQETTGTPRSDTVPSPRDLQFVEVTDV
İ	ł		KVTIMWTPPESAVTGYRVDVIPVNLPGEHGQRLPLSRNTF\AEN
1	1		TGLSPGVTYYFKVFAVSHGRESKPLTAQQTTKL\DAPTNLQFVN
}	1		ETDSTVLVRWTPPRAQITGYRLTVGLTRRGQPRQYNVGPSVSKY
			PLRNLQPASEYTVSLVAIKGNQESPKATGVFTTLQPGSSIPPYN
1	1		TEVTETTIVITWTPAPRIGFKLGVRPSQGGEAPREVTSDSGSIV
1		,	VSGLTPGVEYVYTIQVLRDGQERDAP\IVNK\VVTPLSPPTNLH
	i		LEANPDTGVLTVSWERSTTPDITGYRITTTPTNGQQGNSLEEVV HADQSSCTP\DNLFVPGLEYNVSVYTVKDDKESVPISDTIIPAV
1	1		PPPTDLRFTN/ILGPDTMRVTW\APPPSIDLTNFLVRYSPVKNE
1	1		GRMLQSLSIFFLSDN\AVVLTNLLPGTEYVVSVSSVYEQHESTP
1			\LRGRQKTGLDSP\TGIDFS\DITA\NSFT\VHW\IAPRA/TPI
1	,		TGYRIR\HHPEHF\SGRPREDR\VPHSRNSITLTNLTPGTEYVV
İ			SIVALNGREESPLLIGQQSTVSDVPRDLEVVAATPTSLLI\SWD
+	]		APAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATISGLKPGVD
1	}		YTITVYAVTGRGDSPASSKPISINYRTEIDKPSQMQVTDVQDNS
}	ļ		ISVKWLPSSSPVTGYRVTTT\PKNGPG\PTKTKTAGPDQTEMTI
1	ļ .		EGLQPTVEYVVSVYAQNPSGESQPLVQTAVTNIDRPKGLAFTDV
1			DVDSIKIAWESPQGQVSRYRVTYSSPEDGIHELFPAPDGEEDTA
1	1		ELQGLRPGSEYTVSVVALHDDMESQPLIGTQSTAIPAPTDLKFT
1	}		QVTPTSLSAQWTPPNVQLTGYRVRVTPKEKTGPMKEINLAPDSS
ļ	1	·	SVVVSGLMVATKYEVSVYALKDTLTSRPAQGVVTTLENVSPPRR
i	<u> </u>		ARVTDATETTITISWRTKTETITGFQVDAVPANGQTPIQRTIKP
ľ	1		DVRSYTITGLQPGTDYKIYLYTLNDNARSSPVVIDASTAIDAPS
J	)		NLRPLATTPNSLLVSWQPPRARITGYIIKYEKPGSPPREVVPRP
1	j		RPGVTEATITGLEPGTEYTIYVIALKNNQKSEPLIGRKKTDELP
	[		QLVTLPHPNLHGPEILDVPSTVQKTPFVTHPGYDTGNGIQLPGT
1	[		SGQQPSVGQQMIFEEHGFRRTTPPTTATPIRHRPRPYPPNVGQE
1			ALSQTTISWAPFQDTSEYIISCHPVGTDEEPLQFRVPGTSTSAT LTGLTRGATYNIIVEALKDQQRHKVREEVVTVGNSVNEGLNQPT
]	]		DDSCFDPYTVSHYAVGDEWERMSESGFKLLCQCLGFGSGHFRCD
<b>!</b> .			SSRWCHDNGVNYKIGEKWDRQGENGQMMSCTCLGNGKGEFKCDP
[	<b>'</b>		HEATCYDDGKTYHVGEQWQKEYLGAICSCTCFGGQRGWRCDNCR
{			RPGGEPSPEGTTGQSYNQYSQRYHQRTNTNVNCPIECFMPLDVQ
L			ADREDSRE
5366	8066	703	RLCCTGGGEGTPGASGKRGPAATTSLVLCIPSVPPPVPFPTLWP
			PPSWRRQPPGGIRDFSRRLRREANLVATCLPVRASLPHRLNML
	1	i	RGPGPGLLLLAVLCLGTAVPSTGASKSKRQAQQMVQPQSPVAVS
j.	j	J	QSKPGCYDNGKHYQINQQWERTYLGNALVCTCYGGSRGFNCESK
		ĺ	PEAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS
	1	1	CTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEWT
	1		CKPIAEKCFDHAAGTSYVVGETWEKPYQGWMMVDCTCLGEGSGR
	}	i	ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLOCICTGNGRG
	1		EWKCERHTSVQTTSSGSGPFTDVRAAVYQPQPHPQPPPYGHCVT
		I.	DSGVVYSVGMQLA*KTQGNKQML\CTCLGNGVSCQETAVTOTYG
			GNSNGEPCVLPFTYNGRTFYSCTTEGRQDGHLWCSTTSNYEQDQ

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
. МО :	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
- 1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
j	to first	amino acid	P=Proline, Q=Glutamine, N=Asparagine,
1	amino acid	residue of	S-Serine, T-Threonine, V-Valine,
1	residue of	amino acid	Wermontonhan Verwagies W. Trib
1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ł	sequence	224401166	Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
<del>                                     </del>			(=possible nucleotide insertion)
			KYSFCTDHTVLVQTRGGNSNGALCHFPFLYNNHNYTDCTSEGRR
	j		DNMKWCGTTQNYDADQKFGFCPMAAHEEICTTNEGVMYRIGDQW
		'	DKQHDMGHMMRCTCVGNGRGEWTCIAYSQLRDQCIVDDITYNVN
ŀ			DTFHKRHEEGHMLNCTCFGQGRGRWKCDPVDQCQDSETGTFYQI
ł	1		GDSWEKYVHGVRYQCYCYGRGIGEWHCQPLQTYPSSSGPVEVFI
			TETPSQPNSHPIQWNAPQPSHISKYILRWRPKNSVGRWKEATIP
1	1		GHLNSYTIKGLKPGVVYEGQLISIQQYGHQEVTRFDFTTTSTST
J	1	•	PVTSNT\VTGETTPFSPLVATSESVTEITASSFVVSWVSASDTV
1	l I		SGPRVEYELSEEGDEPQYLVLPSTATSV\NIP\DLLPGRKYIVN
1			VYQISEDGEQSLILSTSQTTAPDAPPDPTVDQVDDTSIVVRWSR
1		•	PQAPITGYRIVYSPSVEGSSTELNLPETANSVTLSDLQPGVQYN
			ITIYAVEENQESTPVVIQQETTGTPRSDTVPSPRDLQFVEVTDV
1	1		KVTIMWTPPESAVTGYRVDVIPVNLPGEHGQRLPLSRNTF\AEN
1			TGLSPGVTYYFKVFAVSHGRESKPLTAQQTTKL\DAPTNLQFVN
	1 !		ETDSTVLVRWTPPRAQITGYRLTVGLTRRGQPRQYNVGPSVSKY
1	1		PLRNLQPASEYTVSLVAIXGNQESPKATGVFTTLQPGSSIPPYN
ľ	1		TEVTETTIVITWTPAPRIGFKLGVRPSQGGEAPREVTSDSGSIV
1			VSGLTPGVEYVYTIQVLRDGQERDAP\IVNK\VVTPLSPPTNLH
			LEANPDTGVLTVSWERSTTPDITGYRITTTPTNGQQGNSLEEVV
1	1		IIADQSSCTF\DNLEVPGLEYNVSVYTVKDDKESVPISDTIIPAV
1	1		PPPTDLRFTN/ILGPDTMRVTW\APPPSIDLTNFLVRYSPVKNE
ļ	]		GRMLQSLSIFFLSDN\AVVLTNLLPGTEYVVSVSSVYEQHESTP
1	]		\LRGRQKTGLDSP\TGIDFS\DITA\NSFT\VHW\IAPRA/TPI
1			TGYRIR\HHPEHF\SGRPREDR\VPHSRNSITLTNLTPGTEYVV
1	1		SIVALNGREESPLLIGQQSTVSDVPRDLEVVAATPTSLLI\SWD
1	1		APAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATISGLKPGVD
1			YTITVYAVTGRGDSPASSKPISINYRTEIDKPSQMQVTDVQDNS
ł	1		ISVKWLPSSSPVTGYRVTTT\PKNGPG\PTKTKTAGPDQTEMTI
1			EGLQPTVEYVVSVYAQNPSGESQPLVQTAVTNIDRPKGLAFTDV
	)		DVDSIKIAWESPQGQVSRYRVTYSSPEDGIHELFPAPDGEEDTA
ļ			ELQGLRPGSEYTVSVVALHDDMESQPLIGTQSTAIPAPTDLKFT
1			QVTPTSLSAQWTPPNVQLTGYRVRVTPKEKTGPMKEINLAPDSS
	i		SVVVSGLMVATKYEVSVYALKDTLTSRPAQGVVTTLENVSPPRR
	j J		ARVTDATETTITISWRTKTETITGFQVDAVPANGQTPIQRTIKP
1	ŀ		DVRSYTITGLQPGTDYKIYLYTLNDNARSSPVVIDASTAIDAPS
1			NLRPLATTPNSLLVSWQPPRARITGYIIKYEKPGSPPREVVPRP
1			RPGVTEATITGLEPGTEYTIYVIALKNNQKSEPLIGRKKTDELP
1			QLVTLPHPNLHGPEILDVPSTVQKTPFVTHPGYDTGNGIQLPGT
J i			SGOOPSVGQQMIFEEHGFRRTTPPTTATPIRHRPRPYPPNVGQE
j l	1	ĺ	ALSQTTISWAPFQDTSEYIISCHPVGTDEEPLQFRVPGTSTSAT
1	ŀ		LTGLTRGATYNI IVEALKDQQRHKVREEVVTVGNSVNEGLNQPT
1		i	DDSCFDPYTVSHYAVGDEWERMSESGFKLLCQCLGFGSGHFRCD
j i	1		SSRWCHDNGVNYKIGEKWDRQGENGQMMSCTCLGNGKGEFKCDP
			HEATCYDDGKTYHVGEQWQKEYLGAICSCTCFGGQRGWRCDNCR
1 1	}	. 1	RPGGEPSPEGTTGQSYNQYSQRYHQRTNTNVNCPIECFMPLDVQ ADREDSRE
5367	235	3591	
		2321	KKILNMLCKKNIVIEYLADILYEYLYGFCFSGIKKYLIIHVLRL
1 1	ſ	ĺ	ILELWMTRLLLEKSVSLQTQYLLLIVKILSWFPGKEMRHHLQIM
1		İ	EVMMRKQDS/RIVGNGSEQQLQKELADVLMDPPMDDQPGEKBLV
1 1		1	KRSQLDGEGDGPLSNQLSASSTINPVPLVGLQKPEMSLPVKPGQ
, 1	]		GDSEASSPFTPVADEDSVVFSKLTYLGCASVNAPRSEVEALRMM
į J		j	SILRSQCQISLDVTLSVPNVSEGIVRLLDPQTNTEIANYPIYKI
} I			LFCVRGHDGTPESDCFAFTESHYNAELFRIHVFRCEIQEAVSRI
]			LYSFATAFRRSAKQTPLSATAAPQTPDSDIFTFSVSLEIKEDDG
1		ļ	KGYFSAVPKDKDRQCPKLRQGIDKKIVIYVQQTTNKELAIERCF
t 1	ľ	1	GLLLSPGKDVRNSDMHLLDLESMGKSSDGKSYVITGSWNPKSPH
<u> </u>	ĺ		FQVVNEETPKDKVLFMTTAVDLVITEVQEPVRFLLETKVRVCSP
1 1	. [	- 1	NERLFWPFSKRSTTENFFLKLKQIKQRERKNNTDTLYEVVCLBS
			ESERERRKTTASPSVRLPQSGSQSSVIPSPPEDDEEEDNDEPLL
1 1	1	1	SGSGDVSKECAEKILETWGELLSKWHLNLNVRPKQLSSLVRNGV
			PEALRGEVWQLLAGCHNNDHLVEKYRILITKESPQDSAITRDIN

Doginning	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Rolectide   Coration Corresponding to first amino acid saino acid saino acid castine of tract amino acid saino acid saino acid saino acid saino acid saino acid saino acid saino acid saino acid saino acid sequence   Sectine, T-Threonine, Vevaline, sequence   Sectine, T-Threonine, Vevaline, sequence   Sectine, T-Threonine, Vevaline, sequence   Sectine, T-Threonine, Vevaline, sequence   Sectine, T-Threonine, Vevaline, sequence   Sectine, T-Threonine, Vevaline, sequence   Sectine, T-Threonine, Vevaline, sequence   Sectine, T-Threonine, Vevaline, sequence   Sectine, T-Threonine, Vevaline, sequence   Sectine, T-Threonine, Vevaline, sequence   Sectine, T-Threonine, vevaline, sequence   Sectine, T-Threonine, vevaline, sequence   Sectine, T-Threonine, vevaline, sequence   Sectine, T-Threonine, vevaline, sequence   Sectine, T-Threonine, vevaline, sequence   Sectine, T-Threonine, vevaline, sequence   Sectine, T-Threonine, vevaline, sequence   Sectine, T-Threonine, vevaline, sequence   Sectine, T-Threonine, vevaline, sequence   Sectine, T-Threonine, vevaline, sequence   Sectine, T-Threonine, vevaline, sequence   Sectine, T-Threonine, vevaline, sequence   Section, sequence   Section, sequence   Section, sequence   Section, sequence   Section, sequence   Section, sequence   Section, sequence   Section, sequence   Section, sequence   Section, sequence   Section, sequence   Section, sequence   Section, sequence   Section, sequence   Section, sequence   Section, sequence   Section, sequence   Section, sequence   Section, sequence   Section, sequence   Section, sequence   Section, sequence   Section, sequence   Section, sequence   Section, sequence   Section, sequence   Section, sequence   Section, sequence   Section, sequence   Section, sequence   Section, sequence   Section, sequence   Section, sequence   Section, sequence   Section, sequence   Section, sequence   Section, sequence   Section, sequence   Section, sequence   Section, sequence   Section, sequence   Section, sequence   Section, sequence   Section, sequence   Sec	1 .			(Amalanine, CoCysteine, Delenartic Acid Re
Cortesponding   to first   amino acid   residue of   amino acid   residue of   amino acid   residue of   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   am	NO:		location	Glutamic Acid. F=Phenylalanine. G=Glycine
Corresponding	ļ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine
amino acid residue of amino acid residue of amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid		corresponding	to first	L-Leucine, M-Methionine, N-Asparagine,
amino acid maino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence		1	amino acid	P=Proline, Q=Glutamine, R=Arginine,
residue of amino acid sequence    Sequence	ı	1	residue of	S=Serine, T=Threonine, V=Valine,
amino acid sequence  Codon, /-possible nuclecticé deletion, /-possible nuclecticé de deletion, /-possible nuclecticé de deletion, /-possible nuclecticé de deletion, /-possible nuclecticé de deletion, /-possible nuclecticé de deletion, /-possible nuclecticé de deletion, /-possible nuclecticé de deletion, /-possible nuclecticé de deletion, /-possible nuclecticé de deletion, /-possible nuclecticé de deletion, /-possible nucleur de deletion /-possible nucleur de deletion /-possible nucleur de deletion /-possible nucleur de deletion /-possible nucleur de deletion /-possible proposible deletion /-possible proposible de deletion /-possible proposible deletion /-possible proposible deletion /-possible proposible deletion /-possible proposible deletion /-possible deletion /-possible deletion /-possible deletion /-possible deletion /-possible deletion /-possible deletion /-possible deletion /-possible deletion /-possible deletion /-possible deletion /-possible deletion /-possible deletion /-possible deletion /-possible deletion /-possible deletion /-possible deletion /-possible deletion /-possible deletion /-possible deletion /-possible deletion /-possible deletion /-possible deletion /-possible deletion /-possible deletion /-possible deletion /-possible deletion /-possible deletion /-possible deletion /-possible deletion /-possible deletion /-possible deletion /-possible deletion /-possible deletion /-possible deletion /-possible deletion /-possible deletion /-possible deletion /-possible deletion /-possible deletion /-possible deletion /-possible deletion /-possible deletion /-possible deletion /-possible deletion /-possible deletion /-possible deletion /-possible deletion /-possible deletion /-possible /-possible deletion /-possible deletion /-possible deletion /-possible deletion /-possible deletion /-possible deletion /-possible deletion /-possible deletion /-possible deletion /-possible deletion /-possible deletion /-possible deletion /-possible deletion /-possible deletion /-possible deletion /-possible deletion /			amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Appasable nucleotide insertion	ì		sequence	Codon, /=possible nucleotice deletion,
AVLILIAMERGAPSVILVKIMEDYSCHEDIFACHEDIFACHYPUMPH  RIMOSYT POLIVINHED SICHAMWASOCHFILTFARKPINAVHH  IIDLLUCGSISVIPRVALGLIKTSKODLIKTOFGRALKFRYOUL  PRYRESENAKUBLICAMINI SOKKIKYKERSHTHARQOAQO  EDPIERFERENRELGEANNRUEGENDOLAHBUTSKIALKOUL  NAEKKADALNSELIKAT KOLLDAEERSKERJESSBAILKOUCH  RAEKADALNSELIKAT KOLLDAEERSKERJESSBAILKOUCH  ANAEKADALNSELIKAT KOLLDAEERSKERJESSBAILKOUCH  CAMAGESIKKNISSIIGDYKOICSOLSERLEKQOTAKVEIEKIR  QVVDOCERCREPFRATAGOUKSTC  LOKASSIKKNISSIIGDYKOICSOLSERLEKQOTAKVEIEKIR  REMELBLAQTKUQUKTA CAKTOOCHERPY*GLEPFNEVIELAKLE  GAAAGAADPRRSISCEGTHUEDFAITPAVTELLALUGAVIJVIJADA  KINNNENISSIITATATOOCKETC  ROAGA DEITPTERKOULDIDINASSIHEPIVALIBERYDPVS  PROFORELVUSLOTUOLKOHINDNKTILD/IP*NAEVILIVOSTA  WOCCE*KE VORKKUN KORMOVIDSIISANDHALLKIDEBLIDKHISY  PROFORELVUSLOTUOLKOHINDNKTILD/IP*NAEVILIVOSTA  WOCCE*KE VORKKUN KORMOVIDSIISANDHALLKIDEBLIDKHISY  PROFORELVUSLOTUOLKOHINDNKTILD/IP*NAEVILIVOSTA  WOCCE*KE VORKKUN KORMOVIDSIISANDHALLKIDEBLIDKHISY  PROFORELVUSLOTUOLKOHINDNKTILD/IP*NAEVILIVOSTA  AUMILITSBEVOKUN BERNOVIDSIISANDHALLKIDEBLIDKHISY  PROFORENTA SICHAMANOVIDSIISANDHALLKIDEBLIDKHISY  PROFORENTA SICHAMANOVIDSIISANDHALLKIDEBLIDKISY  PROFORENTA SICHAMANOVIDSIISANDHALLKIDEBLIDKISY  PROFORENTA SICHAMANOVIDSIISANDHALLKIDEBLIDKISY  PROFORENTA SICHAMANOVIDSIISANDHALLKIDEBLIDKISY  PROFORENTA SICHAMANOVIDSIISANDHALLKIDEBLINKISY  PROFORENTA SICHAMANOVIDSIISANDHALLKIDEBLINKISY  PROFORENTA SICHAMANOVIDSIISANDHALLKIDAINAN TUKKANOVIDSIISANDHALLKIDAINAN TUKKANOVIDSIISANDHALLKIDAINAN TUKKANOVIDSIISANDHALLKIDAINAN TUKKANOVIDSIISANDHALLKIDAINAN TUKKANOVIDSIISANDHALLKIDAINAN TUKKANOVIDSIISANDHALLKIDAINAN TUKKANOVIDSIISANDHALLKIDAINAN TUKKANOVIDSIISANDHALLKIDAINAN TUKKANOVIDSIISANDHALLKIDAINAN TUKKANOVIDSIISANDHALLKIDAINAN TUKKANOVIDSIISANDHALLKIDAINAN TUKKANOVIDSIISANDHALLKIDAINAN TUKKANOVIDSIISANDHALLKIDAINAN TUKKANOVIDSIISANDHALLKIDAINAN TUKKANOVIDSIITADAINAN TUKKANOVIDSIITADAINAN TUKKANOVIDSIITADAINAN TUKKANOVIDSIITADAINAN TUKKANOVIDSIITADAINAN TUKKANOVIDSIITADAINAN TUKKANOVIDSIITADAINAN TUKKANOVIDSIITADAINAN TUKKANOVIDSIITADAINAN TUKK		sequence	i	\=possible nucleotide insertion)
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FETGH\VPLSQHMLGFAMKSUTQMVMGSTERDQDEVIRQCKNHG TWSEIGKFLDGSLUKGMINTKKQYZDALMQLSVLRNI IKERK GRNSGHIFIDSLVGGHLNDOQILEDSMIFSLASCIITAKLCTW ALWFLTTSEVQKKLYEEINQVFGNGPVTPEKIEQLRYCQUVLOP TVTLSVLVKRLHLLSVEGQVIETKYERCEPALTVAKQTVLOP NTWSPRKEPDPRFDBLVMKTFSSLGFSGTQGCPELRFAMVT TVLLSVLVKRLHLLSVEGQVIETKYERCEPALTVSKRY TVLLSVLVKRLHLLSVEGQVIETKYERCEPALTVSKRY TVLLSVLVKRLHLLSVEGQVIETKYERCEPALTVSKRY TVLSVLVKRLHLLSVEGQVIETKYERCEPALTVSKRY TVLSVLKRHLLSVEGQVIETKYERCEPALTVSKRYANGLEF CHCHLFCLADLTGIKKKYTWQGPTABTILFPTTESDFJLSPS GCLKADVLG\VWRRQGRPERRELL*IFWTEGDSNVCTSVEINGHQVV CHCHLFCLADLTGIKKKYTWQGPTABTILFPTTESDFJLSPS GCLKADVLG\VWRRQGRPERRELL*IFWTEGDSNVCTSVEINGHQVV LLSEHITLAQQSNSPFQVILCPFGLNGTLTGQAFKMSDSATKK VNFYEKDEKPINKSEHLSGSFTFFLHGDSNVCTSVEINGHQVV LLSEHITLAQQSNSPFQVILCPFGLNGTLTGQAFKMSDSATKK LIGEKKQFYFSCVLVPQSIPTPSFVGSTKGSSCLGVMQVPASTROPA MSSVLTJPFTSPESVQTVDQSQVKWVKSSVSDGSNSDSTSHH GGKIPRKLANHVVDRVWQECNNNRAQNKRYSASSGLGEATA AKVASNDFVEATGRTNCSCLRHKNLKSNNAGQQGAPSLGQQQQ ILPFHKINNEKQEKSEKPQKRPLTPFHHVSVSDDVMM\ADS\A SQRLV\ISAP\DSQ\VWFSNIE\TNDTAVKYTYGMFTDFLNVGCK PPLKSVPHCOVVDEGVTKTPSTPGGQAPSHTOMSPTPG PPLSF\HCDVVDEGVTKTPSTPGGAPGMFTDENTYSFKMM EURIDSLGSSPPPQYGARVEPTYVYGTAVALEEDBANIAWKYYK PPKKNDVFLPPQLPSDKYKDDFVGFVGDEVTSVTLEIMQCK PLKVSDELVQQYQIKNQCLSATASDARGEKKIDPYAFVEGDEEF LFPKKDXGNSERRACKKIKVEGGTSSVTVLSHEEDANSLFSSS IKQDAFRTSAAPPSSTLIVDSILAVSYTDLDNIFNSDEDELT PGSKRSANGSDDKASCKESKTONLDPLSCISTADLIKMYPTPPS LEGHINGSPNNNNNKEVKSOMTTFGGTUSCNSSCIGAPFKE VDEGFCSPKDESI KDFSYVYKDENQCILVGGSNFAPLKTLPSQY LPLIKLPECTYRQSWTVGKLELLSSGPSNPPIKTBGDGSNNDGS TTPSTFTRGAGGPSAAGGSVKYENSDLYSPASTESTCRFLMSVEP ATTYSTPQTHTSGGMPPSSAPPSNGGALLPSSSTSTCRFLMSVEP ATTYSTPQTHTSGGMPPSSAPPSNGGALLPSSSTRERDRINSVEP ATTYSTPQTHTSGGMPPSSAPPSNGALLSSCLUKDNSCICCVCMNIK GADVGYTPDTGAAPGCTGFSAVNNRKFGNNSGLFFEDELD IGRNYDGCKARKFREPALAPATSAEHVNGGLESSEKLSDLILL LQQCTMLFSPGAADQDFFPKSCVI INWWRVEREDCCNDCVLA LEHGRPPMORNSGGKVDELLVKSSCLHPMSKRNDVMGCSGDIL RMLSLGQVLQDAIQKKRTVAPMGVGTTMQGFTKMGRGSTG TDESPEPLPIFTTLLGYDYDLVLSFFALPAYRGRAGRSG TDESPEPLPIFTTLLGYDYDLVLSFFALPAYRGNAGGSGG TOESPEPLPIFTTLLGYDYDLVLSFFALPAYRGNAGGSGG TOKATA				WWOCE+KP\ORKKLYENGVTDSLKSNFALLLKLDERILDVNI CV
TWESTCKGFLOGSLDKNMTRKGYEDALMQLESULRNIIKERK GRNSGNIFOSLUGANINDOOLLEDAPIPLAGUTITAKLCTW GRNSGORHFOSLUGANINDOOLLEDAPIPLAGUTITAKLCTW ALWFLTTSEEVQKKLYEEINQVFGNGPVTPEKIEQLRYCQHUCC ETVETAKLTPVSADLQDIEGKRIPRIIFERTLULYALGVULQDE NYWEPSHREPDPREDDBLUWKTFSSLEGTQCEPELRFAMMYT TULLSULVRRLHLLSVBGQVIETKYELVTSSREEAMITYSKRY TULLSULVRRLHLLSVBGQVIETKYELVTSSREEAMITYSKRY PRSLCFSLAREAAVLADGGIRRRRRLGKTSASFFYDRAGSLED CHCHLFCLADLTGIKWKKYVWGGFTSAPILFPVTEEDPILSSPS RCLKADVLG/VWRRDGRPERELL*IFPGGESMCTFYBIKGSPY CKKMMCGRMDPPNNAVLCTSKAVINLLERCLMNRNFYBICKW VKPYEKDEKPINKSEHLSCSFTFFLHGDSNUCTSVSINGHQPVY LLSEEHITLAQGSNSPFQVILCPFGLINGTLTGGAFKMSBATKK LLIGEWGPYPISCCLKEMSEEKQEDMDMEDDSLAAVEVLVAGUR MIYPACFVLVPQSDIPTPSPVGSTHCSSSCLGVHQVBASTRDPA MSSVTLTPPTSPBSUTVDPQSVQLWKFESVSDGRNSDSTSHH GGKIPRKLANHVVDRVWQBCMNNRAQNKRYKSASGGLCEATTA AKVASMDFVEATQRTNGCLSCHHMLKSKRNAGQGQAPSLGGQQQ ILLPHKTNBKQBKSEKRPQKRPLTPPHHRVSUSDDUMD\ADS\A SQRLV\ISAP\DSQLYSFSNIKSRNAGQGQAPSLGGQQQ ILLPHKTNBKQBKSEKRPQKRPLTPPHHRVSUSDDUMD\ADS\A SQRLV\ISAP\DSQLYSFSNIKSNIKSHAGQGGAPSLEGQQQ ILLPHKTNBKQBKSEKRPQKRPLTPPHHRVSUSDDUMD\ADS\A SQRLV\ISAP\DSQLYSFSNIKSNIKSHAGQGGAPSLEGQQQ ILLPHKTNBKQBKKSEKRPQKRPTPPGGBSVTSVTELMVCKK PPKKKDVEFLPPQLPSDFKEDDNAGVTPQGBSVTSVTELMVCKK PPKKKDVEFLPPQLPSDFKEDDNAGVTPGGBSVTSVTELMVCKK PLKVSDELVQQYQTKNQCLSATASDAGGEKIDPVAFVEGDEEP LFPDKKRDRSBERGKKKVKVEDTGSVLSHEDBANIAWETYK PPKKRDVEFLPPQLPSDKKKDDDLDSCTSTADLKHYFPTPS LEGHINGFSRNAMNINGVKSMTTTGGSDELT PGSKRSANGSDDKASCKSKTNDDPLSCTSTADLKHYFPTPS LEGHINGFSRNAMNINGVTGMSDILTDHAGTFTPP PGKRSANGSDDKASCKSKTNDLDFLSCTSTADLKHYFPTPS RTPRTPRGAGGPASAGGSVKYENSDLTSPRSTFSTRPFTPTTP RTPRTPRGAGGPASAGGSVKYENSDLTSPRSTFSTRPFTPTTP RTPRTPRGAGGPASAGGSVKYENSDLTSPRSTFSCRMINSG SGADVGYTPDTTGAAYRCCMPPSSAPPSNGGGILPSPSTREPDEDLIL LOQCTNLFSPFGGAADQDFPKGGVLEKSSKLSDLILL LOQCTNLFSPFGGAADQDFPKGGVLEKSSKLSDLILL LOQCTNLFSPFGGAADQDFPKGGGVLEKSSKLSDLILL RMLSLQPVLQDAIQKKRTVSPMCVQGPLITMQCPHKMAGGSTG TDESEPPLPITTLLGYDYDTLVLSFPALPYWERLMLEPYGSGR DIAYVVLCPRNEALLINGAKSFPGDAADGNNEAPSKLKLXLYAQV CRYNLGPYLASPLDDSLLSQPNLVAPTSQSLITPPQMTNTGNA NTPSATLASAASSTMTVTSGVAATANSTLTTASTSSSS SNAMGGVSSNKLBSFPPPRGSMNS				PETOH\VPLSOHMLGFAMKSVTOMVMGSTFEDDOEVIRFOKNHG
GRNFSGHIFIDSLVGGRININDGGLEDSMIFSLASCIITAKLCTW ALWELTISERVOKKLYBERIOLVERGHOEKIGHER TIPRETLVLYALGVVLQDE NTWPSPHKPDPDRFDDELVMKTFSSLGFSGTGGEGEPERRAMVIT TVLLSVLVKRHLLLSVERQVJETKYELVTSREZAMITYSKRY TVLLSVLVKRHLLLSVERQVJETKYELVTSREZAMITYSKRY TVLLSVLVKRHLLLSVERQVJETKYELVTSREZAMITYSKRY TVLLSVLVKRHLLLSVERQVJETKYELVTSREZAMITYSKRY TVLLSVLVKRHLLSVERQVJETKYELVTSREZAMITYSKRY CHCHLFCLADLIGIKKKYVWQGFTSHEFPTFEDFILSFS RCLKADVLG/VWRRDORPERRELL*IFWGEDFVLVLITLFTMTY OKKKMEGGROPPHNAVLCSKALVHLEFVTEEDFILSFS RCLKADVLG/VWRRDORPERRELL*IFWGEDFVLVLITLFTMTY OKKMEGGROPPHNAVLCSKALVHLEFVTEEDFILSFS RCLKADVLG/VWRRDORPERRELL*IFWGEDFANAVLVLAGVR VKPYEKDEKPINKSEHLSCSFTFFLHGDSNVCTSVEIRGHQPVY LLSEHITLAQQSNSFFQVILCPFGLNGTLITGQAFKMEDSATKK KLIGEWKQPYPISCCLKMESEKQENDEDSLAAVEVLVAGVR MIYPACFVLVPQSDIPTPSFVGSTKGSSCLGVHQVPASTRDPA MSSVLTPPFTSFESVQTVPQDSVQKWFSSSSCLGVHQVPASTRDPA MSSVLTPPFTSFESVQTVPQDSVQKWFSSSSGLGDSATSHH GGKIPRKLANHVVDRVMQDECNMRRAQNKRKYSASSGGLGEEATA AKASMDFVEATORTNCSCLRHKNLKSRNGOQAPSLGQQQ LLPHKTNEKQEKSEKPQKRPLTPFHHRVSVSDDVMM\ADS\A SQRLV\ISAP\DSQ\VFSNILTTDHYDAK\TPGMTFDEDFSGSHTSHH GGKIPRCVNDEGFTTNFTTPGGGAPASTGGNTSTTELMVSP EDRIDSLSGSFPPQYGEAVEPTVYGTAVALBEDERNITAKFYKK FPKKKDVFELPPQD-BDSKYKDDPVAGFWGPTFDFTDYGCKK FPKKDVPELPPQD-BDSKKKDDPVAGFWGBTTSVTLEMVQCKK FPKKDVPELPPQD-BDSKKKDDPVAGFWGBTTSVTELMVQCKK FPKKDVPELPPQD-BDSKKKDDPVAGFWGBTSTTSTELMVSP LEPHKNGFSFNNMNNKFYCSMTTGGSTGTTDLHFKNYPTPPS LEPHKNGFSFNNMNNKFYCSMTGTGSTTDLHFKNYPTPPS LEPHKNGFSFNNMNNKFYCSMTGGAGLPFSFSTRETPTFRTP FRFRGAGGFARAGGSTGTTSCHASVER ATTYSIFPSCHAPPSSAAPSSAFVNNKFGNNSGLFFSB IKDDAFRTSGAADGSVTKLLELLSGPSMTFRFTPTRTP RTFTFRGAGGFARAGGSTGTTSCHASVER ATTYSIFPSCHAPPSSAAPSSAFVNNKFGNNSGLFFSB ILGRATDGCKRAKKFPEARAFASAFVNNKFGNNSGLFFSB ILGRAPTGCKRAKFFEARAFASAFVNNKFGNNSGLFFSB ILGRAPTGCKRAKFFEARAFASAFVNNKFGNNSGLFFSB ILGRAPTGCKRAKFFEARAFASAFVNNKFGNNSGLFFSB ILGRAPTGCKRAKFFEARAFASAFVNNKFGNNSGLFFSB ILGRAPTGCKRAKFFEARAFASAFVNNKFGNNSGLFFSB ILGRAPTGCKRAKFFEARAFASAFVNNKFGNNSGLFFSBLILL LQQCTMLFSPGAADQDPFPKSGVINNWFWEEDCCHOCTMAL LEBGRPDNNNSGGRVDELVKSSCLHPMSKNDDVSMGCSGDILL RMLSLGGVFUDANTGGSGSTGTTSGAASSTANTSTETTASTSSSS SNLMSGVSSN	1			TVWSEIGKGFLDGSLDKNMTRKKOYEDALMOLESVLRNIIKERK
ALWFLITSEEVOKKLYEEINQUENGIVENGEVERPEKIEGLRYCQUILC ETVERTAKLTYPSAGLODIEGKINDER 1 FRETLULVALGVULODD NTWPSPHKEPDDRFDDELVMKTFSSLGFSGTQECPELRPAYMYT TVLLSVLVKRLHLLSVEGQUIETKYELVTSSKEBAWITYSKRY TVLLSVLVKRLHLLSVEGQUIETKYELVTSSKEBAWITYSKRY PRSLCFSLWAEBAVLADGGIERREKJEGTSGTQECPELRPAYMYT TVLLSVLVKRLHLLSVEGQUIETKYELVTSSKEBAWITYSKRY RUKADUTG/VWRRODRERREKJ-INGGGDEVALULTIFTMTY OKKKMECGRNDPMADVLCTSKAVHNLLERCLMNRNFVRIGKWF VKPYEKDEKPINKSEHLSCSFTFFLHGDSNVCTSVEINQHQPYV LLSBEHITLAQGSNSPFQVILCPFGLMGTLTGQAFKMSDSATKK LIGEWKQPYPISCCLKEMSEEKQEDMWEDDSLAAVEVLVAGVR MYPACVLVPQSDIPTSPVGSTUSSCLGVAMVRSSSCHOPASTSTEH GGKIPRKLANHVVDRVWQECMNRAQMKKYSASSGLCEBATA AKVASNDFVEATQRTNCSCLTHKNILKSRNAGQOGAPSLGQQQ ILDFHKTNEKGEKSEKPQKRPLTPFHHRVSVSDDVGMD\ADS\A SGRUVISAP\DSGVVRFSINIFYNDAKITYNKTEMDASDGSTSHH GGKIPRKLANHVVDRVWQECMNRAQMKKYSASSGGLCEBATA AKVASNDFVEATQRTNCSCLTHKNILKSRNAGQOGAPSLGQQQ ILDFHKTNEKGEKSEKPQKRPLTPFHHRVSVSDDVGMD\ADS\A SGRUVISAP\DSGVVRFSINIFYNDAKITYKTEMDASDGSTSHH GGKIPRKLONDERVEKTPTTPGSCHPYQMPTDDLPSKMM EDRIDSLSQSPPPQYQEAVEPTVYVGTAVNLEEDEANIAWYXK PPKKKDVEFLPPQLPSNFKDDDVOPGPGGESTSVTVLEMEDAMDLAFSE EDRIDSLSQSPPPQYQEAVEPTVYVGTAVNLEEDEANIAWYXK PPKKKDVEFLPPQLPSNFKDDDVPGPGGGSTTSPLTNMQCKK PLKVSDELVQQYQIKNQCLSAIASDAEQEFKDPYAPVEGDEFF LFPHKKNDRESPERGKKHKYEGTSSVTVLSHEEDMASLFPSS IKQDAPRFTSHARPPSTSLIYDSDLAVSYTDLDMLFNSDEDELT PGKRSANGSDDMASCKISTYGNLDPLSCISTADLHKMYPTPPS LECHIMGFSPMMMNKEYGSMDTTTGGTVLBENSSIGAQFKLE VDBGFCSFKPSEIKDFSYVYKPENCQILVGCGMPAPLKTLPSQY VDBGFCSFKPSEIKDFSYVYKPENCQILVGCGMPAPLKTLPSQY VGTAYTPQTHTSCGMPPSSAPPSNSGAGILPSFSTPRFPPPRP RTTFTRAGGGPASAQGSVKYENSDLYSPASTFSTCRPLNSVEP ATVPSIPEAHSLYVNLILESSYMMIFKRONSGLFFEDELD IIGNRTDGCKBEARFFRALARTAERINNGGLKSSKLSDDLILL LQQCTNLFSIPGAADQDPFFKSGVISNMVWERENDCCNDCVLA LEHGRQFMDNMSGGKVDEALVKSSCLHPWKRNDSMDSMOSGNDIL RMLLSLQPVLQDAIQKRCTVREWQGPLTWQCFKMAGRGSYG TDESPEPLPIFTTLLGYDDYLVLSFFALPYMERMLDEPYGSGR DIAYVVLCPRHEALINAMSFFROLADGRAPSKLLVAQV CRYDLGPYLASLPHAANSKFFROLTATYSCKLIGGMPPSKLL TDGIMRVGSTASKKLESKLVARWFSQAADGNNERFSKLKLVAQV CRYDLGPYLASLPHDSSLLSQPNIVAPTSCSLTIPQDMTNTGNA NTPSATLASAASTMTTGGVALSSTFMORKVGIFTPOGST				GRNFSQHIFIDSLVQGNLNDQQILEDSMIFSLASCIITAKLCTW
ETVARLITYUSAQLQDIEGKIDRFIIPRETIJULYALGVULQDD NWSPSPKKPDDRFIDDELJWMTFSLGFSCTQDCEPELRYAWNY TULLSVLVRRLHLLSVEQQVIETKYELVTSSREEAWITVSKRY TULLSVLVRRLHLLSVEQQVIETKYELVTSSREEAWITVSKRY TULLSVLVRRLHLLSVEQQVIETKYELVTSSREEAWITVSKRY TULLSVLVRRLHLLSVEQQVIETKYELVTSSREEAWITVSKRY CHCHIFCLADLTGIKKKYVQGELRRRRRLLRGTMSASFVPRGASLED CHCHLFCLADLTGIKKKYVQGELRRRRPLLRGTMSASFVPRGASLED OKKMEGGRNDPPMAVLCJSKAVHNLLERCLMNRNFVRIGKWF VKPYEKDEKPINKSEHLSCSFTFFLHODSNVCTSVEINGHQPVY LLSEEHITLAQQSNSPFQVILCPFGLMGTLTQAFKMSDGATKK LIGBWGQPYPISCCKEMSEEKGEDMDWEDDSLAAVEVLVAGVW MIYPACFVLVPQSDIPTTSPVGSTHCSSSCLGVHQVPASTRDPA MSSVTLPPT3PBEVQCTVDPQSVQKWYRSSVSDGFNSDSTSHH GGKIPKLANHVVDRVQECMMRAQNKRYSASSGGLCEBATA AKVASMDFVEATQRTNCSCLRHKNILKSRNAGQGQAPSLGQQQ LICPHKTNTNKQKSKSKEPQKRPLTPHRVSVSDDVGMADANSA SQRLV,ISAP)DSQVQRSNIR,YNDVAK\TPQMHGTEMANSPQ PPPLSP\HPCDVVDEGVTKTPSTPQSGHTYQMFTDDLVSFKMM EURIDSLSGSPPPGVQERVETVTVGTAVNLEEDEANIAWKYYK FPKKKDVFELPPQLPSDKFKDDPVGPFGGESVTSVTELMVQCKK PLKVSDELVQQYQIKNQCLSALASQEPKIDPYAPVGGDEF LFPDKKDVGNSRERAGKKKVEDGTSSVTVLSHEEDAMSLFSPS IKQDAPRTSHARPPSTSLIVOSDLAVSYTIDUNLFNSDEDELT PGSKRSANGSDDKASCKRSKTGKLDDLSCISTADLIKMYPTPPS LEQHIMGFSPNMNNKEYGSMDTTFGGTVLEGNSSIGAQFKIE VDSGFCSPKPESILDPSTVYKPFDCILVEGNSSIGAQFKIE VDSGFCSPKPESILDPSTYVKPFTGTVLEGNSSIGAQFKIE VDSGFCSPKPESILDPSTYVKPFTGTVLEGNSSIGAPFKIE VDSGFCSPKPESILDPSTYVKPFTGTNLSGSSSIGAQFKIE GADWGYIPDTTGGGWAGAGGAVXYENGISPSTFRFTPTPRTP RTFTFRGAGGAPAGGSVXYENGISPSTFRFTPTPRTP RTFTFRGAGGAPAGGSVXYENGISPSTFRFTPTPTRTP RTFTFRGAGGAPAGGSVXYENGISPSTFRFTPTRTPT RTFTFRGAGGAPAGGSVXYENGISPSTFRFTPTPTRTP RTFTFRGAGGAPAGGSVXYENGISPSTFRFTPTPTRTP RTFTFRGAGGAPAGGSVXYENGIPSTRVNGGLKESEKLSDDLILL LQQCTNLFSFGAADQDPFPKSGVISNVVKRERDCCNDCVIA LEHGRGPPUNNGGKVDEALVKSGVIPMSRNDSUFFGGGR DIAYVVLCPRNEALLINGAKSFFROLTHAYFGSGR DIAYVVLCPRNEALLINGAKSFFROLTHAYFGSGR DIAYVVLCPRNEALLINGAKSFFROLTHAYFGSGR DIAYVVLCPRNEALLINGAKSFFROLTHAYFGSGR TDESPEPLPIFTFLGYDDVLVLSFFALPXGNLTTANSTLTTATSTSSSS SNAMGSVSSNLLSFFPPFGSMMSNAAGSMSTYDNTVGGQGLGQQ QYSALGTAGGSGSSSELPTQPHPPUSTSMMDRXMCTPTGGOGG	1 1			AIWFLTTSEEVQKKLYEEINQVFGNGPVTPEKIEQLRYCQHVLC
TVLLSVLVRRIHLLSVEGQVIETKYELVTSSREEAMITVSKRY  PRSLCFSIMABAAVLADGGLRRRRRLIRGTMSASFVPNGASLED  CHCNLFCLADLTGIKWKKYWGGPTSAPILFFVTEEDPILSSPS RCLKADVLG/VWRRDQRPERRE\L*TFMGGEDP\VLLTITMTY  OKKMRGCRMDPPMNAVLCFSKAVINLLERCLWRNPYFIGKWF VKPYEKDEKPINKSEHLSCSFTFFLHGDSDNVCTSVEINQHQPVY LLSEEHITLAQQSNSPFQVILCPFGLNGTLTQAFKKHSBATKK MIYPACTVUPQSDIFTPSPVGSTHCSSSCLGVMQVPASTNDPA MSSVTLTPPTSPEBVQTVDPQSDVKWKFSSVSDGFNSDSTSHH GGKIPRLANHVVDRVWQECNMNRAQNKKKYSASSGLCEATA AKVASWDFVEATORTNCSCLRHKNIKSKNAGQGQAPSLGCQQ ILPRHKTNEKQEKSEKPQKRPLTPFHHRUSVSDDVCMD\ADS\A SQRLV\ISAP\DSQ\VRFSNIR\TNDVKA\TPOMHGTEMANSPD PPLSP\HPCDVVDQCOVTROCLSATASDAEQEPXIDPTAPVEQDEFP LFPKKDVEFLPPQLESDKKKDDPVQFFQGSVTSVTELMVQCKK PPKKKDVEFLPPQLESDKKKDDPVQFFQGSVTSVTTELMVQCKK PFKKKDVEFLPPQLFDKKKDDPVQFFGGSVTSVTELMVQCKK PFKKNDVEFLPPQLFDKKKDDPVQFFGGSVTSVTELMVQCKK PFKKDVGFLPPQLFSDKKKDDPVQFFGGSVTSVTELMVQCKK PFKKDVGFLPPQLFSDKKKDDPVQFFGGSVTSVTELMVQCK PFKKDPSLPQVGRAVEPTVYVGTAVNLEEDEANIAMKYYK PFKKNDVEFLPPQLFSDKKKDDPVQFFGGSVTSVTELMVQCK PFKKDPSLPSPSSLIVADSLASSTADAEQEPXIDPYAFVEGDEFF LFPDKDRGNSSREAGKKHKVEDGTSSVTVLSHEEDMALFSS IKQDAPPTSFARPPSTSLIVADLAVSYTDLDNLFNSDEDELT PGSKRSANGSDKASCKBSKTGNLDPLSCISTADLHKMYPTPPS LEQHINGFSFMMMNKEYGSMDTTFGGTVLEGNSSSIGAQFKLE VDEGFCSPKPSSIKDFSVYVKENCILVGGGMFAPLKTLPSQY LPLIKLPEECIYRQSWTVGKLELLSSGPSMPPIKEGDGSNMQE YGTAYTPQTHTSCGMPPSSAPPSNGGALIDBFSTRFFFPRTF RTFRTFRGAGGFASAQGSVKYENDSLYSPASTFSCRPLNSVEP ATVPSIPEAHSLYVALLLSESVMNLFKDCNSDSCCICVCNMIK GADVGVIPDPTQGAQVTCTGFSAVMNKKFGNNSCLFFEDELD IGNTDCGKEAEKRFBALRATSAEHVWGGLKESEKLSDDLILL LQQCTNLFSPFGAADQDPFPKSCVISMWVVEERDCCNDCVLA GADVGVIPDPTGAADQDPFPKSCVISMWVVEERDCCNDCVLA LEHGRGPMNMSGGKVDEALVKSCLHPWSKRNDSWGCGSODIL RMLSLQPVLQDAIQKKTVPPWGVQGPLTWQOFHKMAGRGSTG TDESPEPLPIPTFLIGNVIVLVLSFFALTHYPFGRWRLL TDGINRVGSTASKKLSEKLVAEWFSQAADGNREAFSKLLKYAQV CKYDLGPVLASLIPLDSSLLSQPRLVAPTSGOLTTPPQMTNTGNA NTPSATLASAASSTMTVTSGVAISTSVATANSTLTTASTSSSSS SNAMSGVSSSSLPTQPHVSSTTDPRRKYGIPDFGDSH	1 !			ETVRTAKLTPVSAQLQDIEGKIDRFIIPRETLVLYALGVVLODP
PRSLCYSLWAEAAVLADGGIRRRRILIRGTMSASFVRRGASLED CHCHLYCLADLTGIKWKKYVWQGPTSAPILFPVTEEDPILSSPS RCLKADVLG/VWRRDQRPERRE\L'IFWGGEDP\VLLTILFTMTY OKKMMEGGRADFPMNAVLCFSKAVHNLLERCLMMRNFVRIGKWF VKPVEKDERPINKSEHLSGS-FHLGDONVCTSVEINGHQPVY LLSERHTILAQQSNSPFQVILCPFGLNGTLTGQAFKMSDSATKK LIGEWKQPYPISCCLKEMSEERQEDMÜMEDDSLAAVEVLVAGVR MIYPACFVLVVQSDIPTSPVGSTHCSSSCLGVMQVPASTRDPA MSSVTLTPPTSPEEVQTVDPQSVQKWVKFSSVSDGFNSDSTSHH GGKIPRLANHVVDRVWQECMMNRAQNKRKYSASSGLCEBATA AKVASWDFVEATQRTNCSCLRKMLKSRNAGQGGAPSLGQQQ ILPRHKTNEKQEKSEKPQKPLTPPHHRAVSDDVGMV\ADS\A SORLV\ISAP\DSQ\VRFSNIR\T\NDVAK\TOPMATSPDPLVPSKM EURIDSLSSSFPPQVGEAVETVYVGTAVNLEEDEANIAWKYYK PFYKKKDVFLIPPQLPSDKKHDDPVGPFGGESVTSVTLMWQCKK PFLKVSDELVQQVQIRNQCLSATASDAGQEPKIDPYAPVEGDEEF LFPDKKDRQNSEREAGKKHKVEDGTSAVTLISHEEDAMSLFSPS IKDDAPRPTSHARPSTSLIVDSDLAVSYTDLDNLFNSDEDELT PGSKRSANGSDDKASCKRSKTGNLDPLSCISTADLHMWPTPPS LEGLIMGFSPMMMNKEVGSMDTTPGGTVLEGNSSSIGAQFKIE VDEGFCSPKPSEIKDFSVVYKPENCQILVGCSMFAPLKTLPSQY LPHIKLPEECIYRQSWTVGKLELLSSGPSPFTRFFPPRPRP RTPRTRGAGGPASAQGSVKYENSDLYSPASTPSTCRPLNSVEP ATVPSIPPAHSLYVNLILISESVMNLFKGNSSGLIFEBELD IGRNTDCGKAERKFRFALRATSAEHVNGGLKESKLSDDLILL LQDQCTNLFSPFGAADQDFFPKSGVISNMVRVEERDCCDCVLA GADVGVYIPDTTQERQVRCTGGSVNNRKFGNSGLFFEDELD IGRNTDCGKAERKFRFALRATSAEHVNGGLKESKLSDDLILL LQDQCTNLFSPFGAADQDDFPKSGVISNMVRVEERDCCDCVLA CERGRGPMDNNSGGKVDEALVKSSCLHPMSKRHOVSMQCSQDIL RMLLSLQPVLQDAIQKKRTVSPWGVQGPLTWQCFHKMAGRGSYG TDESSPPLPIPTFLLGYDDYDLVLSPFALPYWERLMEPYGSQR DLAYVVLCPENEALLNGAKSFYRDLTAIYESCLLGGHRPVSRLL TDGIMRVGSTASKKLSEKLVAEWFSQAADGNBAFSKLKLVAQV CKYDLGPVLASLPDSSLLGQPHLVAPTSGSLTTPDMTTTGNA NTPSATLASAASSTMTVTSGVAISTSVATANSTLTTASTSSSSS SNLNSGVSSSSLPTPPRPLYSSTMDRRVKYEIPDGDSH	1			NTWPSPHKFDPDRFDDELVMKTFSSLGFSGTQECPELRFAYMVT
CHCKLFCLADLTGIKKKYVMGGPTSAPILFPVTEEDPILSSPS RCLKADVIG/WRRDORPERRE\L*ITMGEDP\VLITITTMTY OKKKMEGGRADPPMNAVLGSKAVHNLLERCLMNRNFVRIGKMP VKPYEKDEKPINNSEHLSCSFTFFLHGDSNVCTSVEINGUGPY LLSEEHTILAQGSNSFGVILCPFGLNGTLTGOAFKMSDEATKK LIGEWKGPYPISCICLKEMSEEKGEDMDMEDDSLAAVEVLWAGVR MIYBACFVLVPQSDIPTSPVGSTHCSSSCLGVHQVPASTRDPA MSSVTLTPFTSPESVGTVDPQSVQKWVKKSSVSDGFNSDTSHH GGKIPRKLANHVVDRWQSCINNRAQNIKRKYSASGGLGEATA AKVASWDFVEATGRTRCSCLRKMLKSRNAGQGGAPSLGQQQ ILPKHKTNEKQEKSEKPQKRPLTPPHRVSVSDDVGMOLDABNA SQRLV\ISAP\DSQ\VRFSIIR\TMDVAK\TOCHGTEMANSPQ PPPLSP\HPCDVVDEGVTKTPSTPQSGHFYOMPTDPLVBSKPM EDRIDGLSQSFPPQQQAVEPTVYGTAVNLEEDEANIAWKYYK PPKKKDVEFLPPQLESDKFKDDPVGPFOGESVTSVTELMVQCKK PLKVSDELVQQVQIKNQCLSATASDAEGPRIDPYAFVEDDELT PGSKRSANSSDDKASCKBSKTGNDDPLSCTSTADLHKMYPTPPS LEGHIMGSFSPKMNNKEYGSMDTTFGGTVLEGNSSSIGAQFKIE VDEGFCSPKSEIKDFSVYVKPENCQILVGCSMFAPLKTLPSQY LPLIKLPEECIYRQSWTVGKLELLSSGPSPFIRFTPFTPRTP RTFRTGRGGFASAGGSVKVENSCLISTADLHKMYPTPPS RTFRTFRGRGGFASAGGSVKVENSCLISTADLHKMYPTPPS GANDWGYIFDTTQCACWTGVELLSSGPSPFIRFTPFTPRTP RTFRTFRGRGGFASAGGSKKKTONLDPLSCISTADLHKMYPTPPS ATVPSIPEAHSLYVNLLLSESVMLFKCONSSCCICVCNNNIK GADVGVIFDDTQCACWTCTGFSAVNNRKFGNNSCLFFEDELD IGRNTDCGKAEKRFFEALATSAEHVWGGJKSEKLSDDLILL LQQCTMLFSFPGAADQDPFPKSGVISNWCVESRDCCICVCNNIK GADVGVIFDDTQGEQVRCTTGGFSAVNNRKFGNNSCLFFEDELD IGRNTDCGKGAEKRFFEALRATSAEHVWGGJKSEKLSDDLILL LQQCTMLFSFPGAADQDPFPKSGVISNWVEWERDCCNDCYLA CLEUGRQFMDNNSGGKVDEALVKSSCLHPWSKRNDVSMQCSQDIL RMLLSLQPVLQDAIQKKTVBFWGVQGFLTMQGFHKMAGRGSTG TDESSPFLPIPTFTLGVDYDYLVAPFRSALLFPQMTNTGNA NTPSATLASAASTMTVTSGVAISTSVATANSTLTTASTSSSSS GNLNSGVSSNILBSFFPFGSMNNAAGSMTQANTVQSGLGGG CYSALQTAGISGSSSSEPTGPHDVSSTTDPROKYGIPDSSH SILNAGVSSNILBSFFFFGSMNNAAGSMTQANTVQSGLGGG	6365			TVLLSVLVKRLHLLSVEGQVIETKYELVTSSREEAWITVSKRY
RCLKADVIG/WRRDORPERRE\L=!FWGGEDP\VLLTILFTMTY OKKKMECGRMPPPMANULCFSKAVHILLERCLMRRIFVRIGKWF VKPYEKDEKPINKSEHLSCSFTFFLHGDSNVCTSVETIORIOPYY LLSEEHTILAQQSNSPQVILCPFELINTITGOAFRMSDSATKK LIGEWKGPYPISCCLKEMSEEKQEDMDWEDDSLAAVEVLVAGVR MIYPACFFLVPQSDIPTPSPVGSTHCSSSCLGVHQVPASTRDPA MSSVTLTPFTSPESVGTVDPQSVQKWKFSSVSDGFNSDSTSHH GGKIPRLANKVDRVMQCCMMRRAQNKRKYSASGGLGEATA AKVASWDFVEATORTNCSCLRHKNLKSRNAGQOGQAPSLGOQQQ ILPKHKTNEKQEKSEKPQKRPLTPFHHRVSVSDDVCMD\ADS\A SORLV\ISAR\DSQ\VHFSHR\TNDVAK\TYPOMHTEMANSPQ PPPLSP\HPCDVVDEGVTKTPSTPQSQHFYQMPTPDPLVPSKPM EDRIDSLSGSFPPQYQEAVEPTVYVGTAVNLEEDEANIAWKYYK PPKKKDVEFLPPQLPSDKFKDDPVGPFGGSVTSVTELMVQCKK PLKVSDELVQQYQIKNQCLSAIASDARGEFKIDPYAFVERDEEF LFPNKKDRORSERBACKKHKOGTSSVTULSHEDAMSLFSPS IKQDAPRTSHARPPSTSLIYDSDLAVSYTDLDNLFNSEDDELT PGSKRSANGSDKRSCKBSKTGRLDPLSCTSTADLIKMYPTPPS LEGHIMSFSFMMNNINEYGSMDTTFGGTVLEGNSSIGAPFKIE VDEGFCSPKPSEIKPFSYVYKPENCQILVGCSMFAPLKTLPSQY LPLIKLPEECIYRQSWTVGKLELLSSGFSMPPIKEGDGSNMOQE YGTAYTPQTHTSCGMPPSSAPSNGAGLLPBSTFRFFTPRTP RTFRTFRGAGGPASAGGSVKYENSDLYSPSTFSTCRPLNSVEP ATVPSIPEAHSLYVNLLLSESVMNLFKDCNSDCCICVONNIK GADVGYIPDPTQEAQYRCTCGFSAVMNKKFGNNSGLFFEDELD IIGNYTDCKEAEKFFALRATSAEHVNGGLKESKELDDLILL LQDCYNLFSIPFAADQDPFPKSGVISMVRVEERDCCNDCYLA LEHGRQFMNMNGGGVDEALVKSSCLHPMSKRNDVSMCGSQDIL RMLLSLQPVLQDAIQKKRTVRPWGVGGPLTWQGFKKMAGRGSYG TDESSPEPLEIPFILLGYDVDLVLSPFALPYWERIMLEPYGSQR DLAYVVLCPENEALLNGSKSFFSCAGLHPSKRNDVSMCCSQDIL RMLLSLQPVLQDAIQKKRTVRPWGVGGPLTWQGFKMAGRGSYG TDESSPEPLEIPFILLGYDVDLVLSPFALPYWERIMLEPYGSQR DLAYVVLCPENEALLNGAKSFFROLTAIYESCRIGGHRPVSRLL TDGIHRVGSTASKKLSEKLVAEWFSQAADGNNEAFSKIKLVAQV CCRUDGPYLASLPLDDSSLLSGMSMTANFALTTASTSSSS SNLNSGVSSNKLJESSFSKHVARSSCLITPPOMTYTONA NTPSATLASAASSTMTVTSGVAISTSVATANSTLTTASTSSSS SNLNSGVSSNKLJESSFSKHVDPRDSSTSTDRDKYGIFDDSSH	3309	1	6622	PRSLCFSLWAEAAVLADGGLRRRRRLLRGTMSASFVPNGASLED
QKKMECGRMDFPMNAVLCSSKAVHNLLERCLMMRNFVRIGKWF VKPYEKDEKPINKSEHLSCSFTFFLHGDSNVCTSVEINQHQPYY LLSEEHITLAQQSNSFFQVILCPFGLMGTLTGOAFKMSDSATKK LIGEWKQFYFISCCLKEMSEEKQEBMWEDDSLAAWEVLVAGVR MIYPACFVLVPQSDIPTPSPVGSTHCSSSCLGVHQVPASTRDPA MSSVTLTPPTSPEEVQTVDPQSVQKWVKFSSVSDGFNSDSTSHH GGKIPRKLANHVVDRVWQECNMNRAQNKRKYSASSGGLCEATA AKVASWDFVEATORTNCSCLRHKNLKSRNAGQQQAPSLGQQQ ILPKHKTNERQEKSEKPQKRPLTPFHHRVSVSDDVCMD\ADS\A SQRLV\ISAR\DSQ\VWFSNIR\TNDWAK\TPQMHGTEMNNSPQ PPPLSP\HPQUVDTGGYTKTPSPQSQHPYQMPTPDPLVPSKPM EDRIDSLSQSFPPQYQEAVEPTVYVGTAVNLEEDEANIAWKYYK FPKKKDVEFLPPQLPSDKFKDDPVGFFGQESVTSVTELNVQCKK PLKV9BELVQQYQIKNQCLSAIASDASQEFKIDPYAFVEGDEEF LFPDKKDRQNSEREAGKKHKVEDGTSSVTVUSHEEDAMSLFSPS IKQDAPRPTSHARPPSTSLIYDSDLAVSYTDLDNLFNSDEDELT PGSKRSANGSDDFASCKESKTLDPLSCISTADLHKMYTPPS LEQHIMGFSPMNMNNKEYGSMDTTPGGTVLEGNSSSIGAQFKIE VDBGFCSPKPSEIKDFSYYYKENCOLIVGCSMFAPLKTLPSQY LPLIKLPEECITYRQSHTVGKLELLSSGPSMPFIKEGDGSNMOQE YGTAYTPQTHTSCGMPPSSAPPSNSGAGILPSPSTPFTPTPTP RTPRTPRGAGGPASAGGSVKYENSDLYSPASTPSTCRPLNSVEP ATVPSIPEAHSLYVNLLLSESVMNLFECNSDSCCICVCNNMIK GADUGY IPDPTQEAQYRCTCGFSAVMNRKFGNNSGLFFEDELD IIGRNTDCGKEAEKAFEALRATSAEKTWGELKESEKLSDDLILL LQQCTNLFSIFGAADQDJPFKSGVISNWYWEERDCCNDCVLA LEHGRQFMDNMSGGKVDEALVKSSCLHPWSKRNDVSMQCSQDIL RMLLSQVUQDAIQKKTVRPWGVGGPLTWQGFHKMAGRGSYG TDESSPEPLIPTFLIGYDYDLVLSFFALDYWERRENCEDCYLA LEHGRQFMDNMSGGKVDEALVKSSCLHPWSKRNDVSMQCSQDIL RMLLSQVUQDAIQKKTVRPWGVGGPLTWQGFHKMAGRGSYG TDESSPEPLIPTFLIGYDYDLVLSFFALDYWERLMLGRYSGOG DIAYVVLCPENEALLNGAKSYFRDLTAIYESCRLGQHRPVSRLL TDGIMRVSTASKLESKLVAEWFSQAADGNNEAFSKLKLIAQV CCKYDLGPYLASLPLDSSLLSQPNLWAPFSQSLTPPOMTNTGNA NTPSATLASAASSTMTVTSGVAISTSVATANSTLTTASTSSSSS SNLNSGVSSNKLPSFPFGSNNSNAAGSMSTQAANTVGSQGLGGQ QTSALQTAGISGESSSLFTPQDFPDSSESSSSSSFTQDDFBSSSSSLFTDGDSS				CHCNLFCLADLTGIKWKKYVWQGPTSAPILFPVTEEDPILSSFS
UKPYEKDEKPINKSEHLSCSFTFFLHGDENVCTSVEINGHQPYY LLSEEHITLAQQSNSPFQVILCPFGLNGTLTGQAFKMSDEATKK LIGEWKGPYPISCCLKEMSEEKQEDMDWEDDSLAAVEVLVAGVR MIYPACFVLVPQSDIPTBSPVGSTHCSSSCLGVHQVPASTRDPA MSSVTLTPPTSPEVGTVDPQSVQKWVKFSSVSDGFNSDSTSHH GGKIPRLANHVVDRVWQCKMNRRQNKRKYSASSGGLCEATA AKVASWDFVEATORTNCSCLRIKNLKSRNAGQQGQAPSLGQQQ ILPKHKTNEKQEKSEKPQKRPLTPPHERVSVSDDVSMQADDS\A SQRLV\ISAP\DSQ\VRFSNIR\TNDAK\TPQMHSTEMANSPQ PPPLSP\HPCDVVDEGVTKTPSTPQSQHFYQMPTPDPLVPSKPM EDRIDSLSQSFPPQVQEAVEFTVYVGTAVNLEEDEANIAWKYYK FPPKKKDVEFLPPQLPSDKFKDDPVGPFGGESVTSVTELHVQCKK PLKV3DELVQQYQIKMQCLSAIASDAEQEPKIDPYAFVEGDEEF LFPDKKDRQNSEREAGKKHKVEDGTSSVTVLSHEEDAMSLFSPS IKQDAFRPTSHAPPSTSLIVDSDLAVSYTDLDNLFNSDEDELT PGSKRSANGSDDKASCKESKTGNLDPLSCISTADLHKMYPTPPS LEQHIMGFSPMNNNNKEYGSMDTTPGGTVLEGNSSIGAQFKIE VDEGFCSPKPSEIKDFSVYVKPENCQILVGCGMFAPLKTLPSQY LPLIKLPEECIYRQSWTVGKLELLSSGPSMPFIKEGDGSNMDQE YGTAYTPQTTTSGCMPPSSAPPSNGAGILPSPSTPRFFTPRTP RTFTFRGAGGPASAGGSVXFENSDLSYSPASTPSTCRPLNSVEP ATVPSIPEAHSLYVNLILSESVMNLFKDCNSDSCICUCNNNIK GADVGVIPDPTQEAQYRCTCGFSAVNRKRGNNSGLFFEDELD ILGRNTDCGKAERKPFBALRATSAEHVNGGLKESEKLSDDLILL LQDQCTNLFSFFGAADQDFPKSGVISMVVEVERDCCNDCYLA LEHGRQFMDNMSGGKVDEALVKSSCLHPWSKRNDVSMQCSQDIL RMLLSLQPVLQDAIQKKRTVRFWGVQGPLTWQOFHKMAGRGSYG TDESPEPLIPTFLLGYDYDYLVLSPFALPYWERLMLEPYGSQR TDESPEPLIPTFLLGYDYDYLVLSPFALPYWERLMLEPYGSQR DIAYVVLCPENEALLNGAKSFFRDLTAIYSSCLIGQHRPVSRLL TDGIMRVGSTASKKLSEKLVAEWFSQAADGNNEAFSKLKLYAQV CRYDLGPYLASLPLDSSLISQPNLVAPTSQSLITPPQMTNTGNA NTPSATLASAASSTMTVTSGVAISTSVATANSTLTTASTSSSSS SNLNSGVSSNKLPSFPPFGSMNSNAAGSMSTQANTVGSGCJGGQQ QTSALQTAGISGESSSLPTQPPHPDVSSSTMDRDKYGIPTDGDSH	1 1	1		OKKAMECCEMPERMINING CECANITIVE FERGEDE AND AND AND AND AND AND AND AND AND AND
LISEEHITLAQOSNSPFQVILCPFGLNGTLTGQAFKMSDSATKK LIGEMKQPYPISCCLKEMSEEKQEDMDWEDDSLAAVEVLVAGVR MIYPACFVLVPQSDIPTSPVGSTKGSSCLGVHQVPASTRDPA MSSVTLTPPTSPESVGTVDPQGVQKWVKFSSYSDGFNSDSTSHH GGKIPRKLANHVVDRVWQECMMNRAQNKRKYSASSGSLCEEATA AKVASWDFVEATGRTNGSCLSHKNLKSRNAGQOGQAPSLGQQQQ ILPHHKTNEKQEKSEKPQKRPLTPFHHRVSVSDDVGMD\ADS\A SQRLV\ISAP\DSQ\VRFSNIR\TNDVAK\TPOMHGTEMANSPQ PPPLSP\HPCDVVDEGVTKTTSTPQSQHFYQMFTDPDLVPSKFM EDRIDSLSGSFPPQVGEAVEPTVYVGTAVNLEEDEANIAWKYYK PPKKKDVEFLPPQLPSDKFKDDPVGPFGQESVTSVTLEMVQCKK PPLKV9DELVQQYQIKNQCLSAIASDAEQEPKTDPYAFVEGDEEF LFPPKKDRQNSERSAGKKHKVEDGTSSVTVLSHEEDAMSLFSPS IKQDAPRPTSHARPPSTSLIYDSDLAVSYTDLDNLFNSDEDELT PGSKRSANGSDDKASCKRSKTGNLDPLSCISTADLHKMYPTPPS LEQHIMGFSPMNMNNKEYGSMDTTFGGTVLEGNSSIGAQFKIE VDEGFCSPKPSEIKDPSYVYKPENCQLIVGCSMFAPLKTLPSQY LPLIKLPEECIYRQSWTVQKLELLSGGFSMPPIKEGDGSNMDQE YGTAYTFQTHTSCGMPPSSAPPSNSGAGILPSPSTPRFPTPRTP RTFPTFRAGGPASAQGSVKYENSDLYSPASTFSTCRPLNSVEP ATVPSIPEAHSLVVNLLLSESVMNLFKDCNSDSCCICVCNNNIK GADVGVIPDPTOEAQYRCTGGFSAVNNKKEGNNSGLFFEDELD IIGNTDCGKEAFKPEALRATSAHVVNGGLKESKLSDDLILL LQDQCTNLFSIFGAADQDPFPKSCVISMVWREEDCONDCYLA LEHGROPMDNMSGGKVDEALVKSSCLHPHSKRNDVSMQCSQDIL RMLLSLQPVLQDAIQKKRTVRPHGVGPFLTWQGFIKMAGRGSYG TDESPEPLIPTFLLGYDYDYLVLSFFALPYMEHMLEPYGSQR TDESPEPLIPTFLLGYDYDYLVLSFFALPYMEHMLEPYGSQR DIAYVVLCPENEALLMGAKSFPROLTAIYESCRLGQHRPVSRLL TDGIMRVGSTASKKLSEKLVAEWFSQAADGNNEAFSKLKLYAQV CRYDLGPYLASLPLDSSLISQPNLVAPTSQSLITPPOMTNTGNA NTPSATLASAASSTMTVTSGVAISTSVATANSTLTTASTSSSSS SNLNSGVSSNKLPSFPPFGSMNSNNAAGSMSTQANTVQSQQLGQQ QTSALQTAGISGESSSLPTQPHPDVSSSTMDRNOKYG PTDGDSH	1 1	1		VKPYEKDRKPINKSEHI.SCSETPEI UGDSNIGTSUBTNOUDDIN
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MSSVTLTPFTSPEEVQTVDPQSVQKWVKFSSVSDGFNSDSTSHH GGKIPRKLANHVVDRVWQECMMNRAQNKRKYSASSGICEEATHA AKVASWDFVEATQRTNCSCLRHKNILKSRNAGQGQAPSIGCQQQ ILPKHKTMEKQEKSEKPQKRPLTPPHHRVSVSDDVGMD\ADS\A SQRLV\ISAP\DSQ\VRFSNIR\TMDVAK\TPCMFTEMANSPQ PPPLSP\HPCDVVDGTVKTPSTPQSQHFYQMPFTDPLVPSKPM EDRIDSLSQSFPPQYQEAVEPTVYVGTAVNLEEDEANIAWKYYK FPKKKDVEFLPPQLPSDKFKDDPVGFFGQESVTSVTELMVQCKK PLKV3DELVQQYQIKNQCLSAIASDAEQEPKIDPYAFVEGDEEF LFPDKKDRQNSEREAGKKHKVEDGTSSVTVLSHEEDAMSLFSPS IKQDAPRPTSHARPPSTSLIYDSDLAVSYTDLDNLFNSDEDELT PGSKRSANGSDDKASCKESKTGNLDPLSCISTADLHKMYPTPPS LECHIMGFSPMNMNKEYGSMDTTPGGTVLEGNSSSIGAQFKIE VDEGFCSPKPSEIKDFSYVYKPENCQILVGCSMFAPLKTLPSQY LPLIKLPECIYRGSWTVOKLELLSSGPSMPPIKEGDSNNDQE YGTAYTPQTHT3CGMPPSSAPPSNSGAGILPBFSTPRFPPTRTP RTPRTPRGAGGPASAQGSVKYENSDLYSPASTFSTCRFLNSVEP ATVPSIPEAHSLYVNLILESSVMNLFKDCNSDSCICVCMNNIK GADUGVYIPDPTQEAQYRCTCGFSAVMNKKFGNNSGLFFEDELD IIGRNTDCGKEAEKRFEALRATSAEHVNGGLKESEKLSDDLILL LOOCTNLFSIFGAADQDPFPKSGVISNWVVEERDCCNDCYLA LEHGRQFMDMSGGKVDERLVKSSCLHFWSRNDUSMQCSQDILL RMLSLQPVLQDAIQKKRTVRPWGVGGPLTWQOFHKMAGRSYG TDESPEPLPIPTFILGYDYDYLVLSPFALPYWERLMLEPYGSQR DIAYVVLCPRNEALINGAKSFFRDLTAIYESCRLGGHRPVSRLL TDGIMRWGSTASKKLSEKLVAEWFSQAADGNNEAFSKLKLYAQV CRYDLGPYLASLPLDSSLLSQPNLVAFTSQSLITPPQMTMTGNA NTPSATLASAASSTMTVTGVAISTSVATANSTLTTASTSSSSS SNLNSGVSSNKLPSFPSPFGSMSNAAGSMSTQANTVQSQOLGGQ QTSALQTAGISGESSSLFTQPHEVDVSSSTMDRDKVGIPTGDSSH	1 1			MIYPACFVLVPQSDIPTPSPVGSTHCSSSCLGVHQVPASTRDPA
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GADVGVYIPDPTQEAQYRCTCGFSAVMNRKFGNNSGLFFEDELD IIGRNTDCGKEAEKRFEALRATSAEHVNGGLKESEKLSDDLILL LQDQCTNLFSIFGAADQDPFXSGVISNWVRVEERDCCNDCYLA LEHGRQFMDNMSGGKVDEALVKSSCLHPWSKRNDVSMQCSQDIL RMLLSLQPVLQDAIQKKRTVRPWGVQGPLTWQQFHKMAGRGSYG TDESPEPLPIPTFLLGYDYDYLVLSFFALPYWERLMLEPYGSQR DIAYVVLCPENEALLNGAKSFFRDLTAIYESCRLGQHRPVSRLL TDGIMRVGSTASKKLSEKLVAEWFSQAADGNNEAFSKLKLYAQV CRYDLGPYLASLPLDSSLLSQPNLVAPTSQSLITPPQMTNTGNA NTPSATLASAASSTMTVTSGVAISTSVATANSTLTTASTSSSSS SNLNSGVSSNKLPSFPPFGSMNSNAAGSMSTQANTVQSGQLGGQ QTSALQTAGISGESSSLPTQPHPDVSESTMDRNKVGIPTDGDSH		ļ	ļ	RTPRTPRGAGGPASAQGSVKYENSDLYSPASTPSTCRPLNSVEP
IIGRNTDCGKEAEKRFEALRATSAEHVNGGLKESEKLSDDLILL LQDQCTNLFSIFGAADQDFFPKSGVISMVVRVEERDCCNDCYLA LENGRYMDNMSGGKVDEALVKSSCLHPWSKRNDVSMQCSQDIL RMLLSLQPVLQDAIQKKRTVRPWGVQGPLTWQQFHKMAGRGSYG TDESPEPLPIPTFLLGYDYDYLVLSFFALPYWERLMLEPYGSQR DIAYVVLCPENEALLNGAKSFFRDLTAIYESCRLGQHRPVSRLL TDGIMRVGSTASKKLSEKLVAEWFSQAADGNNEAFSKLKLYAQV CRYDLGPYLASLPLDSSLLISQPNLVAPTSQSLITPPQMTNTGNA NTPSATLASAASSTMTVTSGVAISTSVATANSTLTTASTSSSSS SNLNSGVSSNKLPSFPFGSMNSNAAGSMSTQANTVQSGQLGGQ QTSALQTAGISGESSSLPTQPHPDVSESTMDRNKVGIPTDGDSH			l	ATVESTEEAHSLYVNLILSESVMNLFKDCNSDSCCICVCNMNIK
LQDQCTNLFSPFGAADQDFFPXSGVISNWVRVEERDCCNDCYLA LEHGRQFMDNMSGGKVDEALVKSSCLHPWSKRNDVSMQCSQDIL RMLLSLQPVLQDAIQKKRTVRPWGVQGPLTWQDFHKMAGRGSTG TDESPEPLPIFTFLLGYDYDYLVLSPFALPYWERLMLEPYGSQR DIAYVVLCPENEALLMGAKSFFRDLTAIYESCRLGQHRPVSRLL TDGIMRVGSTASKKLSEKLVAEWFSQAADGNNEAFSKLKLYAQV CRYDLGPYLASLPLDSSLLSQPNLVAPTSQSLITPPQMTNTGNA NTPSATLASAASSTMTVTSGVAISTSVATANSTLTTASTSSSS SNLNSGVSSNKLPSFPFGSMNSNAAGSMSTQANTVQSGQLGGQ QTSALQTAGISGESSSLPTQPHPDVSESTMDRNKVGIPTDGDSH	.			TICHNEDCOVER BY BERLERAL BY BOOK OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STAT
LEHGRQFMDNMSGGKVDEALVKSSCLHPWSKRNDVSMQCSQDIL RMLLSLQPVLQDAIQKKRTVRPWGVQGPLTWQQFHKMAGRGSYG TDESPEPLPIPTFLLGYDYDYLVLSPFALPYWERLMLEPYGSQR DIAYVVLCPENEALLNGAKSFFRDLTAIYESCRLGQHRPVSRLL TDGIMRVGSTASKKLSEKLVAEWFSQAADGNNEAFSKLKYAQV CRYDLGPYLASLPLDSSLLSQPNLVAPTSQSLITPPQMTNTGNA NTPSATLASAASSTMTVTSGVAISTSVATANSTLTTASTSSSSS SNLNSGVSSNKLPSFPFGSMNSNAAGSMSTQANTVQSGQLGGQ QTSALQTAGISGESSSLPTQPHPDVSBSTMDRDKVGIPTDGDSH	] [		,	LODOCTNIES DECARDODE DE LOCALISTE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DEL CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DEL CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE DE LA CONTRE D
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TDESPEPLPIPTFLLGYDYDYLVLSPFALPYWERIMLEPYGSQR DIAYVVLCPENEALLNGAKSFFRDLTAIYESCRLGQHRPVSRLL TDGIMRVGSTASKKLSEKLVAEWFSQAADGNNEAFSKIKLYAQV CRYDLGPYLASLPLDSSLLSQPNLVAFTSQSLITPPQMTNTGNA NTPSATLASAASSTMTVTSGVAISTSVATANSTLTTASTSSSS SNLNSGVSSNKLPSFPFGSMNSNAAGSMSTQANTVQSGQLGGQ QTSALQTAGISGESSSLPTQPHPDVSBSTMDRDKVGIPTDGDSH				RMLLSLOPVLODATOKKRTVRPWGVOGDITWOOFHYMAGDGGVG
DIAYVVLCPENEALLINGAKSFFRDLTAIYESCRLGQHRPVSRLL TDGIMRVGSTASKKLSEKLVAEWFSQAADGNNEAFSKLKLYAQV CRYDLGPYLASLPLDGSLLSQPNLVAPTSQSLITPPQMTNTGNA NTPSATLASAASSTMTVTSGVAISTSVATANSTLTTASTSSSS SNLNSGVSSNKLPSFPFGSMNSNAAGSMSTQANTVQSGQLGGQ QTSALQTAGISGESSSLPTQPHPDVSESTMDRDKVGIPTDGDSH				TDESPEPLPIPTFLLGYDYDYLVLSPFALPYWERI.MI.EDVCQOD
TDGIMRVGSTASKKLSEKLVAEWFSQAADGNNEAFSKLKLYAQV CRYDLGPYLASLPLDSSLLISQPNLVAPTSQSLITPPQMTNTGNA NTPSATLASAASSTMTVTSGVAISTSVATANSTLTTASTSSSSS SNLNSGVSSNKLPSFPFGSMN3NAAGSMSTQANTVQSGQLGGQ QTSALQTAGISGESSSLPTQPHPDVSESTMDRDKVGIPTDGDSH				DIAYVVLCPENEALLNGAKSFFRDLTAIYESCRLGOHRPUSBLI.
CRYDLGPYLASLPLDSSLLSQPNLVAPTSQSLITPPQMTNTGNA NTPSATLASAASSTMTVTSGVAISTSVATANSTLTTASTSSSSS SNLNSGVSSNKLPSFPPFGSMN9NAAGSMSTQANTVQSGQLGGQ QTSALQTAGISGESSSLPTQPHPDVSESTMDRDKVGIPTDGDSH		j		TDGIMRVGSTASKKLSEKLVAEWFSQAADGNNEAFSKLKLYAOV
NTPSATLASAASSTMTVTSGVAISTSVATANSTLTTASTSSSSS SNLNSGVSSNKLPSFPPFGSMN9NAAGSMSTQANTVQSGQLGGQ QTSALQTAGISGESSSLPTQPHPDVSESTMDRDKVGIPTDGDSH		j	1	CRYDLGPYLASLPLDSSLLSQPNLVAPTSQSLITPPOMTNTGNA
SNLNSGVSSNKLPSFPPFGSMN9NAAGSMSTQANTVQSGQLGGQ QTSALQTAGISGESSSLPTQPHPDVSESTMDRDKVGIPTDGDSH			1	NTPSATLASAASSTMTVTSGVAISTSVATANSTLTTASTSSSSS
QTSALQTAGISGESSSLPTQPHPDVSESTMDRDKVGIPTDGDSH AVTYPPAIVVYIIDPFTYENTDESTNSSSVWTLGLLRCFLEMVQ	.		ł	SNLNSGVSSNKLPSFPPFGSMNSNAAGSMSTQANTVQSGOLGGO
AVIYPPALVVYIIDPFTYENTDESTNSSSVWTLGLLRCFLEMVQ		į.	İ	QTSALQTAGISGESSSLPTQPHPDVSBSTMDRDKVG1PTDGDSH
				AVIIPPALVVYIIDPFTYENTDESTNSSSVWTLGLLRCFLEMVQ

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F-Phenylalanine, G-Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ļ	amino acid	sequence	Codon, /=possible nucleotide deletion,
ł	sequence	•	\=possible nucleotide insertion)
			TLPPHIKSTVSVQIIPCQYLLQPVKHEDREIYPQHLKSLAFSAP
ļ			TQCRRPLPTSTNVKTLTGFGPGLAMETALRSPDRPECIRLYAPP
{	i		FILAPVKDKQTELGETFGEAGQKYNVLFVGYCLSHDQRWILASC
ł		•	TDLYGELLETCIINIDVPNRARRKKSSARKFGLQKLWEWCLGLV
			QMSSLPWRVVIGRLGRIGHGELKDWSCLLSRRNLQSLSKRLKDM
1			CRMCGISAADSPSILSACLVAMEPQGSFVIMPDSVSTGSVFGRS
1	i '		TTLNMQTSQLNTPQDTSCTHILVFPTSASVQVASATYTTENLDL
1			APNPNNDGADGMGIFDLLDTGDDLDPDIINILPASPTGSPVHSP
1			GSHYPHGGDAGKGQSTDRLLSTEPHEEVPNILQOPLALGYFVST
j			AKAGPLPDWFWSACPQAQYQCPLFLKASLHLHVPSVQSDELLHS
1			KHSHPLDSNQTSDVLRFVLEQYNALSWLTCDPATQDRRSCLPIH
			FVVLNQLYNFIMNML
5370	1226	716	RWSRKLELRRAAQATESRPPQSQEMHPPTGKEVHALKRLRDSAN
1			ANDVETVQQLLEDGADPCAADDKGRTALHFASCNGNDQIVQLLL
-			DHGADPNQRDGLGNTPLHLAACTNHVPVITTLLRGGARVDALDR
			AGRTPLHLAKSKLNILQEGHAQCLKAVR/HGGEADHPYAEGVSG
			APRAT*AARCSGVFPSPSRWLGSAPWSRSSCTIWSLPLHEAKCR
ſ			AVRPLSSAAQGSAPSSSSCCTVSTSLALAESLSLFRACTSLPVG
			GCISWL
5371	1331	167	IAAMLWKLLLRSQSCRLCSFRKMRSPPKYRPFLACFTYTTDKQS
1			SKENTRTVEKLYKCSVDIRKIRR*KDGYF*RMKPMLKKLRI/F
1			LQELGADETAVASILERCPEAIVCSPTAVNTQRKLWQLVCKNEE
1			ELIKLIEQFPESFFTIKDQENQKLNVQFFQELGLKNVVISRLLT
1 .			AAPNVFHNPVEKNKQMVRILQESYLDVGGSEANMKVWLLKLLSQ
1			NPFILLNSPTAIKETLEFLQEQGFTSFEILQLLSKLKGFLFQLC
			PRSIQNSISFSKNAFKCTDHDLKQLVLKCPALLYYSVPVLEERM
}			QGLLREGISIAQIRETPMVLELTPQIVQYRIRKLNSSGYRIKDG
			HLANLNGSKKEFEANFGKIQAKKVRPLFNPVAPLNVEE
5372	51	857	SPGAQFLWAAPDMPDPLFSAVQGKDEILHKALCFCPWLGKGGME
1	· ·		PLRLLILLFVTELSGAHNTTVFQGVAGQSLQVSCPYDSMKHWGR
1 1			RKAWCRQLGEKGPCQRVVSTHNLWLLSFLRRWNGSTAITDDTLG
1 (		•	GTLTITLRNLQPHDAGLYQCQSLHGSEADTLRKVLVEVLADPLD
1 1			HRDAGDLWFPG\DLRASRMPMWSTASPGASWKEKSPSHPLPSFS
1			SWPASFSSRF*QPAPSGLQPGMDRSQGHIHPVNWTVAMTQGISS
5373	2814	346	KLCQG
1	2014	340	VKKTKSIFNSAMQEMBVYVENIRRKFGVFNYSPFRTPYTPNSQY
1 1			QMLLDPTNPSAGTAKIDKQEKVKLNFDMTASPKILMSKPVLSGG   TGRRISLSDMPRSPMSTNSSVHTGSDVEQDAEKKATSSHFSASE
1 1			ESMDFLDKSTASPASTKTGQAGSLSGSPKPFSPQLSAPITTKTD
1 1	1		KTSTTGSILNLNLDRSKAEMDLKELSESVQQQSTPVPLISPKRQ
1 1	ļ		IRSRFQLNLDKTIESCKAQLGINEISEDVYTAVEHSDSEDSEKS
] ]			DSSDSEYISDDEQKS*GTSQEDTEDKEGCQMDKEPSAVKKKPKP
[ [	ľ		TNPVEIKEELKSTSPASEKADPGAVKDKASPEPEKDPSGKAKPS
į i	1		PHPIKDKLKGKDETDSPTVHLGLDSDSE\NELVIDLGEDHSGRE
j l	ŀ		GRKNKKEPKEPSPKQDVVGKTPPSTTVGSHSPPETPVLTRSSAQ
1 1	j		TSAAGATATTSTSSTVTVTAPAPAATGSPVKKQRPLLPKE\TAP
] [			AVQRSCGTSSTVQQKEITQSPSTSTITLVTSTQSSPLVTSSGSM
	j		STLVSSVNGDLPIGTASADVAADIAKYTSKL\MDAIKGTM\TEI
] }	1		YNDLSKN\TTWKAQLAEDSQGLRIEIEKLQWLHQQEL\SEMKHN
( 1	1		LELTMAEMRQSWEQERDRLIAEVKKQLELEKQQAVDETKKKOWC
1	į		ANFKKEAIFYCCWNTSYCDYPCQ\QAHWPEH\MXSCTQSATAPO
] [	ļ		\QBADAE\VNTETLNKSSQGSSSSTQSAPSETASA\SKEKETSA
1 1	1	Í	EKSKESGSTLDLSGSRETPSSILLGSNQGSDHSR\SNKSSWSSS
		[	DEKRGS\TRSDHN/TPSTQHGRSLLPGKESRAGTPFLGTSK
5374	2814	346	VKKTKSIFNSAMQEMEVYVENIRRKFGVFNYSPFRTPYTPNSQY
		į	QMLLDPTNPSAGTAKIDKQEKVKLNFDMTASPKILMSKPVLSGG
			TGRRISLSDMPRSPMSTNSSVHTGSDVEQDAEKKATSSHFSASE
		ļ	ESMDFLDKSTASPASTKTGQAGSLSGSPKPFSPQLSAPITTKTD
			KTSTTGSILNLNLDRSKAEMDLKELSESVQQQSTPVPLISPKRQ
[			IRSRFOLNLDKTIESCKAQLGINEISEDVYTAVEHSDSEDSEKS
			DSSDSEYISDDEQKS*GTSQEDTEDKEGCQMDKEPSAVKKKPKP

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	Giutamic Acid, Farnenylaianine, Gaglycine,
İ	corresponding		H=Histidine, I=Isoleucine, K=Lysine,
Į.	to first	to first	L=Leucine, M=Methionine, N=Asparagine,
		amino acid	P-Proline, Q-Glutamine, R-Arginine,
1	amino acid	residue of	S-Serine, T-Threonine, V-Valine,
ł	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
}	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
<b>{</b>	<u> </u>		TNPVEIKEELKSTSPASEKADPGAVKDKASPEPEKDFSGKAKPS
			PHPIKDKLKGKDETDSPTVHLGLDSDSE\NELVIDLGEDHSGRE
		i	GRKNKKEPKEPSPKQDVVGKTPPSTTVGSHSPPETPVLTRSSAQ
	ĺ	1	TSAAGATATTSTSSTVTVTAPAPAATGSPVKKQRPLLPKE\TAP
j .			AVQRSCGTSSTVQQKEITQSPSTSTITLVTSTQSSPLVTSSGSM
ì			STLVSSVNGDLPIGTASADVAADIAKYTSKL\MDAIKGTM\TEI
i			YNDLSKN\TTWKAQLAEDSQGLRIEIEKLQWLHQQEL\SEMKHN
1			LELTMAEMRQSWEQERDRLIAEVKKQLELEKQQAVDETKKKQWC
			ANFKKEAIFYCCWNTSYCDYPCQ\QAHWPEH\MKSCTQSATAPQ
1			\QEADAE\VNTETLNKSSQGSSSSTQSAPSETASA\SKEKETSA
ł ·			EKSKESGSTLDLSGSRETPSSILLGSNQGSDHSR\SNKSSWSSS
1			DEKRGS\TRSDHN/TPSTQHGRSLLPGKESRAGTPFLGTSK
5375	2907	1116	HIFLAEEEPMLERRCRGPLAMGPAQPRLLSGPSQESPQTLGKES
			RGLRQQGTSVA\QSGAQAPGRAHRCAHCRRHFPGWVA\LWLHTR
			RCQA/RGLPLPCPECGRRFRHAPFLALHRQVHAAATPDWGFACH
			LCGQSFRGWVALVLHLRAHSAAKAGPPACPKMARDAFWRRKAAS
			SSILRRCHPSRPRGPRPFICGNCGRSILPTWDQ/LKVAHKRVHV
1 .			SRRP*ERGPPAKVFWGPRPRGPPTGDTPPGPGGDAVDRPF\OCA
]			CCGKRFRHK\PNLIRSHAACTSGERPHQ/CSRECG\KRFTNKPY
			LTS\HRRITHTARQPYPCKECGRRFRHKPNLLSHSKIHKRSEGS
1			AQAAPGPGSPQLPAGPQESAAEPTPAVPLKPAQEPPPGAPPEHP
1			QDPIEAPPSLYSCDDCGRSFRLERFLRAHQRQHTGERPFTCAEC
}			GKNFGKKTHLVAHSRVHSGERPFRLARKCGRRFLPRASOSGRN
			SAEPNAPRFGPFVCPDCGKAFRHKPYLAAHRPIATPAEKPYVCP
}	1		DCRKAFSQKSNL\VSHRRIHTGERPYACPDCDRSFSQKSNLITH
Į į			RKSHIRDGAFCCAICGQTFDDEERLLAHQKKHDV
5376	4504	591	VSTFSLCLWPAGGGGRGRVSNMAQSKRHVYSRTPSGSRMSAEAS
[ [	1	574	ARPLRVGSRVEVIGKGHRGTVAYVGATLFATGKWVGVILDEAKG
! }			KNDGTVQGRKYFTCDEGHGIFVRQSQIQVFEDGADTTSPETPDS
1 1			SASKVLKREGTDTTAKTSKLRGLKPKKAPTARKTTTRRPKPTRP
			ASTGVAGASSSLGPSGSASAGELSSSEPSTPAQTPLAAPIIPTP
1 1			VLTSPGAVPPLPSPSKEEEGLRAQVRDLEEKLETLRLKRAEDKA
ļ.	'		KLKELEKHKIQLEQVQEWKSKMQEQQADLQRRLKEARKEAKEAL
<u> </u>			EAKERYMEEMADTADAIEMATLDKEMAEERAESLQQEVEALKER
í í			DESCRIPTION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY
} [			VDELTTDLEILKAEIEEKGSDGAASSYQLKQLEEQNARLKDALV
			VDELTTDLEILKAEIEEKGSDGAASSYQLKQLEEQNARLKDALV RMRDLSSSEKQEHVK\LQKLMEKKNQELEVVRQQRERLQEELSQ
			VDELTTDLEILKAEIEEKGSDGAASSYQLKQLEEQNARLKDALV RMRDLSSSEKQEHVK\LQKLMEKKNQELEVVRQQRERLQEELSQ AESTIDELKEQVDAALGAEEMVEMLTDRNLNLEEKVRELRETVG
			VDELTTDLEILKAEIEEKGSDGAASSYQLKQLEEQNARLKDALV RMRDLSSSEKQEHVK\LQKLMEKKNQELEVVRQQRERLQEELSQ AESTIDELKEQVDAALGAEEMVEMLTDRNLNLEEKVRELRETVG DLEAMNEMNDBLQENARBTELELREQLDMAGARVREAQKRVEAA
			VDELTTDLEILKAEIEEKGSDGAASSYQLKQLEEQNARLKDALV RMRDLSSSEKQEHVK\LQKLMEKKNQELEVVRQQRERLQEELSQ AESTIDELKEQVDAALGAEEMVEMLTDRNLNLEEKVRELRETVG DLEAMNEMNDBLQENARBTELELREQLDMAGARVREAQKRVEAA QETVADYQQTIKKYRQLTAHLQDVNRELTNQQEASVERQQQPPP
			VDELTTDLEILKAEIEEKGSDGAASSYQLKQLEEQNARLKDALV RMRDLSSSEKQEHVK\LQKLMEKKNQELEVVRQQRERLQEELSQ AESTIDELKEQVDAALGAEEMVEMLTDRNLNLEEKVRELRETVG DLEAMNEMNDBLQENARETELELREQLDMAGARVREAQKRVEAA QETVADYQQTIKKYRQLTAHLQDVNRELTNQQEASVERQQQPPP ETFDFKIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPD
			VDELTTDLEILKAEIEEKGSDGAASSYQLKQLEEQNARLKDALV RMRDLSSSEKQEHVK\LQKLMEKKNQELEVVRQQRERLQEELSQ AESTIDELKEQVDAALGAEEMVEMLTDRNLNLEEKVRELRETVG DLEAMNEMNDBLQENARBTELELREQLDMAGARVREAQKRVEAA QETVADYQQTIKKYRQLTAHLQDVNRELTNQQEASVERQQQPPP ETFDFKIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPD SFLRPGGDHDCVLVLLLMPRLICKAELIRKQAQEKFELSENCSE
			VDELTTDLEILKAEIEEKGSDGAASSYQLKQLEEQNARLKDALV RMRDLSSEKQEHVK\LQKLMEKKNQELEVVRQQRERLQEELSQ AESTIDELKEQVDAALGAEEMVEMLTDRNLNLEEKVRELRETVG DLEAMNEMNDBLQENARBTELELREQLDMAGARVREAQKRVEAA QETVADYQQTIKKYRQLTAHLQDVNRELTNQQEASVERQQQPPP ETTDFKIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPD SFLRPGGDHDCVLVLLLMPRLICKAELIRKQAQEKFELSENCSE RPGLRGAAGEQLSFAAIGLVY\SLMPAAGHRYHRY*CHALSQCR
			VDELTTDLEILKAEIEEKGSDGAASSYQLKQLEEQNARLKDALV RMRDLSSSEKQEHVK\LQKLMEKKNQELEVVRQQRERLQEELSQ AESTIDELKEQVDAALGAEENVEMLTDRNLNLEEKVRELRETVG DLEAMNEMNDBLQENARETELELREQLDMAGARVREAQKRVEAA QETVADYQQTIKKYRQLTAHLQDVNRELTNQQEASVERQQQPPP ETFDFKIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPD SFLRPGGDHDCVLVLILMPRLICKAELIRKQAQEKFELSENCSE RPGLRGAAGEQUSFAAIGLVY\SLMPAAGHRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFLIELLHKDQLDETVNVEPLT
			VDELTTDLEILKAEIEEKGSDGAASSYQLKQLEEQNARLKDALV RMRDLSSSEKQEHVK\LQKLMEKKNQELEVVRQQRERLQEELSQ AESTIDELKEQVDAALGAEEMVEMLTDRNLNLEEKVRELRETVG DLEAMNEMNDBLQENARETELELREQLDMAGARVREAQKRVEAA QETVADYQQTIKKYRQLTAHLQDVNRELTNQQEASVERQQQPPP ETFDFKIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPD SFLRPGGDHDCVLVLLLMPRLICKAELIRKQAQEKFELSENCSE RFGLRGAAGEQLSFAAIGLVY\SLMPAAGHRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFLIELLHKDQLDETVNVEPLT KAIKYYQHLYSIHLAEQPEDCTMQLADHIKFTQSALDCMSVEVG
			VDELTTDLEILKAEIEEKGSDGAASSYQLKQLEEQNARLKDALV RMRDLSSSEKQEHVK\LQKLMEKKNQELEVVRQQRERLQEELSQ AESTIDELKEQVDAALGAEEMVEMLTDRNLNLEEKVRELRETVG DLEAMNEMNDBLQENARETELELREQLDMAGARVREAQKRVEAA QETVADYQQTIKKYRQLTAHLQDVNRELTNQQEASVERQQQPPP ETFDFKIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPD SFLRPGGDHDCVLVLLLMPRLICKAELIRKQAQEKFELSENCSE RPGLRGAAGEQLSFAAIGLVY\SLMPAAGHRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFLIELLHKDQLDETVNVEPLT KAIKYYQHLYSIHLAEQPEDCTMQLADHIKFTQSALDCMSVEVG RLRAFLQGGQBATDIALLLRDLETSCS\DIRQFCKKIRRMPGT
			VDELTTDLEILKAEIEEKGSDGAASSYQLKQLEEQNARLKDALV RMRDLSSSEKQEHVK\LQKLMEKKNQELEVVRQQRERLQEELSQ AESTIDELKEQVDAALGAEEMVEMLTDRNLNLEEKVRELRETVG DLEAMNEMNDBLQENARETELELREQLDMAGARVREAQKRVEAA QETVADYQQTIKKYRQLTAHLQDVNRELTNQQEASVERQQQPPP ETFDFKIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPD SFLRPGGDHDCVLVLLLMPRLICKAELIRKQAQEKFELSENCSE RFGLRGAAGEQLSFAAIGLVY\SLMPAAGRRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFLIELLHKDQLDETVNVEPLT KAIKYYQHLYSIHLAEQPEDCTMQLADHIKFTQSALDCMSVEVG RLRAFLQGGGBATDIALLRDLETSCS\DIRQFCKKIRRMPGT DAPGIPAALAFGPQVSDTLLDCRKHLTWVVAVLQEVAAAAAQLI
			VDELTTDLEILKAEIEEKGSDGAASSYQLKQLEEQNARLKDALV RMRDLSSSEKQEHVK\LQKLMEKKNQELEVVRQQRERLQEELSQ AESTIDELKEQVDAALGAEEMVEMLTDRNLNLEEKVRELRETVG DLEAMNEMNDBLQENARETELELREQLDMAGARVREAQKRVEAA QETVADYQQTIKKYRQLTAHLQDVNRELTNQQEASVERQQQPPP ETFDFKIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPD SFLRPGGDHDCVLVLLLMPRLICKAELIRKQAQEKFELSENCSE RFGLRGAAGEQLSFAAIGLVY\SLMPAAGHRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFLIELLHKDQLDETVNVEPLT KAIKYYQHLYSIHLAEQPEDCTMQLADHIKFTQSALDCMSVEVG RLRAFLQGGQBATDIALLRDLETSCS\DIRQFCKKIRRMPGT DAPGIPAALAFGPQVSDTLLDCRKHLTWVVAVLQEVAAAAAQLI APLAENEGLLVAALEELAFKASEQIYGTPSSSPYECLRQSCNIL
			VDELTTDLEILKAEIEEKGSDGAASSYQLKQLEEQNARLKDALV RMRDLSSEKQEHVK\LQKLMEKKNQELEVVRQQRERLQEELSQ AESTIDELKEQVDAALGAEEMVEMLTDRNLNLEEKVRELRETVG DLEAMNEMNDBLQENARBTELELREQLDMAGARVREAQKRVEAA QETVADYQQTIKKYRQLTAHLQDVNRELTNQQEASVERQQQPPP ETFDFKIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPD SFLRPGGDHDCVLVLLLMPRLICKAELIRKQAQEKFELSENCSE RPGLRGAAGEQLSFAAIGLVY\SLMPAAGHRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFLIELLHKDQLDETVNVEPLT KAIKYYQHLYSIHLAEQPEDCTMQLADHIKFTQSALDCMSVEVG RRLRAFLQGGQBATDIALLRDLETSCS\DIRQFCKKIRRRMPGT DAPGIPAALAFGPQVSDTLLDCRKHLTWVAVLQEVAAAAAQLI APLAENEGLLVAALEELAFKASEQIYGTPSSSPYECLRQSCNIL ISTMNK\LVTAMQEGEYDAERPPSKPPP\VELRAAALRAEITDA
			VDELTTDLEILKAEIEEKGSDGAASSYQLKQLEEQNARLKDALV RMRDLSSEKQEHVK\LQKLMEKKNQELEVVRQQRERLQEELSQ AESTIDELKEQVDAALGAEENVEMLTDRNLNLEEKVRELRETVG DLEAMNEMNDBLQENARETELELREQLDMAGARVREAQKRVEAA QETVADYQQTIKKYRQLTAHLQDVNRELTNQQEASVERQQQPPP ETTDFKIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPD SFLRPGGDHDCVLVLLLMPRLICKAELIRKQAQEKFELSENCSE RPGLRGAAGEQLSFAAIGLVY\SLMPAAGHRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFLIELLHKDQLDETVNVEPLT KAIKYYQHLYSIHLAEQPEDCTMQLADHIKFTQSALDCMSVEVG RLRAFLQGGQBATDIALLRDLETSCS\DIRQFCKKIRRRMPGT DAPGIPAALAFGPQVSDTLLDCRKHLTWVVAVLQEVAAAAQLI APLAENEGLLVAALEELAFKASEQIYGTPSSPYECLRQSCNIL ISTMNK\LVTAMQEGEYDAERPPSKPPP\VELRAAALRAEITDA EGLGLKLEDRETVIKBLKKSLKIKGEELSEANVRLTTLLEKKLDS
			VDELTTDLEILKAEIEEKGSDGAASSYQLKQLEEQNARLKDALV RMRDLSSSEKQEHVK\LQKLMEKKNQELEVVRQQRERLQEELSQ AESTIDELKEQVDAALGAEEMVEMLTDRNLNLEEKVRELRETVG DLEAMNEMNDBLQENARETELELREQLDMAGARVREAQKRVEAA QETVADYQQTIKKYRQLTAHLQDVNRELTNQQEASVERQQQPPP ETFDFKIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPD SFLRPGGDHDCVLVILLMPRLICKAELIRKQAQEKFELSENCSE RPGLRGAAGEQLSFAAIGLVY\SLMPAAGHRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFLIELLHKDQLDETVNVEPLT KAIKYYQHLYSIHLAEQPEDCTMQLADHIKFTQSALDCMSVEVG RLRAFLQGGQBATDIALLLRDLETSCS\DIRQFCKXIRRMPGT DAPGIPAALAFGPQVSDTLLDCRKHLTWVVAVLQEVAAAAAQLI APLAENEGLLVAALEELAFKASEQIYGTPSSSPYECLRQSCNIL ISTMNK\LVTAMQEGEYDAERPPSKPPP\VELRAALRAEITDA EGLGLKLEDRETVIKELKKSLKIKGEELSEANVRLTLLEKKLDS AAKDADERIEKVQTRLEETQALLRKKEKEFEETMDALQADIDQL
			VDELTTDLEILKAEIEEKGSDGAASSYQLKQLEEQNARLKDALV RMRDLSSSEKQEHVK\LQKLMEKKNQELEVVRQQRERLQEELSQ AESTIDELKEQVDAALGAEEMVEMLTDRNLNLEEKVRELRETVG DLEAMNEMNDBLQENARETELELREQLDMAGARVREAQKRVEAA QETVADYQQTIKKYRQLTAHLQDVNRELTNQQEASVERQQQPPP ETFDFKIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPD SFLRPGGDHDCVLVLLLMPRLICKAELIRKQAQEKFELSENCSE RFGLRGAAGEQLSFAAIGLVY\SLMPAAGRRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFLIELLHKDQLDETVNVEPLT KAIKYYQHLYSIHLAEQPEDCTMQLADHIKFTQSALDCMSVEVG RLRAFLQGGQBATDIALLLRDLETSCS\DIRGFCKKIRRMPGT DAPGIPAALAFGPQVSDTLLDCRKHLTWVVAVLQEVAAAAAQLI APLAENEGLLVAALEELAFKASEQIYGTPSSSPYECLRQSCNIL ISTMNK\LVTAMQEGEYDAERPPSKPPPVVELRAAALRAEITDA EGLGLKLEDRETVIKELKKSLKIKGEELSEANVRLTLLEKKLDS AAKDADERIEKVQTRLEETQALLRKKEKEFEETMDALQADIDQL EAEKAELKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQR
			VDELTTDLEILKAEIEEKGSDGAASSYQLKQLEEQNARLKDALV RMRDLSSSEKQEHVK\LQKLMEKKNQELEVVRQQRERLQEELSQ AESTIDELKEQVDAALGAEEMVEMLTDRNLNLEEKVRELRETVG DLEAMNEMNDBLQENARETELELREQLDMAGARVREAQKRVEAA QETVADYQQTIKKYRQLTAHLQDVNRELTNQQEASVERQQQPPP ETFDFKIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPD SFLRPGGDHDCVLVLLLMPRLICKAELIRKQAQEKFELSENCSE REGLRGAAGEQLSFAAIGLVY\SLMPAAGHRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFLIELHKDQLDETTNVEPLT KAIKYYQHLYSIHLAEQPEDCTMQLADHIKFTQSALDCMSVEVG RLRAFLQGGQRATDIALLRDLETSCS\DIRGFCKKIRRMPGT DAPGIPAALAPGPQVSDTLLDCRKHLTWVVAVLQEVAAAAAQLI APLAENEGLLVAALEELAFKASEQIYGTPSSSPYECLRQSCNIL ISTMNK\LVTAMQEGEYDAERPPSKPPP\VELRAALRAEITDA EGLGLKLEDRETVIKELKKSLKIKGEELSEANVRLTLLEKKLDS AAKDADERIEKVQTRLEETQALLRKKEKEFEETMDALQADIDQL EAEKAELKQRLNSQSKRTIEGLRGPPPSGTATLVSGIAGEEQQR GAIFGQAPGSVPGPGLVKDSPLLLQQISAMRLHISQLQHENSIL
			VDELTTDLEILKAEIEEKGSDGAASSYQLKQLEEQNARLKDALV RMRDLSSSEKQEHVK\LQKLMEKKNQELEVVRQQRERLQEELSQ AESTIDELKEQVDAALGAEEMVEMLTDRNLNLEEKVRELRETVG DLEAMNEMNDBLQENARETELELREQLDMAGARVREAQKRVEAA QETVADYQQTIKKYRQLTAHLQDVNRELTNQQEASVERQQQPPP ETFDFKIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPD SFLRPGGDHDCVLVLLLMPRLICKAELIRKQAQEKFELSENCSE REGLRGAAGEQLSFAAIGLVY\SLMPAAGHRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFLIELLHKDQLDETVNVEPLT KAIKYYQHLYSIHLAEQPEDCTMQLADHIKFTQSALDCMSVEVG RLRAFLQGGQRATDIALLRDLETSCS\DIRQFCKKIRRMPGT DAPGIPAALAFGPQVSDTLLDCRKHLTWVVAVLQEVAAAAAQLI APLAENEGLLVAALEELAFKASEQIYGTPSSSPYECLRQSCNIL ISTMNK\LVTAMQEGEYDAERPPSKPPP\VELRAAALRAEITDA EGLGLKLEDRETVIKELKKSLKIKGBELSEANVRLTLLEKKLDS AAKDADERIEKVQTRLEETQALLRKKEKEFEETMDALQADIDQL EAEKAELKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQR GAIPGQAPGSVPGPGLVKDSPLLLQQISAMRLHISQLQHENSIL KGAQMKASLASLPPLHVAKLSHEGPGSELPAGALYRKTSQLLET
			VDELTTDLEILKAEIEEKGSDGAASSYQLKQLEEQNARLKDALV RMRDLSSSEKQEHVK\LQKLMEKKNQELEVVRQQRERLQEELSQ AESTIDELKEQVDAALGAEEMVEMLTDRNLNLEEKVRELRETVG DLEAMNEMNDBLQENARETELELREQLDMAGARVREAQKRVEAA QETVADYQQTIKKYRQLTAHLQDVNRELTNQQEASVERQQQPPP ETFDFKIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPD SFLRPGGDHDCVLVLLLMPRLICKAELIRKQAQEKFELSENCSE RFGLRGAAGEQLSFAAIGLVY\SLMPAAGHRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFLIELLHKDQLDETVNVEPLT KAIKYYQHLYSIHLAEQPEDCTMQLADHIKFTQSALDCMSVEVG RRLRAFLQGGQBATDIALLRDLETSCS\DIRQFCKKIRRMPGT DAPGIPAALAFGPQVSDTLLDCRKHLTWVVAVLQEVAAAAAQLI APLAENEGLLVAALEELAFKASEQIYGTPSSSPYECLRQSCNIL ISTMNK\LVTAMQEGEYDAERPPSKPPP\VELRAAALRAEITDA EGLGLKLEDRETVIKELKKSLKIKGBELSEANVRLTLLEKKLDS AAKDADERIEKVQTRLEETQALLRKKEKFEETMDALQADIDQL EAEKAELKQRLNSQSKRTIEGLRGPPSGIATLVSGIAGEEQQR GAIPGQAPGSVPGPGLVKDSPLLLQQISAMRLHISQLQHENSIL KGAQMKASLASLPPLHVAKLSHEGPGGELPAGALYRTSQLLET LNQLSTHTHVVDITRTSPAAKSPSAQLMEQVAQLKSLSDTVEKL
			VDELTTDLEILKAEIEEKGSDGAASSYQLKQLEEQNARLKDALV RMRDLSSSEKQEHVK\LQKLMEKKNQELEVVRQQRERLQEELSQ AESTIDELKEQVDAALGAEEMVEMLTDRNLNLEEKVRELRETVG DLEAMNEMNDBLQENARBTELELREQLDMAGARVREAQKRVEAA QETVADYQQTIKKYRQLTAHLQDVNRELTNQQEASVERQQQPPP ETFDFKIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPD SFLRPGGDHDCVLVLLLMPRLICKAELIRKQAQEKFELSENCSE RPGLRGAAGEQLSFAAIGLVY\SLMPAAGHRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFLIELLHKDQLDETVNVEPLT KAIKYYQHLYSIHLAEQPEDCTMQLADHIKFTQSALDCMSVEVG RRLRAFLQGGQBATDIALLRDLETSCS\DIRQFCKKIRRMMPGT DAPGIPAALAFGPQVSDTLLDCRKHLTWVVAVLQEVAAAAAQLI APLAENEGLLVAALEELAFKASEQIYGTPSSSPYECLRQSCNIL ISTMNK\LVTAMQEGEYDAERPPSKPPP\VELRAAALRAEITDA EGLGLKLEDRETVIKELKKSLKIKGEELSEANVRLTLLEKKLDS AAKDADERIEKVQTRLEETQALLRKKEKEFFETMDALQADIDQL EAEKAELKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQR GAIPGQAPGSVPGPGLVKDSPLLLQQISAMRLHISQLQHENSIL KGAQMKASLASLPPLHVAKLSHEGPGSELPAGALYRKTSQLLET LNQLSTHTHVVDITRTSPAAKSPSAQLMEQVAQLKSLSDTVEKL
5377	752		VDELTTDLEILKAEIEEKGSDGAASSYQLKQLEEQNARLKDALV RMRDLSSSEKQEHVK\LQKLMEKKNQELEVVRQQRERLQEELSQ AESTIDELKEQVDAALGAEEMVEMLTDRNLNLEEKVRELRETVG DLEAMNEMNDBLQENARETELELREQLDMAGARVREAQKRVEAA QETVADYQQTIKKYRQLTAHLQDVNRELTNQQEASVERQQQPPP ETFDFKIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPD SFLRPGGDHDCYLVILLMPRLICKAELIRKQAQEKFELSENCSE RPGLRGAAGEQLSFAAIGLVY\SLMPAAGHRYHRY*CHALSQCR RLD\VYKKVGSLYPEMSAHERSLDFLIELLHKDQLDETVNVEPLT KAIKYYQHLYSIHLAEQPEDCTMQLADHIKFTQSALDCMSVEVG RLRAFLQGGQBATDIALLLRDLETSCS\DIRQFCKXIRRMPGT DAPGIPAALAFGPQVSDTLLDCRKHLTWVVAVLQEVAAAAAQLI APLAENEGLLVAALEELAFKASEQIYGTESSFYECLRQSCNIL ISTMNK\LVTAMQEGEYDAERPPSKPPP\VELRAAALRAEITDA AEGLGLKLEDRETVIKELKKSLKIKGEELSEANVRLTLLEKKLDS AAKDADERIEKVQTRLEETQALLRKKEKEFEETMDALQADIDQL EAEKAELKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQR GAIPGQAPGSVPGPGLVKDSPLLLQQISAMRLHISQLQHENSIL KGAQMKASLASLPPLHVAKLSHEGFGSELPAGALYRKTSQLLET LNQLSTHTHVVDITRTSPAAKSPSAQLMEQVAQLKSLSDTVEKL KDEVLKETVSQRPGATVPTDFATFPSSAFLRAKEEQQDDTVYMG KVTFSCAAGFGQRHRLVLTQEQLHQLHSRLIS
5377	762	1106	VDELTTDLEILKAEIEEKGSDGAASSYQLKQLEEQNARLKDALV RMRDLSSSEKQEHVK\LQKLMEKKNQELEVVRQQRERLQEELSQ AESTIDELKEQVDAALGAEEMVEMLTDRNLNLEEKVRELRETVG DLEAMNEMNDBLQENARETELELREQLDMAGARVREAQKRVEAA QETVADYQQTIKKYRQLTAHLQDVNRELTNQQEASVERQQQPPP ETFDFKIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPD SFLRPGGDHDCVLVLLLMPRLICKAELIRKQAQEKFELSENCSE RFGLRGAAGFGQLSFAAIGLVY\SLMPAAGRRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFLIELLHKDQLDETVNVEPLT KAIKYYQHLYSIHLAEQPEDCTMQLADHIKFTQSALDCMSVEVG RLRAFLQGGQBATDIALLLRDLETSCS\DIRGFCKKIRRMPGT DAPGIPAALAFGPQVSDTLLDCRKHLTWVVAVLQEVAAAAAQLI AFLAENEGLLVAALEELAFKASEQIYGTPSSSPYECLRQSCNIL ISTMNK\LVTAMQEGEYDAERPPSKPPPVVELRAAALRAEITDA EGLGLKLEDRETVIKELKKSLKIKGEELSEANVRLTLLEKKLDS AAKDADERIERVQTRLEETQALLRKKEKEFEETMDALQADIDQL EAEKAELKQRLNSQSKRTIEGLRGPPPSGIATLVSGTAGEEQQR GAIFGQAPGSVPGPGLVKDSPLLLQQISAMRLHISQLQHENSIL KGAQMKASLASLPPLHVAKLSHEGFGSELPAGALYRKTSQLLET LNQLSTHTHVVDITRTSPAAKSPSAQLMEQVAQLKSLSDTVEKL KDEVLKETVSQRPGATVPTDFATFPSSAFLRAKEEQQDDTVYMG KVTFSCAAGFGQRHRLVLTQEQLHQLHSRLIS DVPCKRVLPAEAQEKGQITLSCGESGEEG\F*YHEVRQAEGES*
5377	762	1106	VDELTTDLEILKAEIEEKGSDGAASSYQLKQLEEQNARLKDALV RMRDLSSSEKQEHVK\LQKLMEKKNQELEVVRQQRERLQEELSQ AESTIDELKEQVDAALGAEEMVEMLTDRNLNLEEKVRELRETVG DLEAMNEMNDBLQENARETELELERQLDMAGARVREAQKRVEAA QETVADYQQTIKKYRQLTAHLQDVNRELTNQQEASVERQQQPPP ETFDFKIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPD SFLRPGGDHDCVLVLLLMPRLICKAELIRKQAQEKFELSENCSE REGLRGAAGEQLSFAAIGLVY\SIMPAAGRRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFLIELLHKDQLDETVNVEPLT KAIKYYQHLYSIHLAEQPEDCTMQLADHIKFTQSALDCMSVEVG RLRAFLQGGGRATDIALLRDLETSCS\DIRGFCKKIRRMPGT DAPGIPAALAFGPQVSDTLLDCRKHLTWVVAVLQEVAAAAAQLI AFLAENEGLLVAALEELAFKASEQIYGTPSSSPYECLRQSCNIL ISTMNK\LVTAMQEGEYDAERPPSKPPP\VELRAAALRAEITDA EGLGLKLEDRETVIKELKKSLKIKGEELSEANVRLTLLEKKLDS SAKDADERIEKVQTRLEETQALLRKKEKEFFETMDALQADIDQL EAEKAELKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQR GAIPGQAPGSVPGPGLVKDSPLLLQQISAMRLHISQLQHENSIL KGAQMKASLASLPPLHVAKLSHEGPGSELPAGALYRKTSQLLET LNQLSTHTHVVDITRTSFAAKSPSAQLMEQVAQLKSLSDTVEKL KDEVLKETVSQRPGATVPTDFATFPSSAFLRAKEQQDDTVYMG KVTFSCAAGFGQRHRLVLTQEQLHQLHSRLIS DVPCKRVLPAEAQEKGQITLSCGESGEG\F*YHEVRQAEGES* /WFGPNVRLVHTQLKTKKPSGTLKAKFYLHTGSTKFAARISCTX
			VDELTTDLEILKAEIEEKGSDGAASSYQLKQLEEQNARLKDALV RMRDLSSSEKQEHVK\LQKLMEKKNQELEVVRQQRERLQEELSQ AESTIDELKEQVDAALGAEEMVEMLTDRNINLEEKVRELRETVG DLEAMNEMNDBLQENARETELELEQLDMAGARVREAQKRVEAA QETVADYQQTIKKYRQLTAHLQDVNRELTNQQEASVERQQQPPP ETFDFKIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPD SFLRPGGDHDCVLVLLLMPRLICKAELIRKQAQEKFELSENCSE REGLRGAAGEQLSFAAIGLVY\SLMPAAGHRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFLIELHKDQLDETVNVEPLT KAIKYYQHLYSIHLAEQPEDCTMQLADHIKFTQSALDCMSVEVG KRIRAFLQGGGRATDIALLRDLETSCS\DIRQFCKKIRRMPGT DAPGIPAALAPGPQVSDTLLDCRKHLTWVVAVLQEVAAAAAQLI APLAENEGLLVAALEELAFKASEQIYGTPSSSPYECLRQSCNIL ISTMNK\LVTAMQEGEYDAERPPSKPPP\VELRAAALRAEITDA EGLGKLEDRETVIKELKKSLKIKGEELSEANVRLTLLEKKLDS AAKDADERIEKVQTRLEETQALLRKKEKEFEETMDALQADIDQL EAEKAELKQRLNSQSKRTIEGLRGPPPSGTATLVSGIAGESQQR GAIPGQAPGSVPGPGLVKDSPLLLQQISAMRLHISQLQHENSIL KGAQMKASLASLPPLHVAKLSHEGPGSELPAGALYRKTSQLLET LNQLSTHTHVVDITRTSPAAKSPSAQLMEQVAQLKSLSDTVEKL KDEVLKETVSQRPGATVPTDFATFPSSAFLRAKEEQQDDTVYMG KVTFSCAAGFGQRHRLVLTQEQLHQLHSRIS VFGPNVRLVHTQLKTKKPSGTLKAKFYLHTGSTKFAARISCTX SS*WPGYDGWWGGQYIFIFRGMRWEEQP
5377	762	1106	VDELTTDLEILKAEIEEKGSDGAASSYQLKQLEEQNARLKDALV RMRDLSSSEKQEHVK\LQKLMEKKNQELEVVRQQRERLQEELSQ AESTIDELKEQVDAALGAEEMVEMLTDRNLNLEEKVRELRETVG DLEAMNEMNDBLQENARETELELERQLDMAGARVREAQKRVEAA QETVADYQQTIKKYRQLTAHLQDVNRELTNQQEASVERQQQPPP ETFDFKIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPD SFLRPGGDHDCVLVLLLMPRLICKAELIRKQAQEKFELSENCSE REGLRGAAGEQLSFAAIGLVY\SIMPAAGRRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFLIELLHKDQLDETVNVEPLT KAIKYYQHLYSIHLAEQPEDCTMQLADHIKFTQSALDCMSVEVG RLRAFLQGGGRATDIALLRDLETSCS\DIRGFCKKIRRMPGT DAPGIPAALAFGPQVSDTLLDCRKHLTWVVAVLQEVAAAAAQLI AFLAENEGLLVAALEELAFKASEQIYGTPSSSPYECLRQSCNIL ISTMNK\LVTAMQEGEYDAERPPSKPPP\VELRAAALRAEITDA EGLGLKLEDRETVIKELKKSLKIKGEELSEANVRLTLLEKKLDS SAKDADERIEKVQTRLEETQALLRKKEKEFFETMDALQADIDQL EAEKAELKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQR GAIPGQAPGSVPGPGLVKDSPLLLQQISAMRLHISQLQHENSIL KGAQMKASLASLPPLHVAKLSHEGPGSELPAGALYRKTSQLLET LNQLSTHTHVVDITRTSFAAKSPSAQLMEQVAQLKSLSDTVEKL KDEVLKETVSQRPGATVPTDFATFPSSAFLRAKEQQDDTVYMG KVTFSCAAGFGQRHRLVLTQEQLHQLHSRLIS DVPCKRVLPAEAQEKGQITLSCGESGEG\F*YHEVRQAEGES* /WFGPNVRLVHTQLKTKKPSGTLKAKFYLHTGSTKFAARISCTX

SEO	T Dwod3 - 5 - 2	T 20 - 27 - 2 - 3	
ID	Predicted beginning	Predicted end	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
""	location	corresponding	Glutamic Acid, F=Phenylaianine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
}	amino acid	sequence	Codon, /=possible nucleotide deletion,
}	sequence	Sequence	\=possible nucleotide insertion)
J	33,330	<del> </del>	SFSFRNSKQTYSGVPIIAANMDTVGTFEMAKVLCKS*VPGSFWD
1		}	VPQMGCVFLIYKLFTLKWKMLLLSVLLPASILVAEKFSLFTAVH
Į.		ŀ	KHYSLVQWQEFAGQNPDCLEHLAASSGTGSSDFEQLEQILEAIP
ļ		j	QVKYICLDVANGYSEHFVEFVKDVRKRFPQHTIMAGNVVTGEMV
ļ	1	l _i	EELILSGADIIKVGIGPGSVCTTRKKTGVGYPQLSAVMECADAA
	1	ľ	HGLKGHIISDGGCSCPGDVAKAFGAGADFVMLGGMLAGHSESGG
1	}		BLIERDGKKYKLFYGMSS*I\AM\KKYAGGVAEYRASEGKTVEV
1	1	j	PFKGDVEHTIRDILGGIRSTCTYVGAAKLKELSRRTTFIRVTQQ
1			VNPIFSEAC
5379	2009	664	
	1	, ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	QASGTTLRPLPDLPQLKRREATSRNRALKPRGRLVLMTSCLPAL RFIATPRLSAMPHIDNDVKLDFKDVLLRPKRSTLKSRSEVDLTR
1	1		SPSFRNSKQTYSGVPIIAANMDTVGTFEMAKVLCKS*VPGSFWD
1			VPQMGCVFLIYKLFTLKWKMLLLSVLLPASILVAEKFSLFTAVH
1	1		KHYSLVQWQEFAGQNPDCLEHLAASSGTGSSDFEQLEQILEAIP
			QVKYICLDVANGYSEHFVEFVKDVRKRFPQHTIMAGNVVTGEMV
			EELILSGADIIKVGIGPGSVCTTRKKTGVGYPQLSAVMECADAA
1	ĺ		HGLKGHIISDGGCSCPGDVAKAFGAGADFVMLGGMLAGHSESGG
ļ	i .		ELIERDGKKYKLFYGMSS*I\AM\KKYAGGVAEYRASEGKTVEV
l			PFKGDVEHTIRDILGGIRSTCTYVGAAKLKELSRRTTFIRVTOO
ı			VNPIFSEAC
5380	2	2050	PSRAGGAERGRAAAARSPGGSAAGWECPSVLDEAGACTMSSCVS
1			SQPSSNRAAPQDELGGRGSSSSESQKPCEALRGLSSLSIHLGME
ł			SFIVVTECEPGCAVDLGLARDRPLEADGQEVPLDTSGSQARPHL
1			SGRKLSLQERSQGGLAAGGSLDMNGRCICPSLPYSPVSSPQSSP
ì			RLPRRPTVESHHVSITGMQDCVQLNQYTLKDEIGKGSYGVVKLA
			YNENDNTYYAMKVLSKKKLIRQAAFPRRPPPRGTRPAPGGCIQP
			RGPI\EQVYQEIA\ILKKLDHPNVV\KLVEVL\DDPNEDHLYMV
	•		F\ELVNQGPVMEVPTLKPLSEDQARFYFQDLIKGIEYLHYQKII
1			H\RDIKPSNLLVGEDGHIKIADFGVSNEFKGSDALLSNTVGTPA
Ì			FMAPESLSETRKIFSGKALDVWAMGVTLYCFVFG*CPFMDERIM
1			CLHSKIKSQALEFPDQPDİABDLKDLITRMLDKNPESRIVVPEI
			KLHPWVTRHGAEPLPSEDENCTLVEVTEEEVENSVKHIPSLATV
1	1		ILVKTMIRKRSFGNPFEGSRRBERSLSAPGNLLTKKPTRECESL
3			SELKT*KISPLPACCKVT*EFPHPSGCRPSCWQPPFLHTHSQPR
			*PEPPRTDBALCPYETGRTCWAPLLQVLWWVGTPLPFPLSTSWL
L			PDLVGAPGSHFCFLNIALLRYNSHTM
5381	2	2050	PSRAGGAERGRAAAARSPGGSAAGWECPSVLDEAGACTMSSCVS
] [			SQPSSNRAAPQDELGGRGSSSSESQKPCEALRGLSSLSIHLGME
[ · ]			SFIVVTECEPGCAVDLGLARDRPLEADGQEVPLDTSGSQARPHL
	1	'	SGRKLSLQERSQGGLAAGGSLDMNGRCICPSLPYSPVSSPQSSP
; l	J		RLPRRPTVESHHVSITGMQDCVQLNQYTLKDEIGKGSYGVVKLA
j			YNENDNTYYAMKVLSKKKLIRQAAFPRRPPPRGTRPAPGGCIQP
	ĺ		RGPI\EQVYQEIA\ILKKLDHPNVV\KLVEVL\DDPNEDHLYMV
	ł		F\ELVNQGPVMEVPTLKPLSEDQARFYFQDLIKGIEYLHYQKII
	J		H\RDIKPSNLLVGEDGHIKIADFGVSNEFKGSDALLSNTVGTPA
	{		FMAPESLSETRKIFSGKALDVWAMGVTLYCFVFG*CPFMDERIM
( /	i		CLHSKIKSQALEFPDQPDIAEDLKDLITRMLDKNPESRIVVPEI
1 1	j		KLHPWVTRHGAEPLPSEDENCTLVEVTEEEVENSVKHIPSLATV
	Į		ILVKTMIRKRSFGNPFEGSRREERSLSAPGNLLTKKPTRECESL
]	ſ		SELKT*KISPLPACCKVT*EFPHPSGCRPSCWQPPFLHTHSQPR
	1	l	*PEPPRTDEALCPYETGRTCWAPLLQVLWWVGTPLPFPLSTSWL
<del></del>			PDLVGAPGSHFCFLNIALLRYNSHTM.
5382	1536	203	GARGSQQDAPALQEABVRGPERAQPARGRMTKARLPRLWLVLGS
	1		VFMILLIIVYWDSAGAAHFYLHTSFSRPHTGPPLPTPGPDRDRE
			LTADSDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMRESVRG
			YDWSPRDARRSPDQGRQQAERRSVLRGFCANSSLAFPTKERPFD
	ĺ		DIPNSELSHLIVDDRHGAIYCYVPKVACTNWKRVMIVLSGSLLH
1			RGAPYRDPLRIPREHVHNASAHLTFNKFWRRYGKLSRHLMKVKL
	j		KKYTKFLFVRDPFVRLISAFRSKFELENEEF/*PQVRRAHAAAV
			RQPHQPARLGARGLPRWPQ\VSFANFIQYLLDPHTEKLAPFNEH
	L		WRQVYRLCHPCQIDYDFVGKLETLDEDAAQLLQLLQVDLAAPLP

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalarine, G=Glycine,
Į.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
- I	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
Ĭ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
J	sequence	•	\=possible nucleotide insertion)
	<b></b>		PELPGTGPPSSWEEDWFAKIPLAWRQQLYKLYEADFVLFGYPKP
1			ENLLRD
5383	45	5250	VERLLGCRNSKRTWRMLISKNMPWRRLQGISFGMYSAEELKKLS
1	1		VKSITNPRYLDSLGNPSANGLYDLALGPADSKEVCSTCVQDFSN
1 .			CSGHLGHIELPLTVYNPLLFDKLYLLLRGSCLNCHMLTCPRAVI
	}		HLLLCQLRVLEVGALQAVYELERILSRFLEENADPSASEIREEL
1	1		EQYTTEIVQNNLLGSQGAHVKNVCESKSKLIALFWKAHMNAKRC
[	<b>i</b>		PHCKTGRSVVRKEHNSKLTITFPAMVHRTAGQKDSEPLGIEEAQ
ì	1		IGKRGYLTPTSAREHLSALWKNEGFFLNYLFSGMDDDGMESRFN
1			PSVFFLDFLVVPPSRSRPVSRLGDQMFTNGQTVNLQAVMKDVVL
1			IRKLLALMAQEQKLPEEVATPTTDEEKDSLIAIDRSPLSTLPGQ
		ı	SLIDKLYNIWIRLQSHVNIVFDSEMDKLMMDKYPGIRQILEKKE
	(		GLFRKHMMGKRVDYAARSVICPDMYINTNEIGIPMVFATKLTYP
1			QPVTPWNVQELRQAVINGPNVHPGASMVINEDGSRTALSAVDMT
1			QREAVAKQLLTPATGAPKPQGTKIVCRHVKNGDILLLNRQPTLH
			RPSIQAHRARILPEEKVLRLHYANCKAYNADFDGDEMNAHFPQS
			ELGRAEAYVLACTDQQYLVPKDGQPLAGLIQDHMVSGASMTTRG
			CFFTREHYMELVYRGLTDKVGRVKLLSPSILKPFPLWTGKQVVS
		•	TLLINIIPEDHIPLNLSGKAKITGKAWVKETPRSVPGFNPDSMC
1			ESQVIIREGELLCGVLDKAHYGSSAYGLVHCCYEIYGGETSGKV
1			LTCLARLFTAYLQLYRGFTLGVEDILVKPKADVKRQRIIEESTH
(			CGPQAVRAALNLPEAASYDEVRGKWQDAHLGKDQRDFNMIDLKF
			KEEVNHYSNEINKACMPFGLHRQFPENTLQLMVQSGAKGSTVNT
1			MQISCI,LGQIELEGRSTPLMASGKSLPCFEPYEFTPRAGGFVTG
]			RFLTGIKPPEFFHCMAGREGLVDTAVKTSRSGYLQRCIIKHLE
[			GLVVQYDLTVRDSDGSVVQFLYGEDGLDIPKTQFLQPKQFPFLA
1			SNYEVIMKSQHLHEVLSRADPKKALHHFRAIKKWQSKHPNTLLR
			RGAPLSYSOKIOEAVKALKLESENRNGR/RPWDS/G/RMLRMWY
			ELDEESRRKYQKKAAACPDPSLSVWRPDIYPASVSETFETKVDD
			YSQEWAAQTEKSYEKSELSLDRLRTLLQL\KWQRSLCEPGEAVG
1	1		LLAAQSIGEPSTOMTLNTFHFAGRGEMNVTLGIPRLREILMVAS
			ANIKTPMMSVPVLNTKKALKRVKSLKKQLTRVCLGEVLQKIDVQ
			ESFCMEEKQNKFQVYQLRFQFLPHAYYOOEKCLRPEDILRFMET
1 1			RFFKLLMESIKKKNNKASAFRNVNTRRATORDLDNAGELGRSRG
			EQEGDEEEEGHIVDAEAEEGDADASDAKRKEKOEEEVDYESEEE
	. 1		EEREGEENDDEDMQEERNPHREGARKTQEODEEVGL/GH*GGPV
1 1			PSRPPDAAPETHPQPGAPGA\EAMERRVQAVREIHPFIDDYOYD
} !	1.	j	TEESLWCQVTVKLPLMKINFDMSSLVVSLAHGAVIYATKGITRC
1 1		ł	LLNETTNNKNEKELVLNTEGINLPELFKYAEVLDLRRLYSNDIH
			AIANTYGIEAALRVIEKEIKDVFAVYGIAVDPRHLSLVADYMCF
1			EGVYKPLNRFGIRSNSSPLQQMTFETSFQFLKQATMLGSHDELR
5384			SPSACLVVGKVVRGGTGLFELKQPLR
5364	196	886	QSCGQRLPTVL+L+GPPGSCPCILSLF\PGRPHALPKIRPYINI
[	1	Į	TILKGDKGDPGPMGLPGYMGREGPQGEPGPQGSKGDKGEMGSPG
ļ l	1	1	APCQKRFFAFSVGRKTALHSGEDFOTLLFERVFVNLDGCFDMAT
1 1	1	ł	GQFAAPLRGIYFFSLNVHSWNYKETYVHIMHNOKEAVILYAOPS
1 1	1	1	ERSIMQSQSVMLDLAYGDRVWVRLFKRQRENAIYSNDFDTYITF
5385		200	SGHLIKAEDD
2303	326	799	LMVPRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVESHKKNKIHM
1	j	ļ	SPTFRRPKTL*LRRQPKYPWKSTPRRNKLDHHVIIKFPLTTE*A
į į	İ		VKKIENNSLLVFTVDVKANKHQIKQAVKK/LCDIDVAKVNTLIO
5386	- 336		SDGERKAYVRLAPDYDALVVATKIGIT
9900	326	799	LMVPRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVHSHKKNKIHM
1		- 1	SPTFRRPKTL*LRRQPKYPWKSTPRRNKLDHHVIIKFPLTTE*A
i i		- 1	VKKIENNSLLVFTVDVKANKHOIKOAVKK/LCDIDVAKVNTLTO
5387			SDGERKAYVRLAPDYDALVVATKIGIT
330/	2	2117	FVVAASGGCWFVLGERRAGSLLSASYGTFAMPGMVLFGRRWAIA
]	]		SDDLVFPGFFELVVRVLWWIGILTLYLMHRGKLDCAGGALLSSY
	1	. [	LIVLMILLAVVICTVSAIMCVSMRGTICNPGPRKSMSKLLYIRL
1	1	į.	ALFPPEMVWASLGAAWVADGVOCDRTVVNGIIATVVVSWIIIAA
			TVVSIIIVFDPLGGKMAPYSSAGPSHLDSHDSSQLLNGLKTAAT

SEO	Predicted	Predicted end	Dmino poid govern
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	1	Glutamic Acid, F=Phenylalanine, G=Glycine,
j.	corresponding	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
Ì	to first	to first	L=Leucine, M=Methionine, N=Asparagine,
ŧ	1	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ł	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
[	amino acid	sequence	Codon, /=possible nucleotide deletion.
L	sequence	ł	\=possible nucleotide insertion)
1	1	1	SVWETRIKLLCCCIGKDDHTRVAFSSTAELFSTYFSDTDLVPSD
i	ļ		IAAGLALLHQQQDNIRNNQEPAQVVCHAPGSSQEADLDAELKNC
1	1	1	HHYMQFAAAAYGWPLYIYRNPLTGLCRIGGDCCRSKNPQTMT/M
i	j		VGCDOLOL (CTCARTA UTILITA ALIGICAL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CON
ı	ļ.		VGGDQLQL/CTSAPILHTHRAAVQGLHPRQLPWTRFTELPFLVA
1		,	LDHRKESVVVAVRGTMSLQDVLTDLSAESEVLDVECEVQDRLAH
1	1	!	KGISQAARYVYQRLINDGILSQAFSIAPEYRLVIVGHSLGGGAA
J		]	ALLATMVRAAYPQVRCYAFSPPRGLWSKALQEYSQSFIVSLVLG
l l			KDVIPRLSVTNLEDLKRRILRVVAHCNKPKYKILLHGLWYELFG
1	[	ĺ	GNPNNLPTELDGGDQEVLTQPLLGEQSLLTRWSPAYSFSSDSPL
į	}	J	DSSPKYPPLYPPGRIIHLQEEGASGRFGCCSAAHYSAKWSHEAE
ì			FSKILIGPKMLTDHMPDILMRALDSVVSDRAACVSCPAQGVSSV
1	(	ļ	DVA
5388	1569	753	TADGGAGGGRRQAGVRRHYLYPFTGGYRRRRAACQAERPAARS
1	1	/33	KOTOLA A VOYCOU CHOT DIVING COMMING CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACT
1			KDTDLAAYQKGNLGVQLRNMAQETNHSQVPMLCSTGCGFYGNPR
1	1	1	TNGMCSVCYKEHLQRQNSSNGRISPPVQCTDGSVPEAQSALDST
1	1		SSSMQPSPVSNQSLLSESVASSQLDSTSVDKAVPETEDVQASVS
1	Į l		DTAQQPSEEQSKSLE\NRNKKRIAVSCAGRKWDLLGLNAGVEMF
1			TVVYTVTQMYTIALTITKQMLKNFVFQQEFKSFGSFHQQLLEYK
			ILEHLQTKN
5389	1569	753	TADGGAGGGRRQAGVRRHYLYPFTGGYRRRAACQAERPAARS
ĺ	į l		KDTDLAAYQKGNLGVQLRNMAQETNHSQVPMLCSTGCGFYGNPR
1	i i		TNGMCSVCYKBHLQRQNSSNGRISPPVQCTDGSVPZAQSALDST
	[ [		SSSMQPSPVSNQSLLSESVASSQLDSTSVDKAVPETEDVQASVS
	i		DENOTOR OF A NOW AND A STATE OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OF THE OWNER OWNER OF THE OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER OWNER O
ł	i i		DTAQQPSEEQSKSLE\NRNKKRIAVSCAGRKWDLLGLNAGVEMF
1	j ;		TVVYTVTQMYTIALTITKQMLKNFVFQQEFKSFGSFHQQLLEYK
5390	217		ILEHLQTKN
3370	1 24, 1	1332	EDPRKLMEDKMWSECEGPEMSLVCLTDFQAHAREQLSKSTRDFI
1	i j		EGGADDSITRDDNIAAFKRIRLRPRYLRDVSEVDTRTTIQGEEI
			SAPICIAPTGFHCLVWPDGEMSTARAAQAA\GICYITSTFASCS
			LEDIVIAAPEGLRWFQLYVHPDLQLNKQLIQRVESLGFKALVIT
			LDTPVCGNRRHDIRNQLRRNLTLTDLQSPKKGNAIPYFQMTPIS
1 1			TSLCWNDLSWFQSITRLPIILKGILTKEDAELAVKHNVQGIIVS
1.			NHGGRQLDEVLASIDALTEVVAAVKGKIEVYLDGGVRTGNDVLK
1 1	1		ALALGAKCIFLGDAILWALASKGEHGVKEVLNILTNEFHTSMA\
1 1			LTGCRSVAEINRNLVQFSRL
5391	1	1292	VKKAAGRSRGPPTAGGQRCEEAPGTVMERRLGVRAWVKENRGSF
	, , , , , , , , , , , , , , , , , , ,		QPPVCNKLMHQEQLKVMFVGGPNTRKDYHIEEGEEVFYQLEGDM
1 1			ALDIN BOOKREDAMILACORIES A STATEMENT STREET STATEMENT STREET STATEMENT STREET STATEMENT STREET STATEMENT STREET STATEMENT STREET STATEMENT STREET STATEMENT STREET STATEMENT STREET STATEMENT STREET STATEMENT STREET STATEMENT STREET STATEMENT STREET STATEMENT STREET STATEMENT STATEMENT STREET STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STAT
1 1			VLRVLEQGKHRDVVIRQGEIFLLPARVPHSPQRFANTVGLVVER
	Į		RRLETELDGLRYYVGDTMDVLFEKWFYCKDLGTQLAPIIQEFFS
]. {	ſ	· .	SEQYRTGKPIPDQLLKEPPFPLSTRSIMEPMSLDAWLDSHHREL
] [	ſ		QAGTPLSLFGDTYETQVIAYGQGSSEGLRQNVDVWLWQLEGSSV
1 I	!		VTMGGRRLSLGPWMDSLLVLSWGPSY\AW\ERTOGSVALSVT\O
	ł		DPACKKSPWGEPSCHGLKAATGVPSTLEVPSLPNNSPSPHYLSV
1 I	}		YCRCVPHRPAHCCHPPSCPSQPRCHAPGRAAAPHLLWOTOPTAL
L			PVLPGGLPPAPLLPIPLSLQTQCSTSTPRRPSIKAS
5392	1	1623	IRGSNAQKVVGASGSGGAGPQPDPAGPGGVPALAAAVLGACEPR
			CAAPCPLPALSRCRGAGSRGSRGGRGAAGSGDAAAAAEWIRKGS
į į		J	FILINDAUGHI UDDADH CDOUGHI DANGGODHAAAAEWIRKGS
, ,		. [	FIHKPAHGWLHPDARVLGPGVSYVVRYMGCIEVLRSMRSLDFNT
ţ l		ļ	RTOVTREAINRLHEAVPGVRGSWKKKAPNKALASVLGKSNLRFA
1 1	ł		GMSISIHISTDGLSLSVPATRQVIANHHMPSISFASGGDTDMTD
į l			YVAYVAKDPINQRACHILECCEGL\AQSIISTVGQAFELRFKOY
			LHSPPKVALPPERLAGPEESAWGDEEDSLEHNYYNSIPGKEPPL
	1		GGLVDSRLALTQPCALTALDQGPSPSLRDACSLPWDVGSTGTAP
, ,	ł	Ĭ	PGDGYVQADARGPPDHEEHLYVNTQGLDAPEPEDSPKKDLFDMR
	ĺ	. 1	PFEDALKLHECSVAAGVTAAPLPLEDQWPSPPTRRAPVAPTEEQ
1 1	1	. 1	LEGEDWYRGENGED A REMI DA DODOW INDOORSE TOURS
ļ .	ĺ	1	LRQEPWYHGRMSRRAAERMLRADGDFLVRDSVTNPGQYVLTGMH
	ļ	}	AGQPKHLLLVDPEGVVRTKDVLFESISHLIDHHLQNGQPIVAAE
5393			SELHLRGVVSREP
	4	982	GGDSAGMTMETQMSQNVCPRNLWLLQPLTVLLLLASADSQAAAP
<u>l</u> .			PKAVLKLEPPWINVLQ\EDSVTLTCQGAPQP/ERSDSIQWFHNG

SEQ	Predicted	Predicted end	The sold constant
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
Į.	corresponding	to first	L-Leucine, M-Methionine, N-Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
]	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	acquence	\=possible nucleotide insertion)
<b></b>		<del> </del>	\nLipthtqps\yrfkannn\dsgeytcqtgqtsl\sdpvhltv
1	1	1	TERULU ORDUL BEOFGERTAL BOYES (SEPERT)
1		1	LSEWLVLQTPHLEFQEGETIMLRCHS\WRDKP\LVKVTFFQNGK
			SQKFSHLDPTFSIPQANHSHSGDYHCTGNIGYTLFSSKPVTITV
-			QVPSMGSSSPMGIIVAVVIATAVAAIVAAVVALIYCRKKRISAN
ì		ł	STDPVKAAQFEPPGRQMIAIRKRQLEETNNDYETADGGYMTLNP
5394	2	982	RAPTDDDKNIYLTLPPNDHVNSNN
3394	1 4	982	GGDSAGMTMETQMSQNVCPRNLWLLQPLTVLLLLASADSQAAAP
1		}	PKAVLKLEPPWINVLQ\EDSVTLTCQGAPQP/ERSDSIQWFHNG
1.		j	\NLIPTHTQPS\YRFKANNN\DSGEYTCQTGQTSL\SDPVHLTV
-	1		LSEWLVLQTPHLEFQEGETIMLRCHS\WRDKP\LVKVTFFQNGK
-	ſ		SQKFSHLDPTFSIPQANHSHSGDYHCTGNIGYTLFSSKPVTITV
1	}		QVPSMGSSSPMGIIVAVVIATAVAAIVAAVVALIYCRKKRISAN
J	1		STDPVKAAQFEPPGRQMIAIRKRQLEETNNDYETADGGYMTLNP
5395	2725		RAPTDDDKNIYLTLPPNDHVNSNN
3395	3135	531	RASDAKNQEGLLNTRRKSTDSVPISKSTLSRSLSLQASDPDGAS
1			SSGNPEAVALAPDAYSTGSSSASSTLKRTKKPRPPSLKKKQTTK
Ì			KPTETPPVKBTQQEPDEBSLVPSGENLASETKTESAKTEGPSPA
			LLBETPLEPAAGPKAACPLDSESVEGVVPPASGGGRVQNSPPVG
1	}		RKTLPLTTAPEAGEVTPSDSGGQEDSPAKGHSVRLEFDYSEDKS
1			SWDNQQENPPPTKKIGKKPVAKMPLRRPKMKKTPEKLDNTPASP
			PRSPAEPNDIPIAKGTYTFDIDKWDDPNFNPFSSTSKMQESPKL
1			PQQSYNFDPDTCDESVDPFKTSSKTPSSPSKSPASFEIPASAME
1			ANGVDGDGLNKPAKKKTPLKTDTFRVKKSPKRSPLSDPPSQDP
1			TPAATPETPPVISAVVHATDEEKLAVTNQKWTCMTVDLRADKQD
	1		YPQPSDLSTFVNETKFSSPTEELDYRNSYRIEYMEKIGSSLPQD
ļ			DDAPKKQALYLMFDTSQESPVKSSPVRMSESPTPCSGSSFEETE
)			ALVNTAAKNOHPVPRGLAPNQESHLQVPEKSSQKELEAMGLGTP
			SEAIEITAPEGSFASADALLSRLAHPVSLCGALDYLEPDLAEKN
1 1			PPLFAQKLQRRAAHPTDVSISKTALYSRIGTAEVEKPAGLLFQQ
			PDLDSALQIARAEIITKEREVSEWKDKYEESRREVMEMRKIVAE
			YEKTIAQMIEDEQREKSVS\HQTVQQLVLEKEQA\LADLNSVEK
1 1			\SLADLFRRYEKMKEVLEGFRKNEEVLKRCAQEYLSRVKKEEQR
1	<u> </u>		YQALKVHA\EEKLDRANAB\IAQVRGKAQQEQAAHQASLAERSS
5396	3135		CRV\DALERTLEQKNKEIBELTKICDELIAKMGKS
[ 3336 ]	3133	531	RASDAKNQEGLLNTRRKSTDSVPISKSTLSRSLSLQASDFDGAS
1 1			SSGNPEAVALAPDAYSTGSSSASSTLKRTKKPRPPSLKKKQTTK
1 1			KPTETPPVKETQQEPDEESLVPSGENLASETKTESAKTEGPSPA
ļ. <b>!</b>			LLEETPLEPAAGPKAACPLDSESVEGVVPPASGGGRVQNSPPVG
j <b>i</b>			RKTLPLTTAPEAGEVTPSDSGGQEDSPAKGHSVRLEFDYSEDKS
			SWDNQQENPPPTKKIGKKPVAKMPLRRPKMKKTPEKLDNTPASP
1			PRSPAEPNDIPIAKGTYTFDIDKWDDPNFNPFSSTSKMQESPKL
1			PQQSYNFDPDTCDESVDPFKTSSKTPSSPSKSPASFEIPASAME
J	Į.		ANGVDGDGLNKPAKKKTPLKTDTFRVKKSPKRSPLSDPPSQDP
] . ]	1		TPAATPETPPVISAVVHATDEEKLAVTNQKWTCMTVDLEADKQD
1 1	Í	İ	YPOPSDLSTFVNETKFSSPTEELDYRNSYEIEYMEKIGSSLPQD
1 1	1	į	DDAPKKQALYLMFDTSQESPVKSSPVRMSESPTPCSGSSFEETE
, ,	1	j	ALVNTAAKNOHPVPRGLAFNOESHLOVPEKSSOKELEAMGLGTP
[ [	İ		SEAIBITAPEGSFASADALLSRLAHPVSLCGALDYLEPDLAEKN
{ l	{		PPLFAQKLQREAAHPTDVSISKTALYSRIGTAEVEKPAGLLFQQ
1	}	}	PDLDSALQIARAEIITKEREVSEWKDKYEESRREVMEMRKIVAE
]			YEKTIAQMIEDEQREKSVS\HQTVQQLVLEKEQA\LADLNSVEK
	ı		\SLADLFRRYEKMKEVLEGFRKNEEVLKRCAQEYLSRVKKEEQR
[ ]			YQALKVHA\EEKLDRANAE\IAQVRGKAQQEQAAHQASLAERSS
			CRV\DALERTLEQKNKEIEELTKICDELIAKMGKS
5397	3135	531	RASDAKNQEGLLNTRRKSTDSVPISKSTLSRSLSLQASDFDGAS
		1	SSGNPEAVALAPDAYSTGSSSASSTLKRTKKPRPPSLKKKQTTK
j }		ļ	KPTETPPVKETQQEPDEESLVPSGENLASETKTESAKTEGPSPA
		1	LLEETPLEPAAGPKAACPLDSESVEGVVPPASGGGRVQNSPPVG
[ [	Į.	l	RKTLPLTTAPEAGEVTPSDSGGQEDSPAKGHSVRLEFDYSEDKS
]		}	SWDNQQENPPPTKKIGKKPVAKMPLRRPKMKKTPEKLDNTPASP
<u> </u>			PRSPAEPNDIPIAKGTYTFDIDKWDDPNFNPFSSTSKMQESPKL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ľ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
ı	sequence	_	\=possible nucleotide insertion)
		<del>                                     </del>	POOSYNFDPDTCDESVDPFKTSSKTPSSPSKSPASFEIPASAME
1			ANGVDGDGLNKPAKKKKTPLKTDTFRVKKSPKRSPLSDPPSQDP
1		1	TPAATPETPPVISAVVHATDEEKLAVTNQKWTCMTVDLEADKQD
1		}	YPQPSDLSTFVNETKPSSPTEELDYRNSYEIEYMEKIGSSLPQD
ŀ			DDAPKKQALYLMFDTSQESPVKSSPVRMSESPTPCSGSSFEETE
[	<u> </u>	ĺ	ALVNTAAKNOHPVPRGLAPNOESHLQVPEKSSQKELEAMGLGTP
j		[	SEATE ITAPEGS FASADALLS RLAHPVSLCGALDY LEPDLAEKN
		[	PPLFAQKLQREAAHPTDVSISKTALYSRIGTAEVEKPAGLLFQQ
ſ	ł	ł	PDLDSALQIARAEIITKEREVSEWKDKYEESRREVMEMRKIVAE
	j		YEKTIAQMIEDEQREKSVS\HQTVQQLVLEKEQA\LADLNSVEK
			\SLADLFRRYEKMKEVLEGFRKNEEVLKRCAQEYLSRVKKEEQR
			YQALKVHA\EEKLDRANAE\IAQVRGKAQQEQAAHQASLAERSS
1			CRV\DALERTLEQKNKEIBELTKICDELIAKMGKS
5398	56	5426	SGEVCRMESNFNQEGVPRPSYVFSADPIARPSEINFDGIKLDLS
1	1		HEFSLVAPNTEANSFESKDYLQVCLRIRPFTQSEKELESEGCVH
1	}	•	ILDSQTVVLKEPQCILGRLSEKSSG\QM\AQKFSFPPGFLGPAT
}			TQKEFFQGCIMHP\VKDLLKGQSRLIFTYGLTNSGKTYTFQGTE
	<b>{</b>		ENIRILPRTLNVLPDSLQERLYTKMNLKPHRSRBYLRLSSEQEK
ļ	i		BEIASKSALLRQIKEVTVHNDSDDTLYGSLTNSLNISEFEESIK
1			DYEQANLNMANSIKFSVWVSFFEIYNEYIYDLFVPVSSKFQKKK
i	ĺ		MLRLSQDVKGYSFIKDLQWIQVSDSKEAYRLLKLGIKHQSVAFT
1	}		KLNNASSRSHSIFTVKILQIEDSEMSRVIRVSELSLCDLAGSER
			TMKTQNEGERLRETGNINTSLLTLGKCINVLKNSEKSKFOOHVP
1			FRESKLTHYF/QSFFNGKGKICMIVNISQCYLAYDETLNVLKFS
1			AIAQKVCVPDTLNSSQEKLFGPVKSSQDVSLDSNSNSKILNVKR
			ATISWENSLEDLMEDEDLVEELENAEETED/VGETKLLDEDLDK
1 1		•	TLEENKAFISHEEKRKLLDLIEDLKKKLINEKKEKLTLEFKIRE
1 1			EVTQEFTQYWAQREADFKETLLQEREILEENAERRLAIFKDLVG
'			KCDTREEAAKDICATKVETEEATACLELKFNOIKAELAKTKGEL
1 !			IKTKEELKKRENESDSLIQELETSNKKIITQNQRIKELINIIDO
1			KEDTINEFQNLKSHMENTFKCNDKADTSSLIINNKLICNETVEV
			PKDSKSKICSERKRVNENELQQDEPPAKKGSIHVSSAITEDOKK
1 1			SEEVRPNIAEIEDIRVLQENNEGLRAFLLTIENELKNEKEEKAE
1 1	ļ		LNKQIVHFQQELSLSEKKNLTLSKEVQQIQSNYDIAIAELHVOK
			SKNQEQEEKIMKLSNEIETATRSITNNVSQIKLMHTKIDELRTL
(	i		DSVSQISNIDLLNLRDLSNGSEEDNLPNTQLDLLGNDYLVSKQV
1 1	1		KEYRIQEPNRENSFHSSIEAIWEECKEIVKASSKKSHQIEELEQ
l l	i		QIEKLQAEVKGYKDENNRLKEKEHKNQDDLLKEKETLIQQLKEE
!!			LQEKNVTLDVQIQHVVEGKRALSELTQGVTCYKAKIKELETILE
1 1	l l		TQKVERSHSAKLEQDILEKESIILKLERNLKEFQEHLQD8VKNT
1 1			KDLNVKELKLKEEITQLTNNLQDMKHLLQLKEEEEETNRQETEK
l f			LKEBLSASSARTQN\LNADLQRKEEDYADLKEKLTDAKKQIKQV
		•	QKEVSVMRDEDKLLRIKINELEKKKNQCSQELDMKQR\TIQQLK
	i		EQLINQKVEEAIQQYERACKDLNVKEKIIEDMRMTLEEQEQTQV
i i	ľ		EQDQVL\EAKLEEVERLATELDRWRVKCNDLETKNNQRSNKEHE
			NNTDVLGKLTNLQDBLQESEQKYNADRKKWLEEKMMLITQAKEA
1		j	ENIRNKEMKKYAEDRERFFKQQNEMEILTAQLTEKDSDLQKWRE
1			erdolvaaleiolkalissnvokdneieolkriisetskietoi
	1		MDIKPKRISSADPDKLQTEPLSTSFEISRNKIEDGSVVLDSCEV
		İ	STENDOSTRFPXPELBIQFTPLQPNKMAVKHPGCTTPVTVKIPK
1	ĺ		ARKRKSNEMEEDLVKCENKKNATPRTNLKFP1SDDRNSSVKKEQ
ŀ	1	1	KVAIRPSSKKTYSLRSQASIIGVNLATKKKEGTLQKFGDFLQHS
	1.		PSILQSKAKKIIETMSSSKLSNVEASKENVSQPKRAKRKLYTSE
5399	705		ISSPIDISGQVILMDQKMKESDHQIIKRRLRTKTAK
	,03	230	GPRMAKFLSQDQINEYKECFSLYDKQQRGKIKATDLMVAMRCLG
ļ	]	ŀ	ASPTPGEVQRHLQTHGIDGNGELDFSTFLTIMHMQIKQEDPKKE
	1	į.	ILLAMLMVDKEKKGYVMASDLRSKLTSLGEKLTHKEV\DDLFRE
5400	931	546	\ADIEPNGKVKYDEFIHKITSYLDGTY
	731	248	SHCSSGMEIPPTNYPASRAALVAQNYINYQQGTPHRVFBVQKVK
- 1		ł	QASMEDIPGRGHKYRLKFAVEEIIQKQVKVNCTAEVLYPSTGQE
			TAPEVNFTFEGETGKNPDEEDNTFYQRLKSMKEPLEAQNI\PDN

SEO	7 8		
ID	Predicted beginning	Predicted end	Amino acid segment containing signal peptide
NO:	nucleotide	nucleotide location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO.	location		Glutamic Acid, F=Phenylalanine, G=Glycine,
1	corresponding	corresponding to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	boqueinos	\=possible nucleotide insertion)
	3-1	<del></del>	FGNVSPEMTLVLHLAWVACGYIIWQNSTEDTWYKMVKIOTVKOV
1			QRNDDFIELDYTILLHNIASQEIIPWQMQVLWHPQYGTKVKHNS
1			RLPKEVOLE
5401	3	1360	TGWSYGPTTSLAFLAPRDFPFPPKLLIHPQAVVRLSCGAGSMGS
			QAAAEWRNWASWEGSSSLSGCSMGCFKDDRIVFWTWMFSTYFME
1	1	ĺ	KWAPRQDDMLFYVRRKLAYSGSESGADGRKAAEPEVEVEVYRRD
f	1		SKKLPGLGDPDIDWEESVCLNLILQKLDYMVTCAVCTRADGGDI
	1		HIHKKKSQQVFASPSKHPMDSKGEESKISYPNIFFMIDSF\BE\
1			VFSDMTVGKGEMVCVELVASDKTNTFQGVIFQGSIRYEALKKVY
			DNRVSVAARMAQK\MSFGFSKYSNMEF\VR\MKGPQGKGHAEMA
1			VSRVSTGDTSPCGTEEDSSPASPMHERVTSFSTPPTPERNNRPA
i	[		FFSPSLKRKVPRNRIAEMKKSHSANDSEEFFREDDGGADLHNAT
1			NLRSRSLSGTGRSLVGSWLKLNRADGNFLLYAHLTYVTLPLHRI
1			LTDILEVRQKPILMT
5402	3445	1563	GECFIMAAVVQQNDLVFEFASNVMEDERQLGDPAIFPAVIVEHV
	1		PGADILNSYAGLACVEEPNDMITESSLDVAEEEIIDDDDDDITL
			TVEASCHDGDETIETIEAAEALLNMDSPGPMLDEKRINNNIFSS
ł		·	PEDDMVVAPVTHVSVTLDGIPEVMETQQVQEKYADSPGASSPEQ
1	1.		PKRKKGRKTKPPRPDSPATIPNISVKKKNKDGKGNTIYLWEFLL .
1	1		ALLQDKATCPKYIKWTQREKGIFKLVDSKPVSRLWRKHKNKP\D
			MNYEPMGRALRYYYQRGILAKVEGQRLVYQFKEMPKDLIYINDE
1			DPSSSIESSDPSLSSSATSNRNQTSRSRVSSSPGVKGGATTVLK
ł	•		PGNSKAAKPKDPVEVAQPSEVLRTVQPTQSPYPTQLFRTVHVVQ
			PVQAVPEGEAARTSTMQDETLNSSVQSIR\TIQAPTQVPVVVSP
ł	1		RNQQ\LHTVTLQTVPLTTVIASTDPSAGTGSQKFILQAIPSSQP
1			MTVLKENVMLQSQKAGSPPSIVLGPARV\QQVLTSNVQTICNGT
1			VSV\ASSPSFS\ATAPVVTLFLLGSSQLVAHPPGTVITSVIKTQ
·	]		ETKTLTQEVEKKESEDHLKENTEKTEQQPQPYVMVVSSSNGFTS
5403	3445	1563	QVAMKQNELLEPNSF GECFIMAAVVQQNDLVFEFASNVMEDERQLGDPAIFPAVIVEHV
1		-505	PGADILNSYAGLACVEEPNDMITESSLDVAEEEIIDDDDDDITL
j			TVEASCHDGDETIETIEAAEALLNMDSPGPMLDEKRINNNIFSS
	ļ		PEDDMVVAPVTHVSVTLDGIPEVMETQQVQEKYADSPGASSPEO
			PKRKKGRKTKPPRPDSPATTPNISVKKKNKDGKGNTIYLWEFLL
ľ			ALLQDKATCPKYIKWTQREKGIFKLVDSKPVSRLWRKHKNKP\D
			MNYEPMGRALRYYYQRGILAKVEGQRLVYQFKEMPKDLIYINDE
1			DPSSSIESSDPSLSSSATSNRNQTSRSRVSSSPGVKGGATTVLK
			PGNSKAAKPKDPVEVAQPSEVLRTVQPTQSPYPTQLFRTVHVVQ
	ļ		PVQAVPEGEAARTSTMQDETLNSSVQSIR\TIQAPTQVPVVVSP
			RNQQ\LHTVTLQTVPLTTVIASTDPSAGTGSQKFILQAIPSSQP
1			MTVLKENVMLQSQKAGSPPSIVLGPARV\QQVLTSNVQTICNGT
1			VSV\ASSPSFS\ATAPVVTLFLLGSSQLVAHPPGTVITSVIKTQ
			ETKTLTQEVEKKESEDHLKENTEKTEQQPQPYVMVVSSSNGFTS
	105		QVAMKQNELLEPNSF
5404	187	1111	LPVTLIFAKMKTLQSTLLLLLVPLIKPAPPTQQDSRIIYDYGT
1			DNFEESIFSQDYEDKYLDGKNIKEKETVIIPNEKSLQLQKDEAI
			TPLPPKKENDEMPTCLLCVCLSGSVYCEEVDIDAVPPLPKESAY
	[		LYARPNKIKKLT\AKDFADIPNLRRLDFTGNLIEDIEDGTFSKL
[	1		SLVEBLSLAENQLLKLPVLPPKLTLFNAKYNKIKSRGIKANAFK
	1		KLNNLTFLYLDHNALESVPLNLPESLRVIHLQFNNIASITDDTF
5405	2199	1220	CKANDTSYIRDRIEEIRLEGNPIVLGKHPNSFICLKRLPIGSYF
	""	1240	QNSRSLHMDPQNQHGSGSSLVVIQQPSLDSRPRLDYEREIQPTA
			ILSLDQIKAIRGSNEYTEGPSVVKRPAPRTAPRQEKHERTHEII
j i			PINVNNNYEHRHTSHLGHAVLPSNARGPILSRSTSTGSAASSGS NSSASSEQGLLGRSPPTRPVPGHRSERAIRTOPKOLIVDDLKGS
	1		LKEDLTQHKFICEOCGKCKCGECTAPRTLPSCLACNROCLCSAE
	ĺ		SMVEYGTCMCL\VKGIFYHCSNDDEGDSYSDNPCSCSQSHCCSR
	}		YLCMGAMSLFLPCLLCYPPAKGCLKLCRRCYDWIHRPGCRCKNS
			NTVYCKLESCPSRGQGKPS
5406	279	2732	RWRTYNVEGPLTFMDVAIEFCLEEWQCLDTAQQNLYRNVMLENY
· · · · · · · · · · · · · · · · · · ·	·		

SEQ	Predicted	Predicted end	The first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and the first and th
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	corresponding	Glutamic Acid, F-Phenylalanine, G-Glycine,
İ	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
i	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
1	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	bequence	Codon, /=possible nucleotide deletion,
<del> </del>		<del> </del>	\=possible nucleotide insertion)
ł			RNLVFLG/TIAVSKPDLITCLEQEKEPWEPMRRHEMVAKPPVMC
ì		1	SHFTQDFWPEQHIKDPFQKATLRRYKNCEHKNVHLKKDHKSVDE
			CKVHRGGYNGFNQCLPATQSKIFLFDKCVKAFHKFSNSNRHKIS
I			HTEKKLFKCKECGKSFCMLSHLAQHKIIHTRVNFCKCEKCGKAF
			NCPSIITKHKRINTGEKPYTCEBCGKVFNWSSRLTTHKKNYTRY
1	}		KLYKCEECGKAFNKSSILTTHKIIRTGEKFYKCKECAKAFNOSS
}		}	NLTEHKKIHPGEKPYKCEECGKAFNWPSTLTKHKRIHTGEKPYT
1			CEECGKAFNQFSNLTTHKRIHTA\EKFYKCTECGEAFSRS\SNL TKHKEIHTEKKPYKCBECGKAFKWSSKLTEHKLTHTGEKPYKCE
1			VCCVA ENGRET TOWNS THE CENTRE OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE
1	1	1	KCGKAFNCPSIITKHNRINTGEKPYTCEECGKVFNWSSRLTTHK
	1	1	KNYTRYKLYKCEECGKAFNKSSILTTHKKIHIEKKFYKCEECGK AFKWSSKLTBHKITHTGEK?YKCEECGKAFNHFSILTKHKRIHT
į			GREDVECED CENTER THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE
ŀ			GEKPYKCEECGKAFTQSSNLTTHKKIHTGBKFYKCEECGKAFTQ
1		<b>J</b>	SSNLTTHKKIHTGGKPYKCEECGKAFNQFSTLTKHKIIHTEEKP YKCEECGKAFKWSSTLTKHKIIHTGEKPYKCEECG\KAFKLSST
			LSTHKIIHTGEKPYKCEKCGKAFNRPSNLIEHKKIHTGEQPYKC
1			EECGKAFNYSSHLNTHKRIHTKEQPYKCKECGKAFNQYSNLTTH
}			NKIHTGEKLYKPEDVTVILTTPQTFSNIK
5407	. 3	659	RPRRRQSSCCTGWLAGWLLRAAPRFCRRTETDMEQGKGLAVLIL
1			AIILLOGTLAQSIKGNHLVKVYDYQEDGSVLLTCDAEAKNITWF
	•		KDGKMIGFLTEDKKKWNLGSNAKDPRGMYQCKGSQNKSKPLQVY
1 4		•	YRMCQNCIELNAATISGFLFAEIVSIFDLAVGVYFIAGTGMEFR
L			QS\RASDKQTLLP\NDPAPTQPLKDPRKMTQYSHLQGN\QLRRN
5408	2745	6128	QGSKGTCHPQAQQPWDEGVWQEAPSQSEPWGQSQEPPTMPQRLP
1 1			HARQHTPLPLGSADYRRVVSVRPQGPHRDPXDSRDAAKREQGSL
			APRPVPASRGGKTLCKGYRQAPPGPPAQFQRPICSASPPWASRF
1 1			STPCPGGAVREDTYPVGTQGVPSLALAQGGPQGSWRFLEWKSMP
1 1			RLPTDLDIGGPWFPHYDFERSCWVRAISQEDQLATCWQAEHCGE
} [			VRNKDMSWPEEMSFIANSSKIDRHKVPTEKGATGLSNLGNTCFM
ł			NSSIQCVSNTQPLTQYFISGRHLYELNRTNPIGMKGHMAKCYGD
· i			LVQELWSGTQKNVAPLKLRWTIAKYAPRFNGFQOODSOELLAFI,
			LDGLHEDLNRVHEKPYVELKDSDGRPDWEVAAEAWDNHLRRNRS
1 . 1			IVVDLFHGQLRSQVKCKTCGHISVRFDPFNFLSLPLPMDSYMHL
			EITVIKLDGTTPVRYGLRLNMDEKYTGLKKOLSDLCGLNSBOIL
! ' !	}		LAEVHGSNIKNFPQDNQKVRLSVSGFLCAFEIPVPVSPISASSP
1 1			TQTDFSSSPSTNEMFTLTTNGDLPRPIFIPNGMPNTVVPCGTEK
i l			NFTNGMVNGHMPSLPDSPFTGYIIAVHRKMMRTELYFLSSQKNR
			PSLFGMPLIVPCTVHTRKKDLYDAVWIQVSRLASPLPPOEASNH
1 1			AQDCDDSMGYQYPFTLRVVQKDGNSCAWCPWYRFCRGCKIDCGE
	j		DRAFIGNAYIAVDWHPTALHLRYQTSQERVVDEHESVEQSRRAQ
	ļ		VEPINLDSCLRAFTSEEELGENEMYYCSKCKTHCLATKKLDLWR
	ı		LPPILIIHLKRFQFVNGRWIKSQKIVKFPRESFDPSAFLVPRDP
}	j		ALCOHKPLTPQGDELSEPRILAREVKKVDAQSSAGEEDVLLSKS
	1	[	PSSLSANI ISSPKGSPSSSRKSGTSCPSSKNSSPNSSPRTLGRS
) }			KGRLRLPQIGSKNKLSSSKENLDASKENGAGQICELADALSRGH
	1	1	VINESCIPELIUS DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DEL COMPANIA DE LA COMPANIA DEL COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DEL COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DEL COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DEL COMPANIA DE LA COMPANIA DE LA COMPANIA DEL COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DE LA COMPANIA DEL COMPANIA DEL COMPANIA DEL COMPANIA DE LA COMPANIA DEL COMPAN
ľ	1		VLGGSQPELVTPQDHEVALANGFLYEHEACGNGCGNGYSNGQLG
			NHSEEDSTDDQREDTRIKPIYNLYAISCHSGILGGGHYVTYAKN
			NHSEEDSTDDQREDTRIKPIYNLYAISCHSGILGGGHYVTYAKN PNCKWYCYNDSSCKELHPDEIDTDSAYILFYEOOGIDYAOFI,PK
5409	2745	6128	NHSEEDSTDDQREDTRIKPIYNLYAISCHSGILGGGHYVTYAKN PNCKWYCYNDSSCKELHPDEIDTDSAYILFYEQQGIDYAQFLPK TDGKKMADTSSMDEDFESDY\EKYCVLQ
5409	2745	6128	NHSEEDSTDDQREDTRIKPIYNLYAISCHSGILGGGHYVTYAKN PNCKWYCYNDSSCKELHPDEIDTDSAYILFYEQQGIDYAQFLPK TDGKKMADTSSMDEDFESDY\EKYCVLQ QGSKGTCHPQAQQPWDEGVWQEAPSQSEPWGQSQEPPTMPORLP
5409	2745	6128	NHSEEDSTDDQREDTRIKFIYNLYAISCHSGILGGGHYVTYAKN PNCKWYCYNDSSCKELHPDEIDTDSAYILFYEQQGIDYAQFLPK TDGKKMADTSSMDEDFESDY\EKYCVLQ QGSKGTCHPQAQQPWDEGVWQEAPSQSEPWGGSQEPPTMPQRLP HARQHTPLPLGSADYRRVVSVRPQGPHRDPXDSRDAAKREOGSL
5409	2745	6128	NHSEEDSTDDQREDTRIKFIYNLYAISCHSGILGGGHYVTYAKN PNCKWYCYNDSSCKELHPDEIDTDSAYILFYEQQGIDYAQFLPK TDGKKMADTSSMDEDFESDY\EKYCVLQ OGSKGTCHPQAQQPWDEGVWQEAPSQSEPWGQSQEPPTMPQRLP HARQHTPLPLGSADYRRVVSVRPQGPHRDPKDSRDAAKREQGSL APRPVPASRGGKTLCKGYRQAPPGFFAQFORFICSASPPWASRF
5409	2745	6128	NHSEEDSTDDQREDTRIKPIYNLYAISCHSGILGGGHYVTYAKN PNCKWYCYNDSSCKELHPDEIDTDSAYILFYEQQGIDYAQFLPK TDGKKMADTSSMDEDFESDY\EKYCVLQ OGSKGTCHPQAQQPWDEGVWQEAPSQSEPWGQSQEPPTMPQRLP HARQHTPLPLGSADYRRVVSVRPQGPHRDPKDSRDAAKREQGSL APRPVPASRGGKTLCKGYRQAPPGPFAQFQRPICSASPPWASRF STPCPGGAVREDTYPVGTQGVPSLALAQGGPQGSWRFLEWKSMP
5409	2745	6128	NHSEEDSTDDQREDTRIKPIYNLYAISCHSGILGGGHYVTYAKN PNCKWYCYNDSSCKELHPDEIDTDSAYILFYEQQGIDYAQFLPK TDGKKMADTSSMDEDFESDY\EKYCVLQ QGSKGTCHPQAQQPWDEGVWQEAPSQSEPWGQSQEPPTMPQRLP HARQHTPLPLGSADYRRVVSVRPQGPHRDPXDSRDAAKREQGSL APRPVPASRGGKTLCKGYRQAPPGPPAQFQRPICSASPPWASRF STPCPGGAVREDTYPVGTQGVPSLALAQGGPQGSWRFLEWKSMP RLPTDLDIGGPWFPHYDFERSCWVRAISQEDOLATCWOAEHCGE
5409	2745	6128	NHSEEDSTDDQREDTRIKPIYNLYAISCHSGILGGGHYVTYAKN PNCKWYCYNDSCKELHPDEIDTDSAYILFYEQQGIDYAQFLPK TDGKKMADTSSMDEDFESDY\EKYCVLQ QGSKGTCHPQAQQPWDEGVWQEAPSQSEPWGQSQEPPTMPQRLP HARQHTPLPLGSADYRRVVSVRPQGPHRDPXDSRDAAKREQGSL APRPVPASRGGKTLCKGYRQAPPGPPAQFQRPICSASPPWASRF STPCPGGAVREDTYPVGTQGVPSLALAQGGPQGSWRFLEWKSMP RLPTDLDIGGPWFPHYDFERSCWVRAISQEDQLATCWQAEHCGE VRNKDMSWPEEMSFIANSSKIDRHKVPTEKGATGLSNLGNTCFM
5409	2745	6128	NHSEEDSTDDQREDTRIKFIYNLYAISCHSGILGGGHYVTYAKN PNCKWYCYNDSCKELHPDEIDTDSAYILFYEQQGIDYAQFLPK TDGKKMADTSSMDEDFESDY\EKYCVLQ QGSKGTCHPQAQQPWDEGVWQEAPSQSEPWGQSQEPPTMPQRLP HARQHTPLPLGSADYRRVVSVRPQGPHRDPXDSRDAAKREQGSL APRPVPASRGGKTLCKGYRQAPPGPPAQFQRPICSASPPWASRF STPCPGGAVREDTYPVGTQGVPSLALAQGGPQGSWRFLEWKSMP RLPTDLDIGGPWFPHYDFERSCWVRAISQEDQLATCWQAEHCGE VRNKDMSWPEBMSFIANSSKIDRHKVPTEKGATGLSNLGNTCFM NSSIQCVSNTQPLTQYFISGRHLYELNRTNPIGMKGHMAKCYGD
5409	. 2745	6128	NHSEDSTDDQREDTRIKPIYNLYAISCHSGILGGGHYVTYAKN PNCKWYCYNDSSCKELHPDEIDTDSAYILFYEQQGIDYAQFLPK TDGKKMADTSSMDEDFESDY\EKYCVLQ QGSKGTCHPQAQQPWDEGVWQEAPSQSBPWGQSQEPPTMPQRLP HARQHTPLPLGSADYRRVVSVRPQGPHRDPXDSRDAAKREQGSL APRPVPASRGGKTLCKGYRQAPPGPPAQFQRFICSASPPWASRF STPCPGGAVREDTYPVGTQGVPSLALAQGGPQGSWRFLEWKSMP RLPTDLDIGGPWFPHYDFERSCWVRAISQEDQLATCWQAEHCGE VRNKDMSWPEBMSFIANSSKIDRHVPTEKGATGLSNLGNTCFM NSSIQCVSNTQPLTQYFISGRHLYELNRTNPIGMKGHMAKCYGD LVQELWSGTQKNVAPLKLRWTIAKYAPRFNGFQQQDSOELLAFL
5409	. 2745	6128	NHSEEDSTDDQREDTRIKPIYNLYAISCHSGILGGGHYVTYAKN PNCKWYCYNDSSCKELHPDEIDTDSAYILFYEQQGIDYAQFLPK TDGKKMADTSSMDEDFESDY\EKYCVLQ GOSKGTCHPQAQQPWDEGVWQEAPSQSEPWGQSQEPPTMPQRLP HARQHTPLPLGSADYRRVVSVRPQGPHRDPKDSRDAAKREQGSL APRPVPASRGGKTLCKGYRQAPPGPPAQFQRPICSASPPWASRF STPCPGGAVREDTYPVGTQGVPSLALAQGGPQGSWRFLEWKSMP RLPTDLDIGGPWFPHYDFERSCWVRAISQEDQLATCWQAEHCGE VRNKDMSWPEBMSFIANSSKIDRHKVPTEKGATGLSNLGNTCFM NSSIQCVSNTQPLTQYFISGRHLYELNRTNPIGMKGHMAKCYGD LVQELMSGTQKNVAPLKLRWTIAKYAPRFNGFQQQDSQELLAPL LDGLHEDLNRVHEKPYVELKDSDGRPDWEVAAEAWDNHLRRNRS
5409	2745		NHSEEDSTDDQREDTRIKPIYNLYAISCHSGILGGGHYVTYAKN PNCKWYCYNDSSCKELHPDEIDTDSAYILFYEQQGIDYAQFLPK TDGKKMADTSSMDEDFESDY\EKYCVLQ OGSKGTCHPQAQQPWDEGVWQEAPSQSEPWGQSQEPPTMPQRLP HARQHTPLPLGSADYRRVVSVRPQGPHRDPXDSRDAAKREQGSL APRPVPASRGGKTLCKGYRQAPPGPPAQFQRPICSASPPWASRF STPCPGGAVREDTYPVGTQGVPSLALAQGGPQGSWRFLEWKSMP RLPTDLDIGGPWFPHYDFERSCWVRAISQEDQLATCWQAEHCGE VRNKDMSWPEEMSFIANSSKIDRHKVPTEKGATGLSNLGNTCFM NSSIQCVSNTQPLTQYFISGRHLYELNRTNPIGMKGHMAKCYGD LVQELWSGTQKNVAPLKLRWTIAKYAPRFNGFQQQDSQELLAPL LDGLHEDLNRVHEKPYVELKDSDGRPDWEVAAEAWDNHLRRNRS IVVDLFHGQLRSQVKCKTCGHISVRPDPFNFLSLPLPPMDSYMHI
5409	2745		NHSEEDSTDDQREDTRIKPIYNLYAISCHSGILGGGHYVTYAKN PNCKWYCYNDSSCKELHPDEIDTDSAYILFYEQQGIDYAQFLPK TDGKKMADTSSMDEDFESDY\EKYCVLQ GOSKGTCHPQAQQPWDEGVWQEAPSQSEPWGQSQEPPTMPQRLP HARQHTPLPLGSADYRRVVSVRPQGPHRDPKDSRDAAKREQGSL APRPVPASRGGKTLCKGYRQAPPGPPAQFQRPICSASPPWASRF STPCPGGAVREDTYPVGTQGVPSLALAQGGPQGSWRFLEWKSMP RLPTDLDIGGPWFPHYDFERSCWVRAISQEDQLATCWQAEHCGE VRNKDMSWPEBMSFIANSSKIDRHKVPTEKGATGLSNLGNTCFM NSSIQCVSNTQPLTQYFISGRHLYELNRTNPIGMKGHMAKCYGD LVQELMSGTQKNVAPLKLRWTIAKYAPRFNGFQQQDSQELLAPL LDGLHEDLNRVHEKPYVELKDSDGRPDWEVAAEAWDNHLRRNRS

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H-Histidine, I-Isoleucine, K-Lysine,
i	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ł	to first	amino acid	Debeucine, Mamethionine, NaAsparagine,
1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
1	residue of	l .	S=Serine, T=Threonine, V=Valine,
i	amine acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
		sequence	Codon, /=possible nucleotide deletion,
<b>-</b>	sequence		\=possible nucleotide insertion)
1 .			TOTOFSSSPSTNEMPTLTTNGDLPRPIFIPNGMPNTVVPCGTEK
1			NFTNGMVNGHMPSLPDSPFTGYIIAVHRKMMRTELYFLSSQKNR
}	j	•	PSLFGMPLIVPCTVHTRKKDLYDAVWIQVSRLASPLPPQEASNH
			AQDCDDSMGYQYPFTLRVVQKDGNSCAWCPWYRFCRGCKIDCGE
1	1		DRAFIGNAYIAVDWHPTALHLRYQTSQERVVDEHESVEOSRRAO
			VEPINLDSCLRAFTSEEELGENEMYYCSKCKTHCLATKKLDLWR
Į.	Į .		LPPILIIHLKRFQFVNGRWIKSQKIVKFPRESFDPSAFLVPRDP
1			ALCOHKPLTPQGDELSEPRILAREVKKVDAQSSAGEEDVLLSKS
1	·		PSSLSANIISSPKGSPSSSRKSGTSCPSSKNSSPNSSPRTLGRS
1			KGRLRLPQIGSKNKLSSSKENLDASKENGAGQICELADALSRGH
1			VLGGSQPELVTPQDHEVALANGFLYEHEACGNGCGNGYSNGQLG
1	}		NHSBEDSTDDQREDTRIKPIYNLYAISCHSGILGGGHYVTYAKN
1	]		PNCKWYCYNDSSCKELHPDEIDTDSAYILFYBQQGIDYAQFLPK
Į.			TDGKKMADTSSMDEDFESDY\EKYCVLQ
5410	2	710	LRPPGQARHVWLAARMQAPHKEHLYKLLVIGDLGVGKTSIIKRY
			VHQNFSSHYRATIGVDFALKVLHWDPETVVRLQLWDIAGQERFG
}			NMTRVYYREAMGAFIVFDVTRPATFEAVAKWKNDLDSKLSLPNG
1			KPVSVVLLANKCDQGKDVLMNNGLKMDQFCKEHGFVGWFETSAK
ŀ			ENINIDEASRCLVKHILANECDLMESIEPDVVKPHLTSTKVASC
			SG\CAKILVGTFAGVW
5411	1302	289	TGPAAAGRRKALGSFGKPSPVTGLRAARRRTRPSAPAAPSVGC
1			GKRRESDAGAGGERASVRTGSGRRGGRTMAGDSEQTLQNHQQ?N
			GGEFFLIGVSGGTASGKSSVCAKIVQLLGQNEVDYRQKQVVILS
1.			QDSFYRVLTSEQKAKALKGQFNFDHPDAFDNELILKTLKEITEG
1			KTVQIPVYDFVSHSRKEETVTVYPADVVLFEGILAFYSQER/IR
	.		DLFQMKLFVDTDADTRLSRRVLKDISERGRDLEQILSSSTLRFV
	Ĭ		KPA\FEEFCLPPK\KYADVIIPR\GADN\RVPINLIVQHIQ\DI
1 1			LNGGPS\NRQTNGCLNGYTPSRKRQASESSSRPH
5412	3180	313	QGISNFFHKBANFWFEVSGYLISPLRSPFVDFALEWSLMASPWN
1 1			KMEGESSRFEIHTPVSDKKKKKCSIHKERPQKHSHEIFRDSSLV
	ł		NEQSQITERKKEKKDFQHLISSPLKKSRICDETANATSTLKKEK
1			KRRYSALEVDEBAGVTVVLVDKENINNTPKHFRKDVDVVCVDMS
1	ļ		IEQKLPRK\PKTDKFQVLAKSH\AHKSEALHSKVREKKNKKHQR
		J	KAASWESQRA\RDTLPQSEFPTQEESWLSVGPGGEITELP\ASA
1			HKNKSKKKKKSSNREYET\LAMPEGSQAGREAGTDMQESQPTV
1 [			GLDDETPQLLGPTHKKKSKKKKKKKKKNHQEFESLAMPEGSQVGS
1 1		ł	EVGADMQES\RPAVGLHGETAGIPAPAYKNKSKKKKKSNHQEF
1 1			EAVAMPESLESAYPEGSQVGSEVGTVEGSTALKGFKESNSTKKK
1 1	j		SKKRKLTSVKRARVSGDDFSVPSKNSBSTLFDSVEGDGAMMBEG
1 [		•	VKSRPRQKKTQACLASKHVQEAPRLEPANEEHNVETAEDSEIRY
}			LSADSGDADDSDADLGSAVKQLQEFIPNIKDRATSTIKRMYRDD
1		}	LERFKEFKAOGVAIKFGKFSVKENKOLEKMVEDETALTGTEGAD
1	ļ	ļ	KLLYTDRYPEEKSVITNLKRRYSFRLHIG\RNIARPWKLIYYRA
1	. 1		KKMFDVNNYKGRYSEGDTEKLKMYHSLLGNDWKTIGEMVARRSL
j .	1	1	SVALKFSQISSQRNRGAWSKSETRKLIKAVEEVILKKMSPQBLK
{	1	. 1	EVDSKLQENPESCLSIVREKLYKGISWVEVEAKVQTRNWMQCKS
1 1	1	1	KWTEILTKRMTNGRRIYYGMNALRAKVSLIERLYEINVEDTNEI
1 1	į	ţ	DWEDLASAIGDVPPSYVQTKFSRLKAVYVPFWQKKTFPEIIDYL
1	Ť	Í	YETTLPLLKEKLEKMMEKKGTKIQTPAAPKQVFPPRDIFYYEDD
1	1		SEGGGHRKRKRRPRRHAWFTPVIPVLWEAKAGWII
5413	3753	1304	RFPAGVAPRRAMANVSKKVSWSGRDRDDEEAAPLLRRTARPGGG
1			TPLLNGAGPGAARQSPRSALFRVGHMSSVKLDDELLEP\DMDPP
	ł		HPFPKEIPHNEKLLSLKYESLDYDNSENQLFLEEERRINHTAFR
[			TVELKEWUTCHLIGHT TOLLING OFFICE AND AND AND AND AND AND AND AND AND AND
(	}		TVEIKRWVICALIGILTGLVACFIDIVVENLAGLKYRVIKGNID
1			KFTEKGGLSFSLLLWATLNAAFVLVGSVIVAFIEPVAAGSGIPQ
			IKCFLNGVKIPHVVRLKTLVIKVSGVILSVVGGLAVGKEGPMIH
		1	SGSVIAAGISQGRSTSLKRDFKIFEYLRRDTEKRDFVSAGAAAG
	1		VSAAFGAPVGGVLPSLEEGASFWNQFLTWRIFFASMISTFTLNF
		1	VLSIYHGNMWDLGSPGLINFGRFDSEKMAYTIHEIPVFIAMGVV
	1	į	GGVLGAVFNALNYWLTMFRIRYIHRPCLQVIEAVLVAAVTATVA
<del></del>	<del></del>		FVLIYSSRDCQPLQGGSMSYPLQLFCADGEYNSMAAAFFNTPEK

SEO	Predicted	1 No. 31 1	
ID	beginning	Predicted end	Amino acid segment containing signal peptide
NO:	nucleotide	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ŀ	corresponding	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
Į.		to first	L=Leucine, M=Methionine, N=Asparagine,
ł	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Ston
Ì	amino acid	sequence	Codon, /=possible nucleotide deletion.
L	sequence		\=possible nucleotide insertion)
			SVVSLFHDPPGSYNPLTLGLFTLVYFFLACWTYGLTVSAGVFIP
	-		SLLIGAAWGRLFGISLSYLTGAAIWADPGKYALMGAAAQLGGIV
ı	į.		RMTLSLTVIMMEATSNVTYGFPIMLVLMTAKIVGDVFIEGLYDM
]	1		HIQLQSVPPLHWEAPVTSHSLTAREVMSTPVTCLRRREKVGVIV
	1	}	DVLSDTASNHNGFPVVEHADDTQPARLQGLILRSQLIVLLKHKV
1	1	1	FVERSNLGLVQRRLRLKDFRDAYPRFPPIQSIHVSQDERECTMD
1	Į.	}	T SEEMING DAMPING STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE
1	1		LSEFMNPSPYTVPQEASLPRVPKLFRALGLRHLVVVDNRNQVVG
5414	2130	390	LVTRKDLARYRLGKRGLEELSLAQT
3124	2130	390	GVASAWDRALFSPLLSPTSRVFRTSPPRCVSTETGRRDRARVPS
J	J	·	QWCSVLQGKLPVSGRTSLACVRSILLSPASSPRKVGIVGGTGAR
1	ŀ		AGAAPRDHGRVRHRRPSSARRMTRTTGQCLAPRGCQGPRGTRSP
	1		RSPRSRTRRGCSASPACLP/CRSALIVAVLCYINI,LNYMDRFTV
	1		AGVLPDIEQFFNIGDSSSGLIQTVFISSYMVLAPVFGYLGDRYN
1	·		RKYLMCGGIAFWSLVTLGSSFIPGEHFWLLLLTRGLVGVGEASY
			STIAPTLIADLEVADORSRMLSIFYFAIPVGSGLGYIAGSKVKD
1	į i	1	MAGDWHWALRVTPGLGVVAVLLLFLVVREPPRGAVERHSDLPPI.
l .			NPTSWWADLRALARNPSFVLSSLGFTAVAFVTGSLALWAPARIJ.
			RSRVVLGETPPCLPGDSCSSSDSLIFGLITCLTGVLGVGLGVEI
1	1	,	SRRLRHSNPRADPLVCATGLLGSAPFLFLSLACARGSIVATYIF
	1		IFIGETLLSMNWAIVADILLYVVIPTRRSTAEAFQIVLSHLLGD
1	}		AGSPYLIGLISDRLRRNWPPSFLSEFRALQFSLMLCAFVGALGG
1	!		AAFLGTAHLH
5415	693	2986	IPPKTKLELQKH\LTTLT\NQEQATIFEEVQKLRPRNEQRENEL
	]		IISPLRCLFEBKQKEHIHIGEMKQTSQMAAENIGSELPPSATRF
ŀ	į į		RLDMLKNKAKRSLTESLESILSRGNKARGLQEHSISVDLDSSLS
İ	1 1		STICNTE VEDEVOEWENT PLOCECOPIES CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONT
1	i l		STLSNTSKEPSVCEKEALPISESSFKLLGSSEDLSSDSESHLPE
	1		EPAPLSPQQAFRRRANTLSHFPIECQEPPQPARGSPGVSQRKLM
1	[		RYHSVSTETPHERKDFESKANHLGDSGGTPVKTRRHSWRQQIFL
l	ł . ł		RVATPQKACDSSSRYEDYSELGELPPRSPLEPVCEDGPFGPPPE
1	]		EKKRTSRELRELWQKAILQQILLLRMEKENQKLQASENDLLNKR
]			LKLDYEEITPCLKEVTTVWEKMLSTPGRSKIKFDMEKMHSAVGQ
	!		GVP\RHHRGEIWKFLAEQFHLKHQFPSKQQPKDVPYKELLKQLT
1	l		SQQHAILIDLGRTFPTHPYFSAQLGAGQLSLYNILKAYSLLDQE
1			VGYCQGLSFVAGILLLHMSEEEAFKMLKFLMFDMGLRKOYRPDM
1	l	•	IILQIQMYQLSRLLHDYHRDLYNHLBEHEIGPSLYAAPWFI.TMF
1	1		ASQFPLGFVARVFDMIFLQGTEVIFKVALSLLGSHKPLILOHEN
1 1			LETIVDFIKSTLPNLGLVQMEKTINOVFEMDIAKOLOAYEVEYH
ļ.			VLQEELIDSSPLSDNQRMDKLEKTNSSLRKONLDLLEOLOVANG
ľ			RIQSLEATIEKLLSSESKLKQAMLTLELERSALLQTVEELRRRS
			AKPSDREPECTOPEPTGD
5416	27	4074	KSQLFCFWGGKAGDILSGDQDKEQKDFYFVETFYGYQLDLDFLK
į l		Ť	YVDDIQKGNTIKRLNIQKRRKPSVPCPEPRTTSGQQGIWTSTES
) í	1		LSSSNSDDNKQCPNFLIARSQVTSTPISKPPPPLETSLPFLTIP
1			ENRQLPPPSPQLPKHNLHVTKTLMETRRRLEQERATMQMTPGEF
, ,	j		RRPRLASFGGMGTTSSLPSFVGSGNHNPAKHQLQNGYQGNGDYG
ļ l	İ		SYAPAAPTTSSMGSSIRHSPLSSGISTPVTNVSPMHLQHIRBQM
1 1	İ		AIALKRLKELEEQVRTIPVLQVKISVLQEEKRQLVSQLKNQRAA
ł	1		SOLMICCUBERCY CALL SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE SOLD OF THE
]			SQINVCGVRKRSYSAGNASQLEQLSRARRSGGELYIDYEEEEME
			TVEQSTQRIKEFRQL\TADMQALEQKIQDSSCEASSELRENGEC
i i	i		RSVAVGAEENMNDIVVYHRGSRSCKDAAVGTLVEMRNCGVSVTE
}	1	}	AMLGVMTEADKEIELQQQTIESLKEKIYRLEVQLRETTHDREMT
	<u> </u>	Ì	KLKQELQAAGSRKKVDKATMAQPLVFSKVVEAVVQTRDQMVGSH
ſ			MDLVDTCVGTSVETNSVGISCQPECKNKVVGPELPMNWWIVKER
1	ł		VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTEESVNDLTLLKT
Į.	ł		NLNLKEVRSIGCGDCSVDVTVCSPKECASRGVNTEAVSOVEAAV
ŀ			MAVPRIADQDTSTDLEQVHQPTNTETATLIESCTNTCLSTLDKO
	1	i	TSTQTVETRTVAVGEGRVKDINSSTKTRSIGVGTLLSGHSGFDR
1	į	ļ	PSAVKTKESGVGQININDNYLVGLKMRTIACGPPOLTVGLTASR
ŀ		ĺ	RSVGVGDDPVGESLENPQPOAPLGMMTGLDHYIERIOKLLAGOO
ſ		Ì	TLLAENYSELAEAFGEPHSOMGSLNSOLISTLSSINSVMKSAST
1		l	EELRNPDFQKTSLGKITGSYLGYTCKCGGLQSGSPLSSQTSQPE

SEQ	Predicted	Predicted end	Their and the second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second se
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G-Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Laucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P-Proline, Q=Glutamine, R-Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
- {	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
(	sequence	1	\=possible nucleotide insertion)
		<del> </del>	QEVGTSEGKPISSLDAFPTQEGTLSPVNLTDDQIAAGLYACTNN
1			ESTLKSIMKKKDGNKDSNGAKKNLQFVGINGGYETTSSDDSSSD
		ĺ	ESSSESDDECDVIEYPLEBEEEEEDBDTRGMAEGHHAVNIEGL
1		İ	KSARVEDEMQVQECEPEKVBIRERYELSEKMLSACNLLKNTIND
1	j		PKALTSKDMRFCLNTLQHEWFRVSSQKSAIPAMVGDYIAAFEAI
ł		j	SPDVLRYVINLADGNGNTALHYSVSHSNFEIVKLLIJDADVCNVD
ł	1	ļ	HONKAGYTPIMLAALAAVEAEKDMRIVEELFGCGDVNAKASQAG
1	}	1	QTALMLAVSHGRIDMVKGLLACGADVNIQDDEGSTALMCASEHG
		į	HVEIVKLLLAQPGCNGHLEDNDGSTALSIALEAGHKDIAVLLYA
1		Į.	HVNFAKAQSPGTPRLGRKTSPGPTHRGSFD
5417	27	4074	KSOLECEWCG ZACDIL CODONEO ZONO ZENERO ZONO ZENERO
1	-	30/7	KSQLFCFWGGKAGDILSGDQDKEQKDPYFVETPYGYQLDLDFLK YVDDIQKGNTIKRLNIQKRRKPSVPCPEPRTTSGQQGIWTSTES
ł			LSSSNSDDNKQCPNFLIARSQVTSTPISKPPPPLETSLPFLTIP
ļ	J		ENRQLPPPSPQLPKHNLHVTKTLMETRRRLEQERATMQMTPGEF
			PROBLACECOMETTECL DODUCCONTROL WINE AND
1	<b>{</b>		RRPRLASFGGMGTTSSLPSFVGSGNHNPAKHQLQNGYQGNGDYG SYAPAAPTTSSMGSSIRHSPLSSGISTPVTNVSPMHLQHIREQM
1	]		AIALKRLKELEEQVRTIPVLQVKISVLQEEKRQLVSQLKNQRAA
1	ļ		SQINVCGVRKRSYSAGNASQLEQLSRARRSGGELYIDYEEEEME
1			TVEQSTQRIKEFRQL\TADMQALEQKIQDSSCEASSELRENGEC
	]		RSVAVGAEENMNDIVVYHRGSRSCKDAAVGTLVEMRNCGVSVTE
			AMLGVMTRADKEIELQQQTIESLKEKIYRLEVQLRETTHDREMT
1		i	KLKQELQAAGSRKKVDKATMAQPLVFSKVVEAVVQTRDQMVGSH
1			MDLVDTCVGTSVETNSVGISCQPECKNKVVGPELPMNWWIVKER
1	,		VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTEESVNDLTLLKT
1 .			NLNLKEVRSIGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAAV
1			MAVPRIADQDTSTDLEQVHQFINTETATLIESCINTCLSTLDKQ
1			TSTQTVETRTVAVGEGRVKDINSSTKTRSIGVGTLLSGHSGFDR
i i			PSAVKTKESGVGQININDNYLVGLKMRTIACGPPQI:TVGLTASR
)			RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQQ
			TLLAENYSELAEAFGEPHSQMGSLNSQLISTLSSINSVMKSAST
			EELRNPDFQKTSLGKITGSYLGYTCKCGGLQSGSPLSSQTSQPE
1 1			QBVGTSEGKPISSLDAFPTQEGTLSPVNLTDDQIAAGLYACTNN
			ESTLKSIMKKKDGNKDSNGAKKNLQFVGINGGYETTSSDDSSSD
1 1			ESSSESDDECDVIEYPLEEEEEEEDEDTRGMAEGHHAVNIEGL
1 1			KSARVEDEMQVQECEPEKVEIRERYELSEKMLSACNLLKNTIND
	•	•	PKALTSKDMRFCLNTLQHEWFRVSSQXSAIPAMVGDYIAAFEAI
1 1	1		SPDVLRYVINLADGNGNTALHYSVSHSNFEIVKLLLDADVCNVD
) ]	}	•	HONKAGYTPIMLAALAAVEAEKDMRIVEELFGCGDVNAKASQAG
1			QTALMLAVSHGRIDMVKGLLACGADVNIQDDEGSTALMCASEHG
1	1		HVBIVKLLLAQPGCNGHLEDNDGSTALSIALEAGHKDIAVLLYA
j			HVNFAXAQSPGTPRLGRKTSPGPTHRGSFD
5418	24	1133	SVPRAGGDMBTGAAELYDQALLGILQHVGNVQDFLRVLFGFLYR
1			
1 1	1		RIDFYRLLKHPSDRMGFPPGAAQALVLQVFKTFDHMARQDDEKR RQELEEKIRRKEEEEAKTVSAAAAEKEPVPVPVQEIEIDSTTEL
1		İ	DGHQEVEKVQPPGPVKEMAHGSQEAEAPGAVAGAAEVPR\EPPI
1 1	İ		LPRIQEOFQKNPDSYNGAVRENYTWSQDYTDLEVRVPVPKHVVK
}			GKQVSVALSSSSIRVAMLEENGERVLMEGKLTHKINTESSLWSL
			EPGKCVLVNLSKVGEYWWNAILEGEEPIDIDKINKERSMATVDE
, i		ľ	EEQAVLDRLTFDYHQKLQGKPQSHELKVHEMLKKGWDAEGSPFR
	1.		GQRFDPAMFNISPGAVQF
5419	1395	259	GTHPLDPDLVSRTSVQGPLMTMACPGMSDTEESPFLGPRAAEEG
] . [		433	SESEACEAFGRRKSEEEGRRSDTSGFGRSRKHKVNWKHPERADA
1 1	Į.		KDPASLPQC/LGP/DCVRPAQPSSKYCSDDCGMKLAANRIYEIL
} 1	1		PORTOOWOOSPICTARRUGERY TERTEREOGRAPHICS CONTROL OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERT
( )	ľ	,	PQRIQQWQQSPCIAEEHGKKLLERIRREQQSARTRLQEMERRFH
	}	j	ELEAILLRAKQQAVREDEESNEGDSDDTDLQIFCVSCGHFINPR
	1		VALRHMERCYAKYESQTSFGSMYPTRIEGATRLFCDVYNPQSKT
į į	ţ	ľ	YCKRLQVLCPEHSRDPKVPADEVCGCPLVRDVFELTGDFCRLPK
	}	]	RQCNRHYCWEKLRRAEVDLERVRVWYKLDELFEQERNVRTAMTN RAGLLALMLHQTIQHDPLTTDLRSSADR
5420	117	1733	NEAGGACPFKGGASGRLYLSPRLPRVSVAGCEERPLGWVWVLGG
		-123	MEAGGACPF RGGASGRLYLSPRLPRVSVAGCEERPLGWVWVLGG GGFLPARPPRAQRHLGFSHAEQSMEAPDYEVLSVREQLFHERIR
		i,	TO THE TANKET OF STATE OF STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE

SEO	Predicted	1 man 42 mb - 3	
ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location		Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	corresponding to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
1	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid	I.	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	sequence	Codon, /=possible nucleotide deletion,
<del></del>	sequence	<del> </del>	\=possible nucleotide insertion)
1	1		ECIISTLLFATLYILCHIFLTRFKKPAEFTT\GMMKMPPSTRL/
1	1	}	LLELCTFTLAIALGAVLLLPFSIISNZVLLSLPRNYYIQWLNGS
1			LIHGLWNLVFLFSNLSLIFLMPFAYFFTESEGFAGSRKGVLGRV
1	Ĭ	1	YETVVMLMLLTLLVLGMVWVASAIVDKNKANRESLYDFWEYYLP
1	<b>.</b>		YLYSCISFLGVLLLLVCTPLGLARMFSVTGKLLVKPRLLEDLEE
1			QLYCSAFEEAALTRRICNPTSCWLPLDMELLHRQVLALQTQRVL
			LEKRRKASAWQRNLGYPLAMLCLLVLTGLSVLIVAIHILELLID
1			EAAMPRGMQGTSLGQVSFSKLGSFGAVIQVVLIFYLMVSSVVGF
ì	1		YSSPLFRSLRPRWHDTAMTQIIGNCVCLLVLSSALPVFSRTLGL
			TRFDLLGDFGRFNWLGNFYIVFLYNAAFAGLTTLCLVKTFTAAV
5421	117	1733	RAELIRAFGERE
	/	1/33	NEAGGACPFKGGASGRLYLSPRLPRVSVAGCEERPLGWVWVLGG
1			GGFLPARPPRAQRHLGFSHAEQSMEAPDYEVLSVREQLFHERIR
1	1		ECIISTLLFATLYILCHIFLTRFKKPAEFTT\GMMKMPPSTRL/
1	]		LIELCTFTLAIALGAVLLLPFSIISNEVLLSLPRNYYIQWLNGS
1			LIHGLWNLVFLFSNLSLIFLMPFAYFFTESEGFAGSRKGVLGRV
	1		YETVVMLMLLTLLVLGMVWVASAIVDKNKANRESLYDFWEYYLP YLYSCISFLGVLLLLVCTPLGLARMFSVTGKLLVKPRLLEDLEE
1	l,		QLYCSAFEEAALTRICNPTSCWLPLDMELLHRQVLALQTQRVL
1			LEKRRKASAWQRNLGYPLAMLCLLVLTGLSVLIVAIHILELLID
1			BAAMPRGMOGTSLGOVSFSKLGSFGAVIOVVLIFYLMVSSVVGF
	1		YSSPLFRSLRPRWHDTAMTQIIGNCVCLLVLSSALPVFSRTLGL
	· .		TRFDLLGDFGRFNWLGNFYIVFLYNAAFAGLTTLCLVKTFTAAV
	]		RAELIRAFGERE
5422	3	1263	SCGESLPTWLAGASRPGIGRKGGAWGGRGGSSPAQVLLSPGPVF
	[		KAGCNWWHLSRDQAGVQRCDLGSSQPPPLGFKRFSCLSLPSSWD
1			YRSTVLCVSKMEADLSGFNIDAPRWDQRTFLGRVKHFLNITDPR
			TVFVSERELDWAKVMVEKSRMGVVPPGTQVEQLIJYAKKLYDSAF
		•	HPDTGEKMNVIGRMSFQLPGGMIITGFMLQFYRTMPAVIFWQWV
Į.			NOSFNALVNYTNRNAASPTSVRQMALSYFTATTTAVATAVGMNM
1	ĺ		LTKKAPPLVGRWVPFAAVAAANCVNIPMMRQQELIKGICVKDRN
1			ENEIGHSRRAAAIGITQVVISRITMSAPGMILLPVIMERLEKLH
j ,			FMQKVKVL/SAPLQVMLSGCFLIFMVPVACGLFPQKCELPVSYL
			EPKLQDTIKAKYGELEPYVYFNKGL
5423	3186	905	GVSMALGEEKAEAEASEDTKAQSYGRGSCRERELDIPGPMSGEQ
l	' ·		PPRLEAEGGLISPVWGAEGIPAPTCWIGTDPGGPSRAHOPOASD
			ANREPVAERSEPALSGLPPATMGSGDLLLSGESOVEKTKLSSSE
	× .	,	EFPQTLSLPRTTICSGHDADTEDDPSLADLPOALDLSOOPHSSG
			LSCLSQWKSVLSPGSAAQPSSCSISASSTGSSLQGHQERAEPRG
	· 1		GSLAKVSSSLEPVVPQEPSSVVGLGPRPQWSPQPVFSGGDASGL
1 . 1	· 1		GRRRLSFQAEYWACVLPDSLPPSPDRHSPLWNPNKEYEDLLDYT
			YPLRPGPQLPKHLDSRVPADPVLQDSGVDLDSFSVSPASTLKSP
	<b>_</b>		TNVSPNCPPAEATALPFSGPREPSLKQWPSRVPQKQGGMGLASW
	1	I	SQLASTPRAPGSRDARWERREPALRGAKDRLTIGKHLDMGSPQL
]	1		RTRDRGWPSPRPEREKRTSQSARRPTCTESRWKSEEEVESDDEY
1 1		ļ	LALPARLTQVSSLVSYLGSISTLVTLPTGDIKGQSPLEVSDSDG
]	, 1		PASFPSSSSQSQLPPGAALQGSGDPEGQNPCFLRSFVRAHDSAG
	·		EGSLGSSQALGVSSGLLKTRPSLPARLDRWPFSDPDVEGQLPRK
			GGEQGKESLVQC\VKTFC\CQLEELICWLYNV\ADVTDHGTPAR
	1		SNLTSLK\SSLQLYRQFKKDIDEHQSLTESVLQKGEILLQCLLE
	1	ļ	NTPVLEDVLGRIAKQSGELESHADRLYDSILASLDMLAGCTLIP
5424	3186	905	DKKPMAAMEHPCEGV
		303	GVSMALGEEKAEASEDTKAQSYGRGSCRERELDIPGPMSGEQ
1	1	ì	PPRLEAEGGLISPVWGAEGIPAPTCWIGTDPGGPSRAHQPQASD
	•		ANREPVAERSEPALSGLPPATMGSGDLLLSGESQVEKTKLSSSE
	į.	Į.	EFFOTLSLPRTTICSGHDADTEDDPSLADLPQALDLSQQPHSSG
:	{ _f	i	LSCLSQWKSVLSPGSAAQPSSCSISASSTGSSLQGHQERAEPRG
	1	ĺ	GSLAKVSSSLEPVVPQEPSSVVGLGPRPQWSPQPVFSGGDASGL
1		ł	GRRRLSFQAEYWACVLPDSLPPSPDRHSPLWNPNKEYEDLLDYT YPLRPGPQLPKHLDSRVPADPVLQDSGVDLDSFSVSPASTLKSP
		Í	THYSPHCPPAEATALPFSGPREPSLKQWPSRVPQKQGGMGLASW
		<del></del>	

SEQ	Predicted	Predicted end	12-1
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Cluteria Acid Rephanical acid Re
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	Interest M Mathierica N Park
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid		P=Proline, Q=Glutamine, R=Arginine,
i	residue of	residue of	S=Serine, T=Threonine, V=Valine,
ſ	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	1	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
ĺ	1		SQLASTPRAPGSRDARWERREPALRGAKDRLTIGKHLDMGSPQL
1	1	ļ	RTRDRGWPSPRPEREKRTSQSARRPTCTESRWKSEEEVESDDEY
J	i	j	LALPARLTQVSSLVSYLGSISTLVTLPTGDIKGQSPLEVSDSDG
			PASPPSSSSQSQLPPGAALQGSGDPEGQNPCFLRSPVRAHDSAG
İ		<u> </u>	EGSLGSSQALGVSSGLLKTRPSLPARLDRWPFSDPDVEGQLPRK
į.	į	Ì	GGEQGKESLVQC\VKTFC\CQLEELICWLYNV\ADVTDHGTPAR
ŀ		]	SNLTSLK\SSLQLYRQFKXDIDEHQSLTESVLQKGBILLQCLLB
1		ļ	MADAL EDAL COLLA ACCOLL BOLLA DA LA DATA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DE LA COLLA DEL COLLA DE LA COLLA DE LA COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COLLA DEL COL
1	j	]	NTPVLEDVLGRIAKQSGELESHADRLYDSILASLDMLAGCTLIP
5425	1086		DKKPMAAMEHPCEGV
3423	1088	115	GFCPSPSLGHQPPRVLHPTMSMAVETFGFFMATVGLLMLGVTLP
)	]		NSYWRVSTVHGNVITTNTIFENLWFSCATDSLGVYNCWEFPSML
			ALSGYIQACRALMITAILLGFLGLLLGIAGLRCTNIGGLELSRK
1		l	AKLAATAGAPH\ILPGICGMVAI\SWYAFNITR\DFSDPLYPGT
			KYELGPALYLGNSASLISILGGLCLCSACCCGSDEDPAASARRP
	1		YQAPVSVMPVATSDQEGDSSFGKYGRNALRVAALCRGPRCLPTA
1	1		PKKRGPGRGPFPYSNLRGRPRPVPVAPPRPRPRVLHSHGPSQAK
1	1		NCSWEVAYLPSEAGSLIF
5426	42	3435	ATSSQSLGRADPPRGGTMERSPGEGPSPSPMDQPSAPSDPTDQP
	f I		PAAHAKPDPGSGGQPAGPGAAGEALAVLTSFGRRLLVLIPVYLA
1		7	GAVGLSVGFVLFGLALYLGWRRVRDEKERSLRAARQLLDDEEQL
}			TAKTLYMSHRELPAWVSFPDVEKAEWLNKIVAQVWPFLGQYMEK
ı			LLAETVAPAVRGSNPHLQTFTFTRVELGEKPLRIIGVKVHPGQR
	}		PEOLI I DI MICHIGONO POMPRINA PROPERTI GVENTE CONTROLLO POR PROPERTI GVENTE CONTROLLO POR PROPERTI GVENTE CONTROLLO POR PROPERTI GVENTE CONTROLLO POR PROPERTI GVENTE CONTROLLO POR PROPERTI GVENTE CONTROLLO POR PROPERTI GVENTE CONTROLLO POR PROPERTI GVENTE CONTROLLO POR PROPERTI GVENTE CONTROLLO POR PROPERTI GVENTE CONTROLLO POR PROPERTI GVENTE CONTROLLO POR PROPERTI GVENTE CONTROLLO POR PROPERTI GVENTE CONTROLLO POR PROPERTI GVENTE CONTROLLO POR PROPERTI GVENTE CONTROLLO POR PROPERTI GVENTE CONTROLLO POR PROPERTI GVENTE CONTROLLO POR PROPERTI GVENTE CONTROLLO POR PROPERTI GVENTE CONTROLLO POR PROPERTI GVENTE CONTROLLO POR PROPERTI GVENTE CONTROLLO POR PROPERTI GVENTE CONTROLLO POR PROPERTI GVENTE CONTROLLO POR PROPERTI GVENTE CONTROLLO POR PROPERTI GVENTE CONTROLLO POR PROPERTI GVENTE CONTROLLO POR PROPERTI GVENTE CONTROLLO POR PROPERTI GVENTE CONTROLLO POR PROPERTI GVENTE CONTROLLO POR PROPERTI GVENTE CONTROLLO POR PROPERTI GVENTE CONTROLLO POR PROPERTI GVENTE CONTROLLO POR PROPERTI GVENTE CONTROLLO POR PROPERTI GVENTE CONTROLLO POR PROPERTI GVENTE CONTROLLO POR PROPERTI GVENTE CONTROLLO POR PROPERTI GVENTE CONTROLLO POR PROPERTI GVENTE CONTROLLO POR PROPERTI GVENTE CONTROLLO POR PROPERTI GVENTE CONTROLLO POR PROPERTI GVENTE CONTROLLO POR PROPERTI GVENTE CONTROLLO POR PROPERTI GVENTE CONTROLLO POR PROPERTI GVENTE CONTROLLO POR PROPERTI GVENTE CONTROLLO POR PROPERTI GVENTE CONTROLLO POR PROPERTI GVENTE CONTROLLO POR PROPERTI GVENTE CONTROLLO POR PROPERTI GVENTE CONTROLLO POR PROPERTI GVENTE CONTROLLO POR PROPERTI GVENTE CONTROLLO POR PROPERTI GVENTE CONTROLLO POR PROPERTI GVENTE CONTROLLO POR PROPERTI GVENTE CONTROLLO POR PROPERTI GVENTE CONTROLLO POR PROPERTI GVENTE CONTROLLO POR PROPERTI GVENTE CONTROLLO POR PROPERTI GVENTE CONTROLLO POR PROPERTI GVENTE CONTROLLO POR PROPERTI GVENTE CONTROLLO POR PROPERTI CONTROLLO POR PROPERTI CONTROLLO POR PROPERTI CONTROLLO POR PROPERTI CONTROLLO POR PROPERTI CONTROLLO POR PROPERTI CONTROLLO POR PROPERTI CONTROLLO POR PROPERTI CONTROLLO POR PROPERTI CONTROLLO POR PROPERTI
1			KEQILLDLNISYVGDVQIDVEVKKYFCKAGVKGMQLHGVLRVIL
1	·		BPLIGDLPFVGAVSMFFIRRPTLDINNTGMTNLLDIPGLSSLSD
1	l i		TMIMDSIAAPLVLPNRLLVPLVPDLQDVAQLRSPLPRGIIRIHL
1			LAARGLSSKDKYVKGLIEGKSDPYALVRLGTQTFCSRVIDEELN
!	İ		PQWGETYEVMVHEVPGQEIEVEVFDKDPDKDDFLGRMKLDVGKV
<b>i</b>	ĺ		LQASVLDDWFPLQGGQGQVHLRLEWIJSLLSDAEKLEQVLQWNWG
1.			VSSRPDPPSAAILVVYLDRAQDLPMVTSELYPPQLKKGNKEPNP
i i			MVQLSIQDVTQESKAVYSTNCPVWEEAFRFFLQDPQSQBLDVQV
1 1	,	•	KDDSRALTLGALTLPLARLLTAPELILDQWFQLSSSGPNSRLYM
1			KLVMRILYLDSSEICFPTVPGCPGAWDVDSENPQRGSSVDAPPR
i i			PCHTTPDSQFGTEHVLRIHVLEAQDLIAKDRFLGGLVKGKSDPY
			VKLKLAGRSFRSHVVREDLNPRWNEVFEVIVTSVPGQELEVEVF
1			DKDLDKDDFLGRCKVRLTTVLNSGFLDEWLTLEDVPSGRLHLRL
1 1	1		ERLTPRPTAABLEEVLQVNSLIQTQKSAELAAALLSIYMERAED
	]	i	LPLRKGTKHLSPYATLTVGDSSHKTKTISQTSAPVWDESASFLI
1 1	1	i	RKPHTESLELQVRGEGTGVLGSLSLPLSELLVADQLCLDRWFTL
ļ. J	<b> </b>		SSGQGQVLLRAQLGILVSQHSGVEAHSHSYSHSSSSLSEEPELS
			CODDUTTECADEU DODITHUDGO DA DA COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE
{	į		GGPPHITSSAPEV\RQRLTHVDSPLEAPAGPLGQVKLTLWYYSE
1	İ		ERKLVSIVHGCRSLRQNGRDPPDPYVSLLLLPDKNRGTKRRTSQ
{ ·	İ		KKRTLSPEFNERFEWELPLDEAQRRKLDVSVKSNSSFMSREREL
5427	42		LGKVQLDLAETDLSQGVARWYDLMDNKDKGSS
1 2201	7.4	3435	ATSSQSLGRADPPRGGTMERSPGEGPSPSPMDQPSAPSDPTDQP
]		į (	PAAHAKPDPGSGGQPAGPGAAGEALAVLTSFGRRLLVLIPVYLA
1		. [	GAVGLSVGFVLFGLALYLGWRRVRDEKERSLRAARQLLDDEEQL
1 1		i	TAKTLYMSHRELPAWVSFPDVEKAEWLNKIVAQVWPFLGQYMEK
, 1			LLAETVAPAVRGSNPHLQTFTFTRVELGEKPLRIIGVKVHPGOR
į l		1	KEQILLDLNISYVGDVQIDVEVKKYFCKAGVKGMQLHGVLRVIL
1 /	1		EPLIGDLPFVGAVSMFFIRRPTLDINWTGMTNLLDIPGLSSLSD
j 1			TMIMDSIAAFLVLPNRLLVPLVPDLQDVAQLRSPLPRGIIRIHL
ļ l	į		LAARGLSSKDKYVKGLIEGKSDPYALVRLGTQTFCSRVIDERLN
	l		PQWGETYEVMVHBVPGQEIEVEVFDKDPDKDDFLGRMKLDVGKV
]	j		
	į.	1	LQASVLDDWFPLQGGQGQVHLRLEWLSLLSDAEKLEQVLQWNWG
	1	1	VSSRPDPPSAAILVVYLDRAQDLPMVTSELYPPQLKKGNKEPNP
	į	1	MVQLSIQDVTQESKAVYSTNCPVWEEAFRFFLQDPQSQELDVQV
[ ]		1	KDDSRALTLGALTLPLARLLTAPELILDQWFQLSSSGPNSRLYM
		. }	KLVMRILYLDSSEICFPTVPGCPGAWDVDSENPQRGSSVDAPPR
! !		1	PCHTTPDSQFGTEHVLRIHVLEAQDLIAKDRFLGGLVKGKSDPY
	ŀ	ľ	VKLKLAGRSFRSHVVREDLNPRWNEVFEVIVTSVPGQELEVEVF
			DKDLDKDDFLGRCKVRLTTVLNSGFLDEWLTLEDVPSGRLHLRL
-			

SEO	Predicted	Day = 42 = 4 = -3	
ID	beginning	Predicted end	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	corresponding	to first	
ŀ	to first	amino acid	L=Leucine, M=Methicnine, N=Asparagine,
İ	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
- 1	residue of	amino acid	S-Serine, T=Threonine, V=Valine,
1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, +=Stop
ı	sequence	pedgewee	Codon, /=possible nucleotide deletion,
		<del> </del>	\=possible nucleotide insertion)
1 .			ERLTPRPTAAELEEVLQVNSLIQTQKSAELAAALLSIYMERAED
ì			LPLRKGTKHLSPYATLTVGDSSHKTKTISQTSAPVWDESASFLI
1	1	1	RKPHTESLELQVRGEGTGVLGSLSLPLSELLVADQLCLDRWFTL
-			SSGQGQVLLRAQLGILVSQHSGVEAHSHSYSHSSSLSEEPELS
		}	GGPPHITSSAPEV\RQRLTHVDSPLEAPAGPLGQVKLTLWYYSE
1			ERKLVSIVHGCRSLRQNGRDPPDPYVSLLLLPDKNRGTKRRTSQ
1	1	ŀ	KKRTLSPEFNERFEWELPLDEAQRRKLDVSVKSNSSFMSREREL
5428	3	1839	LGKVQLDLAETDLSQGVARWYDLMDNKDKGSS
		1039	SSRSERLSACATAPPWLVSSRPARPAQLQRPGKMVEDGAEELED
-			LVHFSVSELPSRGYGVMEEIRRQGKLCDVTLKIGDHKFSAHRIV
1	1		LAASIPYFHAMFTNDMMECKQDEIVMQGMDPSALEALINFAYNG
	1	ĺ	NLAIDQQNVQSLLMGASFLQLQSIKDACCTFLRERLHPKNCLGV
1	1	1	ROFAETMMCAVLYDAANSFIHQHFVEVSMSEEFLALPLEDVLEL
			VSRDELNVKSEEQVFEAALAWVRYDREQRGTFL\RNLQSNIRLL
1	]		FCRPQFLSDRVQQDDLVRCCHKCRDLVDEAKDYLLMPERRDHI.D
1	1	1	AFRTRPRCCTSIAGLIYAVGGLNSAGDSLNVVEVFDPIANCWER
1			CRPMTTARSRVGVAVVNGLLYAIGGYDGQLRLSTVQAYNTETDT
1		,	WTRVGSMNSKRSAMGTVVLDGQIYVCGGYDGNSSLSSVETYSPE
1	1 1		TDKWTVVTSMSSNRSAA\GVTVFEGRIYVSGGHDGLQIFSSVEH
1	]		YNHHTATWHPAAGMLNKRCRHGAASLGSKMFVCGGYDGSGFLSI
1	i l		AEMYSSV\ADQWCLIVPM\HTRR\SRVSLGGPAVGRLYAVWGVT
l			TGQSNL\SSVGDVLTPETDCWTFM\APMACHEGGVGVGCIPLLT
5429	828	202	r =
1		202	RREDALSSEGCLWPSESTVSGNGIPEPQVYAPPRPTDRLAVPPF
	, ,		AQRERFHRFQPTYPYLQHEIDLPPTISLSDGEEPPPYQGPCTLQ
1	1		LEDPEQQLELNRESVRAPPNRTIFDSDLMDSARLGGPCPPSSNS
1	j		GISATCYGSGGRMEGPPP\TYSEVIGHYPGSSFQHQQSSGPPSL
5430	441	1507	LEGTRLHHTHIAPLESAAIWSKEKDKQKGHPL
1	1		QKRRKRRKKIMKTIQPKMHNSISWAIFTGLAALCLFQGVPVRS
ļ	1		GDATFPKAMDNVTVRQGESATLRCTIDNRVTRVAWLNRSTILYA
1			GNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTDN
[	i i		HPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEP
. ·			TVTWRHISPKAVGFVSEDEYLEIQGITREQSGDYECSASNDV\A
1	ļ		APV\VRRVKVTVNYPPYISEAKGTGVPVGQKGTLQCEASAVPSA EFQWYKDDKRLI/EGKKGVKVENRPFLSKLIFFNVSEHDYGNYT
	[	•	CVASNKLGHTNASIMLFGPGAVSEVSNGTSRRAGCVWLLPLLVL
	1.		HLLLKF
5431	2	1312	AAAAPGSRRRRPLPDRPHMAHGYEAPPPPAPRSPAWRARSKPV\
			LPGITINP\TIAEGPSP\TSEGASEANLVDLQKKLEELELDEQQ
			KKRLEAFLTQKAKVGELKDDDFERISELGAGNGGVVTKVQHRPS
			GLIMARKLIHLEIKPAIRNQIIRELQVLHECNSPYIVGFYGAFY
			SDGEISICMEHMDGGSLDQVLKEAKRIPEEILGKVSIAVLRGLA
	ł		YLREKHQIMHRDVKPSNILVNSRGEIKLCDFGVSGQLIDSMANS
	ļ	,	FVGTRSYMAPERLQGTHYSVQSDIWSMGLSLVELAVGRYPIPPP
	· •		DAKELEAIFGRPVVDGEEGEPHSISPRPRPPGRPVSGHGMDSRP
1			AMAIFELLDYIVNEPPPKLPNGVFTPDFQEFVNKCLIKNPAERA
	·		DLKMLTNHTFIKRSEVEEVDFAGWLCKTLRLNQPGTPTRTAV
5432	2	1312	AAAAPGSRRRRPLPDRPHMAHGYEAPPPPAPRSPAWRARSKPV\
i			LPGITINP\TIAEGPSP\TSEGASEANLVDLQKKLEELELDEQQ
ł	j	•	KKRLEAFLTOKAKUGEI KDDDEBB TORT GO GOTTOKKURELEDDEQQ
			KKRLEAFLTQKAKVGELKDDDFERISELGAGNGGVVTKVQHRPS
			GLIMARKLIHLEIKPAIRNQIIRELQVLHECNSPYIVGFYGAFY
1	i i	j	SDGEISICMEHMDGGSLDQVLKEAKRIPEEILGKVSIAVLRGLA YLEEKHOIMHDDVKBSNILLNSDGSLKY GDBSLKVSIAVLRGLA
i	1		YLREKHQIMHRDVKPSNILVNSRGEIKLCDFGVSGQLIDSMANS
1	1.	1	FVGTRSYMAPERLQGTHYSVQSDIWSMGLSLVELAVGRYPIPPP
1	ł		DAKELEAI FGRPVVDGEEGEPHS I SPRPRPPGRPVSGHGMDSRP
			AMAIFELLDYIVNEPPPKLPNGVFTPDFQEFVNKCLIKNPAERA
5433	360	1885	DLKMLTNHTFIKRSEVEEVDFAGWLCKTLRLNQPGTPTRTAV
1			SVQEDKVGFEDPLHLCSWRARACPCTWPHC/CTGLLECLGFAGV
			LFGWPSLVFVFKNEDYFKDLCGPDAGPIGNATGQADCKAQDERF
		L	SLIFTLGSFMNNFMTFPTGYIFDRFKTTVARLIAIFFYTTATLI

۲	SEQ	Predicted	Predicted end	I Amino poid
	ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
- 1	NO:	nucleotide	location	Glutamic Acid, F-Phenylalanine, G-Glycine,
ı		location	corresponding	H-Histidine, I-Isoleucine, K-Lysine,
- [		corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
- 1		to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
- [		amino acid	residue of	S=Serine, T=Threonine, V=Valine,
- 1		residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
- 1		amino acid	sequence	Codon, /=possible nucleotide deletion.
L		sequence		\=possible nucleotide insertion)
				IAFTSAGSAVLLFLAMPMLTIGGILFLITNLQIGNLFGQHRSTI
- }				ITLYNGAFDSSSAVFLIIKLLYEKGISLR/VLLHLHLCLOYLAC
- [				STHFPPDAPGAHPIPTAPQLQLWPVPWEWHHKGREG/OOLSMKT
ł				GSYSQRSSFQRRKRPQGQGRSRNSAPSGATL/CSRRFAWHLVWL
				SVIQLWHYLFIGTLNSLLTNMAGGDMARVSTYTNAFAFTQFGVL
				CAPWNGLLMDRLKQKYQKEARKTGSSTLAVALCSTVPSLALTSL
				LCLGFALCASVPILPLQYLTFILQVISRSFLYGSNAAFLTLAFP
1				SEHFGKLFGLVMALSAVVSLLQFPIFTLIKGSLQNDPFYVNVMF
┢	5434	66	652	MLAILLTFFHPFLVYRECRTWKESPSAIA
	1	00	034	RYAALIISLIQHKLLWRNQHCSRCVIMSPAQSAGLNWLP/GSGK
1				HGPFLGCSQYPACDYVRPLKSSADGHIVKVLEGQVCPACGANLV
ĺ	- 1			LRQGRFGMFIGCINYPECEHTELIDKPDETAITCPQCRTGHLVQ
	1	į		RRSRYGKTPHSCDRYPECOFAINFKPIAGECPECHYPLLIEKKT AQGVKHFCASKQCGKPVSAE
	5435	4704	1597	PGDSSQRLAEMSNAKERKHAKKMRNQPINVTLSSGFVADRGVKH
				HSGGEKPFQAQKQEPHPGTSRQRQTRVNPHSLPDPEVNRQSSSK
l				GMFRKKGGWKAGPEGTSQEIPKYITASTFAQARAAEISAMLKAV
	1			TOKSSNSLVFQTLPRHMRRRAMSHNVKRLPRRLQEIAQKEAEKA
	Į.			VHQKKEHSKNKCHKARRCHMNRTLEFNRRQKKNIWLETHIWHAK
	- 1			RFHMVKKWGYCLGERPTVKSHRACYRAMTNRCLLQDLSYYCCLE
1	l l			LKGKEEEILKALSGMCNIDTGLTFAAVHCLSGKROGSLVLYRVN
1	1			KYPREMLGPVTFIWKSQRTPGDPSESROLWIWLHPTLKODILER
1	1	i		IKAACQCVEPIKSAVCIADPLPTPSQEKSOTELPDEKIGKKRKR
	1	1		KDDGENAKPIKKIIGDGTRDPCLPYSWISPTTGIIISDLTMFMN
				RFRLIGPLSHSILTEAIKAASVHTVGEDTEETPHRWWIETCKKD
	ĺ	1		DSVSLHCRQEAIFELLGGITSPABIPAGTILGLTVGDPRINLPQ
1				KKSKALPNPEKCODNEKVROLLLEGVPVECTHSFIWNODICKSV
1	- 1	1		TENKISDQDLNRMRSELLVPGSQLILGPHESKIPILLIQQPGKV
	- (	İ		TGEDRLGWGSGWDVLLPKGWGMAFWIPFIYRGVRYGGLKESAVH
	1			SQYKRSPNVPGDFPDCPAGMLFAEEQAKNLLEKYKRRPPAKRPN
	j	]		YVKLGTLAPFCCPWEQLTQDWESRVQAYEEPSVASSPNGKESDL RRSEVPCAPMPKKTHQPSDEVGTSIEHPREAEEVMDAGCQESAG
1.	- 1	f		PERITDQEASENHVAATGSHLCVLRSRKLLKQLSAWCGPSSEDS
1	1	Į.		RGGRRAPGRGQQGLTREACLSILGHFPRALVWVSLSLLSKGSPE
	ľ			PHTMICVPAKEDFLQLHEDWHYCGPQESKHSDPFRSKILKQKEK
		]		KKREKRQKP\GRASSDGPAGEEPVAGQEALTLGLWSGPLPRVTL
1	1		1	HCSRTLLGFVTQGDFSMAVGCGEALGFVSLTGLLDMLSSQPAAQ
┡				RGLVLLRPPASLQYRFARIAIEV
ĺ	5436	1781	635	ASDS I PWSEARTTRKLAORGCOWSLPERMPLVVFCGLPVSGKSP
	ĺ	· i	!	RABELRVALAAEGRAVYVVDDAAVLGAEDPAVYGDSAREKALRG
1		1	1	ALRASVERRLSRHDVVILDSLNYIKGFRYELY\CLARAARTPLC
1	1	İ		LVYCVRPGGPIAGPQVAGANENPGRNVSVSWRPRAEEDGRACA
ı	- 1		ŧ	GSSVLRELHTADSVVNGSAQADVPKELEREESGAAESPALVTPD
	. 1		ļ	SEKSAKHGSGAFYSPELLBALTLRFEAPDSRNRWDRPLFTLVGL
	i			EEPLPLAGIRSALFENRAPPPHQSTQSQPLASGSFLHQLDQVTS
ļ.				QVLAGLMEAQKSAVPGDLLTLPGTTEHLRFTRPLTMAELSRLRR
	437	739	1672	QFISYTKMHPNNENLPQLANMFLQYLSQSLH CQEAASEFGGPLHTPAMFLRRLGGWLPRPWGRRKPMRPDPPYPE
	}			PRRVDSSENSGSDWDSAPETMEDVGHPKTXDSGALRVSRAASE
l		1	1	PSKEEPQVEQLGSKRMDSLKWDQPISSTQESGRLEAGGASPKLR
!	1	ł	1	WDHVDSGGTRRPGVSPEGGL\GVPGPGAPLEKPGRREKLLGWLR
	}	J		GEPGAPSRYLGGPEECLQISTNLTLHLLELLASALLALCSRPLR
	1		1.	AALDTLGLRGPLGLWLHGLLSFLAALHGLHAVLSLLTAHPLHFA
	- (	Ì	1	CLFGLLQALVLAVSLREPNGDEAATDWBSEGLEREGEEQRGDPG
			J.	KGL
5	438	2443	1152	TKPRKRRHQPASQRQRPWSSDSTGDLLARGKGRKEENKGSDRVS
		1	1 :	LAPPSLRRPMMCQSEARQGPELRAAKWLHPPQLALRRRLGOLSC
	- 1		11	MSRPALKLRSWPLTVLYYLLPFGALRPLSRVGWRPVSRVALYKS
	1		] '	VPTRLLSRAWGRLNQVELPHWLRRPVYSLYIWTFGVNMKEAAVE
	1		[ ]	DLHHYRNLSEFFRRKLKPQARPVCGLHSVISPSDGRILNFGOVK
	<del></del>		1	NCEVEQVKGVTYSLESFLGPRMCTEDLPFPPAASCDSFKNQLVT

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ł	location	corresponding	H-Histidine, I=Isoleucine, K-Lysine.
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine.
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
l	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
[	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
		-	REGNELYHCVIYLAPGDYHCFHSPTDWTVSHRRHFPGSLMSVNP
1		ĺ	GMARWIKELFCHNERVVLTGDWKHGPFSLTAVGAT\NWGSIRIY
		ļ	FDRDLHTNSPRHSKGSYNDFSFVTHTNREGVPMALRGEHLG/QS
F420			FNLGSTIVLIFEAPKDFNFQLKTGQKIRFGEALGSL
5439	2443	1152	TKPRKRRHQPASQRQRPWSSDSTGDLLARGKGRKEENKGSDRVS
1			LAPPSLRRPMMCQSEARQGPELRAAKWLHFPQLALRRRLGQLSC
ĺ	1		MSRPALKLRSWPLTVLYYLLPFGALRPLSRVGWRPVSRVALYKS
1			VPTRLLSRAWGRLNQVELPHWLRRPVYSLYIWTFGVNMKEAAVE
1	}		DLHHYRNLSEFFRRKLKPQARPVCGLHSVISPSDGRILNFGQVK
ĺ			NCEVEQVKGVTYSLESFLGPRMCTEDLPFPPAASCDSFKNQLVT
1	İ		REGNELYHCVIYLAPGDYHCFHSPTDWTVSHRRHFPGSLMSVNP
1	}		GMARWIKELFCHNERVVLTGDWKHGFFSLTAVGAT\NWGSIRIY
			FDRDLHTNSPRHSKGSYNDFSFVTHTNREGVPMALRGEHLG/QS
5440	693	253	FNLGSTIVLIFEAPKDPNFQLKTGQKIRFGEALGSL EPIFVTPDHRLVTMTHIV\QTFSPVNS\GQPPNYEMLKEEQEVA
1	]		MLGAPHNPAPPMSTVIHIRSETSVPDHVVWSLFNTLFMNTCCLG
1	•		FIAFAYSVKSRDRKMVGDVTGAQAYASTAKCLNIWALILGIFMT
1			ILLIIIPVLVVQAQR
5441	2	2054	CRDGGKNGFMVSPMKPLEIKTQCSGPRMDPKICPADPAFFSFIN
			NSDLWVANIETGEERRLTFCHQGLSNVLDDPKSAGVATFVIQEE
			FDRFTGYWWCPTASWEGSEGLKTLRILYEEVDESBVEVIHVPSP
	]		ALEERKTDSYRYPRTGSKNPKIALKLAEFQTDSQGKIVSTQEKE
1			LVQPFSSLFPKVEYIARAGWTRDGKYAWAMFLDRPOOWLOLVLI,
1			PPALPIPSTENEEQ\RLASARAVPRNVQPYVVYEEVTNVWINVH
}			DIFYPFPQSEGEDELCFLRANECKTGFCHLYKVTAVLKSOGYDW
			SEPFSPGEGEQSLTNAIWVNEETKLVYFQGTKDTPLEHHLYVVS
Ì			YEAAGEIVRLTTPGFSHSCSMSQNFDMFVSHYSSVSTPPCVHVY
j,			KLSGPDDDPLHKQPRFWASMMEAAKIFHFHTRSDVRLYGMIYKP
			HALQPGKKHPTVLFVYGGPQVQLVNNSFKGIKYLRLNTLASLGY
1			AVVVIDGRGSCQRGLRFEGALKNQMGQVEIEDQVEGLQFVAEKY
1	]		GFIDLSRVAIHGWSYGGFLSLMGLIHKPQVFKVAIAGAPVTVWM
1	•		AYDTGYTERYMDVPENNQHGYEAGSVALHVEKLPNEPNRLLILH
1 .1	' I		GFLDENVHFFHTNFLVSQLIRAGKPYQLQVALPPVSPQIYPNER HSIRCPESGEHYEVTLLHFLQEYL
5442	1	3474	CGQRSRRSPDMPBAKPANKKAPKGKDAPKGAPKEAPPKEAPAE
	. ]		APKEAPPEDQSPTAEEPTGVFLKKPDSVSVETGKDAVVVAKVNG
			KELPDKPTIKWFKGKWLELGSKSGARFSFKESHNSASNVYTVEL
l i	ì	i	HIGKVVLGDRGYYRLEVKAKDTCDSCGFNIDVEAPRODASGQSL
]			ESFKRTSEKKSDTAGELDFSGLLKKREVVEEEKKKKKKDDDDLG
1			IPPEIWELLKGAKKSEYEKIAFQYGITDLRGMLKRLKKAKVEVK
1	İ	l	KSAAFIKKI, DPAYQVDRGNKIKLMVEISDPDLTLKWPKNGOEIK
	[		PSSKYVFENVGKKRILTINKCTLADDAAYEVAVKDEKCFTELFV
[			KEPPVLIVTPLEDQQVFVGDRVEMAVEVSEEGAQVMWMKDGVEL
1 1			TREDSFKARYRFKKDGKRHILIFSDVVQEDRGRYQVITNGGQCE
			AELIVEEKQLEVLQDIADLTVKASEQAVFKCEVSDEKVTGKWYK
1	1	•	NGVEVRPSKRITISHVGRFHKLVIDDVRPEDEGDYTFVPDGYAL
1			GSLSAKLNFLEIKVEYVPKQ\EPPKIPLGFASGGKTSENAD/IV
]	,		VVAGNKLRLDV\SITGEAPSPFAT\WLKG\DEVFTTTEGRTRIE
	[		KRVDCSSFVIESAQREDEGRYTIKVTNPIGEDVASIFLQVVDVP
	1	. 1	DPPEAVRITSVGEDWAILVWEPPMYDGGKPVTGYLVERKKKGSQ RWMKLNFEVFTETTYESTKMIEGILYEMRVFAVNAIGVSQPSMN
] 1		l	TKPFMPIAPTSEPLHLIVEDVTDTTTLKWRPPNRIGAGGIDGY
		- 1	LVEYCLEGSEEWVPANTEPVERCGFTVKNLPTGARILFRVVGVN
1	İ	ĺ	IAGRSEPATLAQPVTIREIAEPPKIRLPRHLRQTYIRKVGEQLN
	1	1	LVVPFQGKPRPQVVWTKGGAPLDTSRVHVRTSDFDTVFFVRQAA
1	{	1	RSDSGEYELSVQIENMKDTATIRIRVVEKAGPPINVMVKEVWGT
			NALVEWQAPKDDGNSEIMGYFVQKADKKTMEWFNVYERNRHTSC
	İ	]	TVSDLIVGNEYYFRVYTENICGLSDSPGVSKNTARILKTGITFK
	1	1	PPEYKEHDFRMAPKFLTPLIDRVVVAGYSAALNCAVRGHPKPKV
}	ŀ		VWMKNKMEIREDPKFLITNYQGVLTLNIRRPSPFDAGTYTCRAV
			NELGEALAECKLEVRVPQ
_			

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
j	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion.
ļ	sequence	· · · · · ·	\=possible nucleotide insertion)
5443	66	1003	SRGQLDAGQSSEQHGGNRQPEQSRSRSSSSSSSSPRRSRSAAEPA
]		1	MALSMPLNGLKEEDKEPLIELFVKAGSDGESIGNCPFSORLFMI
1			LWLKGVVFSVTTVDLKRKPADLONLAPGTHPPFITFNSEVKTDV
i	İ		NKIEEFLEEVLCPPKYLKLSPKHPESNTAGMDIFAKPSAYIKNS
1		ļ	RPEANEALERGLLKTLQKLDEYLNSPLPDEIDENSMEDIKFSTR
1			KFLDGNEMTLADCNLLPKLHIVKVVAKKYRNFDIPKEMTGIWRY
ł			LTNAYSRDEFTNTCPSDKEVEI\AYSDVAKRLHOVKSRLLKEVS
i	Į.		FMSSP
5444	2	344	SGPIGVTGAQMAKWLRDYLSFGGRRPPPQPPTPDYTESDILRAY
1	_	244	RAQKNLDFEDPY*DSESRLEPDPAGPGDSKNPGDAKYGSPKHRL
1			
}			IKVEAADMARAKALLGGPGEELBADTEYLDPFDAQPHPAPPDDG
ļ			YMEPYDAQWVMSELPGRGVQLYDTPYBEQDPETADGPPSGQKPR
			QSRMPQEDERPADEYDQPWEWKKDHISRAPAVQFDSPEWERTPG
			SAKELRRPPPRSPQPAERVDPALPLEKQPWFHGPLNRADAESLL
			SLCKEGSYLVRLSETNPQDCSLSLRSSQGFLHLKFARTRENQVV
			LGQHSGPFPSVPELVLHYSSRPLPVQGAEHLALLYPVVTQTP*Q
			*PDWGDRRPNGQVATGLPELWGAEAPSAAAHPGLHRERHPEGLP RAEKPGLRGPLLGLREPLGAGPRGPWGLQEPRRCQVWFSOAPAH
₹ .			QGGGCGYGQSQGPSGRPRGGAGSRH
5445	2364	486	
	2304	400	ILSRGFLGSVEICIQLPLPASEPVLLLTWARRRWRETRSRREPT
1			TLRAQSVCPWWI*ETRMNRSIPVEVDESEPYPSQLLKPIPEYSP
			EEESEPPAPNIRNMAPNSLSAPTMLHNSSGDFSQAHSTLKLANH
j			QRPVSRQVTCLRTQVLEDSEDSFCRRHPGLGKAFPSGCSAVSEP ASESVVGALPAEHQFSFMEKRNQWLVSQLSAASPDTGHDSDKSD
1			
1			QSLPNASADSLGGSQEMVQRPQPHRNRAGLDLPTIDTGYDSQPQ DVLGIRQLBRPLPLTSVCYPQDLPRPLRSREFPQFBPQRYPACA
1			QMLPPNLSPHAPWNYHYHCPGSPDHQVPYGHDYPRAAYQQVIQP
[			ALPGQPLFGASVRGLHPVQKVILNYPSPWDQEERPAQRDCSFPG LPRHQDQPHHQPPNRAGAPGESLECPAELRPQVPQPPSPAAVPR
1	· .		PPSNPPARGTLKTSNLPEELRKVFITYSMDTAMEVVKFVNFLLV
j			NGFQTAIDIFEDRIRGIDIIKWMERYLRDKTVMIIVAISPKYKO
1.	·		DVEGAESQLDEDEHGLHTKYIHRMMQIEFIKQGSMNFRFIPVLF
[ ]		•	PNAKKEHVPTWLQNTHVYSWPKNKKNILLRLLREEEYVAPPRGP
1 1			LPTLOVVPL
5446	972	161	SSWSWCTGRMRKTRLWGLLWMLFVSELRAATKLTEEKYELKEGO
		202	
			TLDVKCDYTLEKFASSQKAWQIIRDGEMPKTLACTERPSKNSHP VQVGRIILEDYHDHGLLRVRMVNLQVEDSGLYQCVIYQPPKEPH
1 1	}		MLFDRIRLVVTKGFSGTPGSNENSTQNVYKIPPTTTKALCPLYT
] ]	j		TPRTVTQAPPKSTADVSTPDSEINLTNVTDIIRVPVFNIVILLA
	j	j	GGFLSKSLVFSVLFAVTLRSFVP*AHEPTRMSSDFQPHPSGSCA
1 1	ľ		KGGGRR
5447	207	617	MTARTLSLMASLVAYDDSDSEAETEHAGSFNATGQQKDTSGVAR
] " ]		· · ·	DD005000000000000000000000000000000000
		ĺ	PPGQDFASGTLDVPKAGAQPTKHGSCEDPGGYRLPLAQLGRSDR GSCPSQRLQWPGKEPQVTFPIKEPSCSSLWTSHVPASHMPLAAA
	1		RFKQVKLSRNFPKSSFHAQSESETVGKNGSSFQKKKCEDCVVPY
}	1	ļ	TPRRLRQRQALSTETGKGKDVEPQGPPAGRAPAPLYVGPGVSEF
j	į	ļ	IQPYLNSHYKETTVPRKVLPHLRGHRGPVNTIQWCPVLSKSHML
	Í	ľ	LSTSMDKTFKVWNAVDSGHCLQTYSLHTEAVRAARWAPCGRRIL
	!		SGGFDFALHLTDLETGTQLFSGRSDFRITTLKFHPKDHNIFLCG
}			GFSSEMKAWDIRTGKVMRSYKATIQQTLDILFLREGSEFLSSTD
	1		ASTRDSADRTIIAWDFRTSAKISNQIFHERFTCPSLALHPREPV
	ļ		FILA OTNONVI. AT POTEND VENODE DE PROGRAMA PRESENTATION DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR DE LA CONTRACTOR D
			FLAQTNGNYLALFSTVWPYRMSRRRRYEGHKVEGYSVGCECSPG
	}		GDLLVTGSADGRVLMYSPRTASRACTLQGHTQACVGTTYHPVLP
		į	SVLATCSWGGDMKIWH+AFHWLSLGEAIGDLAPARGYSGPGRSL
5448	194	1833	KSPSPSKSLLVLLCGRAMFQPATCPWQLPALSK
		1033	MASKYTDAIVWYQKKIGAYDQQIWEKSVEQREIKGLRNKPKKTA
	j	ì	HVKPDLIDVDLVRGSAFAKAKPESPWTSLTTKGIVRVVFFPFFFF
	1	1	RWWLQVTSKVIFFWLLVLYLLQVAAIVLFCSTSSPHSIPLTEVI
		,	GPIWLMLLLGTVHCQIVSTRTPKPPLSTGGKRRRKLRKAAHLEV
}	ļ	J	HREGDGSSTTDNTQEGAVQNHGTSTSHSVGTVFRDLWHAAFFLS
			GSKKAKNSIDKSTETDNGYVSLDGKKTVKSGEDGIQNHEPQCET

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
İ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
!	amino acid	residue of	S-Serine, T-Threonine, V-Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
<b>\</b>	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	· -	\=possible nucleotide insertion)
			IRPEETAWNTGTLRNGPSKDTQRTITNVSDBVSSEEGPETGYSL
		ł	RRHVDRTSEGVLRNRKSHHYKKHYPNEJAPKSGTSCSSRCSSSR
į.		i	QDSESARPESETEDVLWEDLLHCAECHSSCTSETDVENHQINPC
1		{	VKKEYRDDPPHQSHLPWLHSSHPGLEKISAIVWEGNDCKKADMS
l		1	VLBISGMIMNRVNSHIPGIGYQIFGNAVSLILGLTPFVFRLSQA
			TDLEQLTAHSASELYVIAFGSNEDVIVLSMVIISFVVRVSLVWI
			FFFLLCVAERTYKQVGIM*TSEGVLRNRKSHHYKKHYPNEDAPK
			SGTSCSSRCSSSRQDSESARPESETEDVLWEDLLHCAECHSSCT
Į			SETDVENHQINPCVKKEYRDDPFHQSHLPWLHSSHPGLEKISAI
İ			VWEGNDCKKADMSVLEISGMIMNRVNSHIPGIGYQIFGNAVSLI
1			LGLTPFVFRLSQATDLEQLTAHSASELYVIAFGSNEDVIVLSMV
L			IISFVVRVSLVWIFFFLLCVAERTYKQVGIM
5449	194	1833	MASKVTDAIVWYQKKIGAYDQQIWEKSVEQREIKGLRNKPKKTA
			HVKPDLIDVDLVRGSAFAKAKPESPWTSLTTKGIVRVVFFPFFF
	1		RWWLQVTSKVIFFWLLVLYLLQVAAIVLFCSTSSPHSIPLTEVI
1			GPIWLMLLLGTVHCQIVSTRTPKPPLSTGGKRRRKLRKAAHLEV
1	1		HREGDGSSTTDNTQEGAVQNHGTSTSHSVGTVFRDLWHAAFFLS
1			GSKKAKNSIDKSTETDNGYVSLDGKKTVKSGEDGIQNHEPQCST
-	i .		IRPEETAWNTGTLRNGPSKDTQRTITNVSDEVSSEEGPETGYSL
1	1		RRHVDRTSEGVLRNRKSHHYKKHYPNEDAPKSGTSCSSRCSSSR
-	1		QDSESARPESETEDVLWEDLLHCAECHSSCTSETDVENHQINPC
	}		VKKEYRDDPFHQSHLPWLHSSHPGLEKISAIVWEGNDCKKADMS
1	1	ı	VLEISGMIMNRVNSHIPGIGYQIFGNAVSLILGLTPFVFRLSQA
1	}		TDLEQLTAHSASELYVIAFGSNEDVIVLSMVIISFVVRVSLVWI
1 .			FFFLLCVAERTYKQVGIM*TSEGVLRNRKSHHYKKHYPNEDA>K
1		•	SGTSCSSRCSSSRQDSESARPESETEDVLWEDLLHCAECHSSCT
1 .	i		SETDVENHQINPCVKKEYRDDPFHQSHLPWLHSSHPGLEKISAI
ì			VWEGNDCKKADMSVLEISGMIMNRVNSHIPGIGYQIFGNAVSLI   LGLTPFVFRLSQATDLEQLTAHSASELYVIAFGSNEDVIVLSMV
ŀ			IISFVVRVSLVWIFFFLLCVAERTYKQVGIM
5450	B136	1242	GQQFASFFG*NHPEVTVAMALTDIDLQLQFSMSQPEALLLLAAG
	1		PADHLLLQLYSGHLQVRLVLGQEELRLQTPAETLLSDSIPHTVV
			LTVVEGWATLSVDGFLNASSAVPGAPLEVPYGLFVGGTGTLGLP
1			YLRGTSRPLRGCLHAATLNGRSLLRPLTPDVHEGCAEEFSASDD
1			VALGFSGPHSLAAFPAWGTQDEGTLEFTLTTQSRQAPLAFQAGG
1 1	1	•	RRGDFIYVDIFEGHLRAVVEKGQGTVLLHNSVPVADGQPHEVSV
i i			HINAHRLEISVDQYPTHTSNRGVLSYLEPRGSLLLGGLDAEASR
1	ļ		HLQEHRLGLTPEATNASLLGCMEDLSVNGQRRGLREALLTRNMA
			AGCRLEEEEYEDDAYGHYEAFSTLAPRAWPAMELPEPCVPEPGL
1	1	•	PPVFANFTQLLTISPLVVAEGGTAWLEWRHVQPTLDLMEAELRK
1 1			SQVLPSVTRGAHYGELELDILGAQARKMFTLLDVVNRKARFIHD
			GSEDTSDQLVLEVSVTARVPMPSCLRRGQTYLLPIQVNPVNDPP
'	[		HIIFPHGSLMVILEHTQKPLGPEVFQAYDPDSACEGLTFQVLGT
( l	·		SSGLPVERRDQPGEPATEFSCRELEAGSLVYVHCGGPAQDLTFR
			VSDGLQASPPATLKVVAIRPAIQIHRSTGLRLAQGSAMPILPAN
<u> </u>	•		LSVETNAVGQDVSVLFRVTGALQFGELQKHSTGGVEGAEWWATQ
1			AFHORDVEQGRVRYLSTDPQHHAYDTVENLALEVQVGQEILSNL
1 1	1		SFPVTIQRATVWMLRLEPLHTQNTQQETLTTAHLEATLEEAGPS
! !		]	PPTFHYEVVQAPRKGNLQLQGTRLSDGQGFTQDDIQAGRVTYGA
, ,			TARASEAVEDTFRFRVTAPPYFSPLYTFPIHIGGDPDAPVLTNV
		1	LLVVPEGGEGVLSADHLFVKSLNSASYLYEVMERPRLGRLAWRG
1		ŀ	TODKTTMVTSFTNEDLLRGRLVYQHDDSETTEDDIPFVATRQGE
			SSGDMAWEEVRGVFRVAIQPVNDHAPVQTISRIFHVARGGRRLL
1. 1		į	TTDDVAFSDADSGFADAQLVLTRKDLLFGSIVAVDEPTRPIYRF
	1		TQEDLRKRRVLFVHSGADRGWIQLQVSDGQHQATALLEVQASEP
			YLRVANGSSLVVPQGGQGTIDTAVLHLDTNLDIRSGDEVHYHVT
}		J	AGPRWGQLVRAGQPATAFSQQDLLDGAVLYSHNGSLSPEDTMAF SVEAGPVHTDATLOVTIALEGRIADIKI VRUKKTYMEGGEARET
	1		SVEAGPVHTDATLQVTIALEGPLAPLKLVRHKKIYVFQGEAAEI RRDQLEAAQEAVPPADIVFSVKSPPSAGYLVMVSRGALADEPPS
			LDPVQSFSQEAVDTGRVLYLHSRPEAWSDAFSLDVASGLGAPLE
i			GVLVELEVLPAAIPLEAQNFSVPEGGSLTLAPPLLRVSGPYFPT
		—————J	

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Cocation   Corresponding to first amino acid residue of residue of anino acid residue of anino acid anino acid sequence   Security   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February				(A=A)anine C-Custoine D-Account and D
Cocresponding   Cofired   Cocresponding   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Cofired   Co	NO:	nucleotide		Glutamic Acid R-Phonulalanian C Cluster
Lequeine, Medethionine, Medegragine, perioduc of first amino acid residue of amino acid residue of amino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence s	ļ			W-Wightidine T-Toolouging W-Living
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residue of amino acid sequence with the provide and the sequence code, /-possible nucleotide deletion, /-possible nucleotide deletion, /-possible nucleotide deletion, /-possible nucleotide deletion, /-possible nucleotide deletion, /-possible nucleotide insertion				Parroline, Qadiutamine, Raarginine,
amino acid sequence    Codon, /=possible nucleotide deletion,    -possible nucleotide sinettion			i	S=Serine, T=Threonine, V=Valine,
Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence				W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
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RAPRINGFLSLVGGGLGPVTRTOADVDSGRLAFVANGSVAGTY  QLSMSGGASPPLPMSLANDLIPSAIRVQLARPLEVPOALGRSS. SQQUAVVSDREEPERAVRLIQGPGYGHLLVGGRPTSAFSOPGY DOGGEVFAFTHYSSSIBHERVALLAGGPGVAVNOTVRALINI WAGGPWPQGATLRLDFTVLDAGELANRTGSVPRFRLLEGPHER WVRVPRARTEPGGSQLVEQPTQGDLEDGRCGLEVEVREPGRAPPG AGDSLTILEHMAQGVPPAVASLDFATEYNAARYSVALLSVPEA ARTEAGKEESSTFTGEGPGWASSPERAVAKGGLSFLEAMMFSV IIMMCLVLLLALIBLELLFYLFURRKRYCKEHVOVUTTAKPRINGLA GUTETFRKUEGGAJPLTAVEGGPPPGGGPDEELLGVCRTPNP ALKNOGYWN  1 PALANGGYWN  TO SESGGRTGDTLGRESACMDALKPPCLWRNHERGKREDGGR GUTETFRKUEGGAJPLTAVEGGPPPGGGPDEELLGVCRTPNP ALKNOGYWN  SMSPAGSPHSLEALIRDAPGGLDVLLHKMPIKSGREDGGR GVSQNNNDLTSCCFSDAKTMYEVFQRGLAVSDNGFCLTYRKFNG PYRHLSYKOVSDRAFYLGSCLLHKGYKSSPDGVVGIFRGNRES GVSQNNDLTSCCFSDAKTMYEVFQRGLAVSDNGFCLTYRKFNG PYRHLSYKOVSDRAFYLGSCLLHKGYKSSPDGVVGIFRGNRESM IISELACYTISMVAVPLVDTLGFBAIVHIVNKADLAWICDTPQ KALVLIGUKKGFTSELKVI ILMDEPDDLAVGRGEKSGIELISL YDABALGKEHFRKPVPSSPEDLSVLCFTSGTTGDVKGMTHON IVSNAAPLKCVBAYPETFDDVAISTLYDLAMPERIVQAVVYS CGARVGFPGGDIRLLADDMKTLKPTLFPAVFRLINRIYDKYOME AKTPLKKELLKLAVSSKFRELQKGII IRHDEFNULGREKGATHEND GGRVRVIVTGAAPMSTSWTFFRAAMGCOVYEAYGGTTCTGGCT FILEGMTSGHGVVBLACHTVKLEDVABMPKLIFAKIQDSL GGRVRVIVTGAAPMSTSWTFFFRAAMGCOVYEAYGGTTCTGGCT FILEGMTSGHGVVBLACHTVKLEDVABMPKLIFAKIQDSL GGRVRVIVTGAAPMSTSWTFFFRAAMGCOVYEAYGGTTCTGGCT FILEGMTSGHGVVBLACHTVKLEDVABMPKLIFAKIQDSL GGRVRVIVTGAAPMSTSWTFFFRAAMGCOVYEAYGGTTCTGGCT FILEGMTSGHGVVBLACHTVKLEDVABMPKLIFAKIQDSL WVPDTDVLBSFAAKLGVUGSFEELCQMCVVPCRAILEDLGKIGKE SGLXFFEQVKATFLIHEEPSIENGLITTTLKKKRGELSKYFRTO VVPDTDVLBSFAAKLGVUGSFEELCQMCVVPCRAILEDLGKIGKE SGLXFFEQVKATFLIHEEPSIENGLITTTLKKKRGELSKYFRTO DDDIGDHQPFBAAHDVLARSRSRANVLNKVEYAQQRMKLQVQEQ RKSYDERHVLS  1333  1138  SRYFSLCLSLSSLSLSFSREPVAGAPGCGTAGPPAMATLMGGLLR CSLSLSSLSLLASVLLLAGGLSDAAMFEDOKKCICPPYKERSG VTIKYTII ILYSLILLLLIVATLUTULEP LIQGLFFCHADLIGS DDDIGDHQPFBAAHDVLARSRSRANVLNKVEYAQQRMKLQVBQ PGERSQQQDDIELETKANGWNSNGGFIKFRYFIENGRUKICL RSWCDRITTSTSKRKDRVSCDSSLEEPPPARSGGGGSAKE PGERSQQODDIELETKANGWNSNGGFIKFRYFIENGEWLIG LEMATLKRSPYSISCHLANGLIFTSTDLERKYPENVELAGEDDGKITA KUMIETEDTIKKLKKKYYBLKKRNSNDGFIKFRYFIENG	ł	İ		TARGGGGTQQDGFHFRAHLQGPAGASVAGPQTSEAFAITVRDVN
QLSMSGASPPLPMSLAVDILIPSAIEVQLRAPLEVPOALGRSSL SQQLAWVSPEEPRAAVPLOQPOYGLHADGYSAFSOPQI DQGEVVFAFTHFSSSIDHFRULALAGUNASAVVNUTVALLIN WAGGNPGGAPLALDTVLDAGSLANTGSVPRAFILLEGPHGR VWRVPRARTEPGGSQLVSQPTQQDLEDGRIGLEVGRPEGRAPOP AGDSLTLELMAQGVPPAVASSLDFATFPYNAARFYSVALLSVPEA ARTEAGKESSTFTGEGPGWASSFERAVAKGGLSFLEAMMFSV IINCLVLLLLALIDELLFYLRRRNTCKHDVQVLTAXPRIGLA GDTETFRKVSEGQAIPLTAVGGQPPPGGGPDELLQFCRTPNP ALKNGYWW  SESSEGSTGDTLGRESACMDALKPPCLMKNEERGKKDDSCGR WISSPOSPHSLEALRDAAPSQGLNPLLLPTKMLFIFNFLFSPLP TPALICILLTFGAAIFLMLTTROPVUPLLDLINNGSVGLGGGAAK GVSQRNNDLTSCCFSDAKTIVSVFGGGAPPGGLCTYRKFNQ PYRMLSYKQVSDRASYLGSCLLHKGYKSSPDOFVGIFGANKPSW IISBLACKTYSMVAPLLDTGGBAINVILVRKADLAMVICOTPQ KADVLIGNVEKGFTPSLKVIILMDPDDDLKQGGKSKSGIEILLL YDARNIGKEHRFKPVPSPSPEDLSVICTFSTDDYGAMTTHON IVSNAAAPLKCVEHAYEFTPDDVAISTLPLANMFREIVQAVVYS CGARVGFFGGIEILLADMARTKLPVLFSPAUTDYGAMTTHON IVSNAAAPLKCVEHAYEFTPDDVAISTLPLANMFREIVQAVVYS CGARVGFFGGIEILLADMARTKLPVLFSPAUTHRIYDYKOME AKTPLKKFLLKLAVSSKFKELQKGIIRHDSFNBULKIIRTYDKVQNE AKTPLKKFLLKLAVSSKFKELQKGIIRHDSFNBULKIIRTYDKVQNE AKTPLKKFLLKLAVSSKFKELQKGIIRHDSFNBULKIIRTYDKVQNE AKTPLKKFLLKLAVSSKFKELQKGIIRHDSFNBULKIIRTYDKVQNE AKTPLKKFLLKLAVSSKFKELQKGIIRHDSFNBULKIIRTYDKVQNE KNIFFLAQGESYLAPKKENTYNKEDFULGTGGGTCGGGT FTLEGDMTSGHVSVLLACHVYKLEVALDMYTTVUNREGEUCIKG WVPDTDULPSFAAKLGVKGSFEELCONGVVRRALLEDLQKIGKE SGLKYFSGVKATFLKVBEPFSIENGLLTTTLKKERGPGLFKGGGGAKE SGLKYFSGVKATFLUNSCPFULGTHGSELRSLVOV VVPDTDULPSFAAKLGVKGSFEELCONGVVRRALLEDLQKIGKE SGLKYFSGVKATFLUNSCPFULGTHGSELRSLVOV VVPDTDULPSFAAKLGVKGSFEELCONGVVRRALLEDLQKIGKE SGLKYFSGVKATFLUNSCPFULGTHGSLRSLVOV VVPDTDULPSFAAKLGVKGSFEELCONGVVRRALLEDLQKIGKE SGLKYFSGVKATFLUNVLETVLEDTLUNGTHUCFTGSGFKKYY VKINTIILTSLIGLLLLAWVYLILVEDTLURRLFGHAALLGS LISSLSLSLALGVULLAGLSDAARNFEDVRCKCICCPPYKERSG VTIKTTIILTSLIGLLLAWVYLILVEDTLURRLFGHAALLGS VTIKTTIILTSLIGLLAWVYLILVEDTLURRLFGHAALLGS DDDIGGDGPFANAHDVLARSRSRANVLNKVEYAQQRNKLQVOQD RASSTVPBSTVLS  S453  111  1520  PSIFAAVGGSAPPERPBEFTVTATATSQVAQQPAAAFGGQAY KGLDTETTVEVANGELQDRKTIKRSRGRPKFEREMLKGLQHNII VKYNDSWESTVSKSTILDHARFPQBETOVRULABEDDGKKIAI KLMLEDIKKLKGKYKONBAIFRIKHKFVVKI	[	{		ERPPOPOASVPLRLTRGSRAPISRAQLSVVDPDSAPGEIEYEVQ
SOQQLEVUSDREBERATURLOGOGILLUGGRPTASPASSORIUS DOGGEVUFAFTHYSSSIBHERFULLARGUNASAVANDTURALLIN WAGGPWPQGATLELIDTYLDAGELANRTCSYPERFILLEGPRIGR VVRYPRARTEPGGSQLVEQPTQQDLEDGRIGLEVERFBGRAPGP AGDSLTILEUNAGVPPAVASLDFATEYNARRYFSVALLSYPEA ARTEAGKEESSTFTGEPGPWASSPERAVAKGGLISFLEAMMFSV IIMNCLVILLALIDELLIFYLRKRINTCKHENVOVLTAKPRIGLA GUTETTRKVERGQAIPLTAVFQGQPPPGGQPDPELLQFCRTPNP ALNINGYWV  5451  1 2274  RDSSEGGRTGDTLGRESACMDALKPPCLWRNHERGKKDRDSCGR KNISPGSPHSLEALRDAPSQGINPILLIPTYMRHIFTEKEPSLE TPALICILTERAAIFLWILTRPQPVLPLIANGSVGEGGARK GVSQKNNDLTSCCFSDAKTHYEVFGRGLAVSDNGPCLGYRKPNO PYRMLSYKOVSDRASYLGSCLLIKKGYKSSPOVGIFFANNESW GVSQKNNDLTSCCFSDAKTHYEVFGRGLAVSDNGPCLGYRKPNO PYRMLSYKOVSDRASYLGSCLLIKKGYKSSPOVGIFFANNESW IISBLACYTYSMVAVPLVDTLGPBGALVSINNGVGLEGGARK GVSQKNNDLTSCCFSDAKTHYEVFGRGLAVSDNGPCLGYRKPNO PYRMLSYKOVSDRASYLGSCLLIKKGYKSSPOVGIFFANNESW IISBLACYTSMVAVPLVDTLGPBGALVSINNGVGLEGARK GVSQKNNDLTSCCFSDAKTHYEVFGRGLAVSDNGPCLGYRKPNO PYRMLSYKOVSDRASYLGSCLLIKKGYKSSPOVGIFFANNESW IISBLACYTSMVAVPLVDTLGPBGALVSINNESWERSHILL YDARNLGKEHFRKPVDPSPDLGVICFTSGTTGDPKGAMITHON IVSNAAAPLKCVEHAYPDTPDDVAISTLDRKGMKSGKSGSGILLL YDARNLGKEHFRKPVDPSPDDVAISTLDRKGMKSGKSGSGILLL YDARNLGKEHFRKPVDPSPDVAISTLDRHFERRICQAVYYS CGRAVGFFCGDIRLADDMKTLKFPLFFANGGOVAGYAGYTGGTCT FILFGDMTSGHVSVVFLACHYVKLEDVADMYFTVNNEGEVCIKG GGVSVIVTOGAAPMSTSWNTFFRAMGCOVARGGTEGCVTKRTGGCT FILFGDMTSGHVSVVFLACHYVKLEDVADMYFTVNNEGEVCIKG KNIFKLAGGSVIAPKEENTYVKLEDVADMYFTVNNEGEVCIKG KNIFKLAGGSVIAPKEENTYVKLEDVADMYFTVNNEGEVCIKG SGLKFFSQVSATPLHPEFFSIENGLIPTTLKARGELSKYPRTQ TOSILEHIQD SLKFFSQVSATPLHPEFFSIENGLIPTLKARGELSKYPRTQ TOSILEHIQD SLKFFSQVSATPLHPEFFSIENGLIPTLKARGCLSKYERSS VTIKVTIIIYLSILGLLLYMVYLTLVEPILGRCHSCKYERSS VTIKVTIIIYLSILGLLLYMVYLTLVEPILGRCHSCKYERSS VTIKVTIIIYLSILGLLLYMVYLTLVEPILGRCHCKYERSS VTIKVTIIIYLSILGLLLYMVYLTLVEPILGRCHCKYERSS VTIKVTIIIYLSILGLLKGKCTULVTELHTSGUTKATLKRFKVKKIKVL RSWCPRHVVLS  111 1520 PSIFAAVPGSAPPEHRETVYTATATSQVAQQPPAAAPGGOAV KGAPSSTVYDSTSIKDRPVSGPSLVSKERSPRINGLQHNI VRYDSWESTVKGKKCIVLVTELHTSFOLLKKONIFTTGPTGSVKIGD LEMATEKSPYSSCONAAQIYRRVTSGWAPASDRKAUPSGKKIQH VCCGDHKTMAKAIKKDRALIKRPOLERG	1	l .		RAPHNGFLSLVGGGLGPVTRFTQADVDSGRLAFVANGSSVAGIF
DQGGVVFAFTHFSSSIDHFRVLALARGVAPANACVMYVRALLHY WARGDWPQCATALRIDPTULDAGELARRTCSPEFRLEGPHER WARVPRAFTEGGGQUVEQFTQQDLEDGRLGLEVGPEFRAPEG AGGDHTLELKMAQGVPPAVASDDFATEPYNAARPYSVALLSVPEA ARTEAGKPESSTPTGEPGPWASSFERAVAKGGLISFLEAMMFSV IIMCLVLLLLALILIPLLFYLRRRNTCKHDVQUVTARFRNGLA GUTETFRKVEDGQATPLTAVPGGQPPEGQDPELLQFCETPTAP ALKNGQYW ALKNGQYW ALKNGQYW ALKNGQYW ALKNGQYW ALKNGQYW ALKNGQYW ALKNGQYW ALKNGQYW ALKNGQYW ALKNGQYW ALKNGQYW ISBERGGRTGDTLGREFSACMDALKPPCLWRNHERGKKDRDSCGR KNSBPGSFHSLEALARDAAPSQGLNFLLLPTKMLFTFNFLSPLD FYALLGILTFAAATFLALITAPQPVLPLLDLINNQSVGIEGGARK GVSQNNNDLTSCCFSDAKTMYEVFQRGLAVSNNGCCLGYRKFNQ PYRKLSYKQVSDAFFLCSCLLHKGYKSSPODFVGIFAQNEPS IISBLACTYTSMVAPLLDTLGFBATHVLNKADLAMVICDTPQ KALVLIGNVEKGFTDSLEVICTGGBATHVINKADLAMVICDTPQ KALVLIGNVEKGFTDSLEVICTGGBATHVINKADLAMVICDTPQ KALVLIGNVEKGFTDSLEVICTGGBATHVINKADLAMVICDTPQ KALVLIGNVEKGFTDSLEVICTGGBATHORNEPS IISBLACTYTSMVAPLDTLGGBATHVINKADLAMVICDTPQ KALVLIGNVEKGFTDSLEVICTGGTDSLAGAMTHON IVSNAAAFLKCVENAYEFTDDDVASTLIPLAHMFERLVQAVYS CGARVGFFOGDISLLADMTLKLPFLIP PALLRRITDKYGME AXTPLKKFLLKLAVSSKFKELQKGI IRRDSFNDKLIFAKIQDSL GGRVEVIVTGAAPMTSVMTPFRAAMGCQVYPARGETCRGGT FTLFGDMTSGHVGVPLACATVKLEDVADMNYFTVNNEGBEVCIKG INVFKGYLKDPEKTQBALDSDGWLHTGDIGRHLPRGTIKKIDRK KNIFKLAGGSYLAPEKIENTYNRSGPVLIFNGSLRAGLKYGV VUPDTDULPSFAAKLGVKGSFEELCONGVVREALILEDLGKIGKE SGLKYFEGVARTIFLHEPEFSIENGLITTPTLKKRGELSKYFRTO IOSLVEHIQD SRYPSLCISLSJSJSFSREPVAGAPGCGTAGPPAMATLWGGLLR LGSLLSLSCLALSVLLLAGLSDAKNIFGDIGRAFLFGHAGLIGS FTLYNTIIILSIGLLLAWWYLTLUEPTLIKRRITGHAGLIGS FTLYNTIIILSIGLLLAWWYLTLUEPTLIKRRITGHAGLIGS FTLYNTIILSIGLLLAWWYLTLUEPTLIKRRITGHAGLIGS FTLYNTIILSIGLLAWWYLTLUEPTLIKRRITGHAGLIGS FTLYNTIILSIGLLAWWYLTLUEPTLIKRRITGHAGLIG DDDIGDRGPFANAHDVLARSRSRANVLNKVEYAQQRWKLQVQQD AAPAPSTVYPSTSTKDRPVSQPSLVGSKEPPPARSGSGGSAKE PQEERSQQQDDIELETKAVGNSINGRFIKRFFUKKIVL RGWCRGLLKGLGFHATTAPTIILBILGKLGNTFITTGPTGWKIGD LGLATLKRASPYSTGKORTVYLTLATTSGTVAGQPBAAAPGGQAV AGPAPSTVPSTSTSLORPYSIJCHARSPGBAGGGGGASKE PQEERSQQQDDIELETKARRPGPEGTOWYAGGMAGH LDMTSSTYPSGTSISLDRAFTSPGTLERNVFDUAGEMOWSG FLECTRONKDBRYSIJCHARPPGGTOWAGPMAAAFGGQAV AGPAPSTVPSTSTSLORPY				QLSMSDGASPPLPMSLAVDILPSAIEVQLRAPLEVPQALGRSSL
DQGGVVFAFTHFSSSIDHFRVLALARGVAPANACVMYVRALLHY WARGDWPQCATALRIDPTULDAGELARRTCSPEFRLEGPHER WARVPRAFTEGGGQUVEQFTQQDLEDGRLGLEVGPEFRAPEG AGGDHTLELKMAQGVPPAVASDDFATEPYNAARPYSVALLSVPEA ARTEAGKPESSTPTGEPGPWASSFERAVAKGGLISFLEAMMFSV IIMCLVLLLLALILIPLLFYLRRRNTCKHDVQUVTARFRNGLA GUTETFRKVEDGQATPLTAVPGGQPPEGQDPELLQFCETPTAP ALKNGQYW ALKNGQYW ALKNGQYW ALKNGQYW ALKNGQYW ALKNGQYW ALKNGQYW ALKNGQYW ALKNGQYW ALKNGQYW ALKNGQYW ALKNGQYW ISBERGGRTGDTLGREFSACMDALKPPCLWRNHERGKKDRDSCGR KNSBPGSFHSLEALARDAAPSQGLNFLLLPTKMLFTFNFLSPLD FYALLGILTFAAATFLALITAPQPVLPLLDLINNQSVGIEGGARK GVSQNNNDLTSCCFSDAKTMYEVFQRGLAVSNNGCCLGYRKFNQ PYRKLSYKQVSDAFFLCSCLLHKGYKSSPODFVGIFAQNEPS IISBLACTYTSMVAPLLDTLGFBATHVLNKADLAMVICDTPQ KALVLIGNVEKGFTDSLEVICTGGBATHVINKADLAMVICDTPQ KALVLIGNVEKGFTDSLEVICTGGBATHVINKADLAMVICDTPQ KALVLIGNVEKGFTDSLEVICTGGBATHVINKADLAMVICDTPQ KALVLIGNVEKGFTDSLEVICTGGBATHORNEPS IISBLACTYTSMVAPLDTLGGBATHVINKADLAMVICDTPQ KALVLIGNVEKGFTDSLEVICTGGTDSLAGAMTHON IVSNAAAFLKCVENAYEFTDDDVASTLIPLAHMFERLVQAVYS CGARVGFFOGDISLLADMTLKLPFLIP PALLRRITDKYGME AXTPLKKFLLKLAVSSKFKELQKGI IRRDSFNDKLIFAKIQDSL GGRVEVIVTGAAPMTSVMTPFRAAMGCQVYPARGETCRGGT FTLFGDMTSGHVGVPLACATVKLEDVADMNYFTVNNEGBEVCIKG INVFKGYLKDPEKTQBALDSDGWLHTGDIGRHLPRGTIKKIDRK KNIFKLAGGSYLAPEKIENTYNRSGPVLIFNGSLRAGLKYGV VUPDTDULPSFAAKLGVKGSFEELCONGVVREALILEDLGKIGKE SGLKYFEGVARTIFLHEPEFSIENGLITTPTLKKRGELSKYFRTO IOSLVEHIQD SRYPSLCISLSJSJSFSREPVAGAPGCGTAGPPAMATLWGGLLR LGSLLSLSCLALSVLLLAGLSDAKNIFGDIGRAFLFGHAGLIGS FTLYNTIIILSIGLLLAWWYLTLUEPTLIKRRITGHAGLIGS FTLYNTIIILSIGLLLAWWYLTLUEPTLIKRRITGHAGLIGS FTLYNTIILSIGLLLAWWYLTLUEPTLIKRRITGHAGLIGS FTLYNTIILSIGLLAWWYLTLUEPTLIKRRITGHAGLIGS FTLYNTIILSIGLLAWWYLTLUEPTLIKRRITGHAGLIG DDDIGDRGPFANAHDVLARSRSRANVLNKVEYAQQRWKLQVQQD AAPAPSTVYPSTSTKDRPVSQPSLVGSKEPPPARSGSGGSAKE PQEERSQQQDDIELETKAVGNSINGRFIKRFFUKKIVL RGWCRGLLKGLGFHATTAPTIILBILGKLGNTFITTGPTGWKIGD LGLATLKRASPYSTGKORTVYLTLATTSGTVAGQPBAAAPGGQAV AGPAPSTVPSTSTSLORPYSIJCHARSPGBAGGGGGASKE PQEERSQQQDDIELETKARRPGPEGTOWYAGGMAGH LDMTSSTYPSGTSISLDRAFTSPGTLERNVFDUAGEMOWSG FLECTRONKDBRYSIJCHARPPGGTOWAGPMAAAFGGQAV AGPAPSTVPSTSTSLORPY				SQQQLRVVSDREEPEAAYRLIQGPQYGHLLVGGRPTSAFSOFOI
WAGGPMPGGATHRIDPTVLDAGELANTGSVERFLLEGPRHGR VVRWPRARPEPGGGGLVEQPTQODLEDGRIGGEVGRPEGRAPG AGDSLTLELWAGGVPRAVASLDFATEPYNAARPYSVALLSVPEA ARTEAGKPESSTPTGEPGPMASSPERAVAKGGFLSFLEAMMFSV IIMCLVLLLLALI LELLFYLDKRNIKATGKHDVQVLTAKPRIGLA GUTETPRKVEDGGAIPLTAVFGGGPPFGGGPDFELLGFCRTPMP ALNINGGYW  5451  1 2274 RDSSEGGRTGDTLGRPSACMDALKPPCLWRNHERGKKDNDSCGR KNSEPGSPHSLEALINDARPSQLWPLLLPKWLPTFNFLFSPLP TPALICILTGAATFLWLITRPQPVLPLLDINNGSVCIEGGARK GVSQKNNILITSCCFSDARTMYEVPQRGLAVSUNGFGLGYRKNOQ PYRMISYKQVSDRAEVLGSCLHHGYKSSPDOFVGIFAGNREBW IISBLACYTYSMVAVPLYDTLGPBAIVHIVNRADIAWICDTPQ KAUVLIGANVERGFTPSLKVIILIMDEFDDLKGRGEKSGIELISL VDARNIGKEHFRKPVPPSPEDLSVICTSTGTDGDKGRMTHHON IVSNAAAPLKCVERAVPPPDDVALSTALHMPFERIVQAVVYS CGARVGFFGGDIRLLADDMKTLKPTLFPAVFRLINTIYDKVONE ANTPLKKELLKLAVSSKYKELQKGIIRHDSFRDKLIFAKQDSL GGGRVAIVIGGABMSTSWATFFRAMGCQVYEAVGGTECTGGCT FTLPGDMTSGHVGVPLACNTYKLEDVADMNYFTVNNBGEVCIKG TNYPKGYLKADPSTALLGUNDSHATHGJARLFAKUDSL KNIFKLAGGEVIAPEKIENIYNRSGPVLQIFYHGESLRSSLVGV VUPDTOULPSFAAKLGVAKSFELCONQVVERAILEDLQKIIGKE SGLKTFEQVKAIFLHPEPPSIENGLIFPTLKAKRGELSKYPRTQ IOSINEHQD  S452  1833  1138 SRYPSLCISISISSFSREPVAGAPGCGTAGPPAMATLWGGLLR LGSLLSISCIALSVLLLAQLSDAARNFEDVRKCCICPYKENSG HYNNKIJSKOCCHLVVEPMPVURGDVRAYCLRCEKKERESS VTIKVTIIIVLSILGLLLLANVYLTLVEPILKRRLFGHAQLIQS DDDIGGHQPFANAHDVLARSRSRANVLNKVEYAQQRMKLQVQEQ RKSVPDRRVVJS  S453  111  1520 PSIFAAVPGSAPPEPHREETVTATATSQVAQQPPAAAAPGGGAKE PQEBRSQQDDIEBLETTAVGMSNDGRFLKFDIEGGSFKTYY KGLDTETTVSVANCKLLOPKEREPERPSTRGGGSAKE PQEBRSQQDDIEBLETTAVGMSNDGRFLKEDTGTGTGVKIGD LEMATSEYPYSSCONAAQIVRRVTSGVKRSERDENDVATGRCM LEMATSEYPYSSCONAAQIVRRVTSGVKRSERDENDVATGRCMC LEMATSEYPYSSCONAAQIVRRVTSGVKRSERDENDVATGRCMC LEMATSEYPYSSCONAAQIVRRVTSGVKRSERDENDVATGRCMC LEMATSEYPYSSCONAAQIVRRVTSGVKRSERDENDVATGRCMC LEMATSEYPYSSCONAAQIVRRVTSGVKRSERDENDVATGRCMC LEMATSEYPYSSCONAAQIVRRVTSGVKRSERDENDVATGRCMC LEMATSEYPYSSCONAAQIVRRVTSGVKRSEPPPARSGSGGSAKE PQEBRSQQODDIEBLETTAVGMSNDGRFLKERDENGGVKIAI LKJURIEDLIKLKGKYKONBAIEFSFDLERNVPEDVAQEMVESG YVCEGDHKTMAKAIKDRVSLIIRKRRGRQQLI*  PSIFRAVPGSAPPBHREEFTVTATATSGVAQOPPAAAAPGGOAV AGPASTVPSSTSSCONAGGTRAKARG				DQGEVVFAFTNFSSSHDHFRVLALARGVNASAVVNVTVRALLHV
VVRVPRAPTEPGGGGLLVGPTGQDLEDGRIGLEVGRPEGRAPGP AGDSLTLELHARQGVPDAVASLDFATEPANARPYSVALLSVPEA ARTEAGKPESSTPTGEPGPMASSPEPAVAKGGFLSTLEAMMFSV IIPMCLVILLILALILELLFYLKKRNKTGKHDVUVLTAKPRINGLA GDTETFRKVEPGGAIPLTAVPGGQPPPGGGPPPELLGCETTPW ALKNIGGYW  5451  1 2274 RDSSEGGRGTGTLGRPSACMDALKPPCLWRNHERGKKORDSGGR KNSBPGSPHSLEALRDAAPSQGLNFLLLFTKMLFIFNFLFSPLP TPALICILTFGAAIFLWILTRPQVUPLLDLINDSVGIBGGARK GVSQKNNDLTSCCFSDAKTMYEVFQRGLAVSONGPLGYRKPNQ PYRMLSYKQVSDRAEVLGSCLLHKGYKSSPDGFVGIFARNEW IISBLACYTYSMVAVPLYDTLGPBAIPUNKADLAVVLCDTPQ KALVLIGNVEKGFTPSLKVIILMDPFDDDLKGRGKSGIBILSL YDARBIGLGHPRKVVPDSPSDLSVICFTSGTTGDPKGMSTHION IVSNAAPLKCVEHAYEPTPDDVAISTULAMMFRIVQAVVYS CGARVGFFCGDIRLLADDHKTLKFTLFPAVPELLMRIYDKVQNE AKTPLKKFLLLLAVSSKFELQKGIILFFANWFLTWINDSEVCIKG GGVRVIVTGAAPMSTSVMTFFRAMGCQVYEAYGQTECTGGCT FTL.FGDWTSGHLVVPLLGAACHYVLEDVAMPTTVMNEGEVCIKG KNIFICLAGGEYIAPEKIENIYNRSQVVLQIFVHGESLRSSLVGV VVDDTDVLDSFAAKLGVAGYSEELCQNQVVERAILDEDLGKKE SGLKFFEQVKAIFLHEEPFSIENGLITPTLKAKRGELSKYFRTQ 105LVEHIQD  5452  1833  1138 SRYPSLCISISLSSFSREPVAGAPGCGTAGPPAMATLWGGLLR KNIFICLAGGEYIAPEKIENIYNRSQVVLQIFVHGESLRSSLVGV VVDDTDVLDSFAAKLGVAGSFEELCQNGVVERAILEDLGKIGKE SGLKFFEQVKAIFLHEEPFSIENGLITPTLKAKRGELSKYFRTQ 105LVEHIQD  5452  1833  1138 SRYPSLCISISLSSJSFSREPVAGAPGCGTAGPPAMATLWGGLLR HYNKNISGKDCDCLHVVEPNPVAGDVBAYCLACECKYERSS VTIKVTIIIVLSILGLLLIYMVITLVEPILKREICTPKRENSG HYNKNISGKDCDCLHVVEPNPVAGDVBAYCLACECKYERSS VTIKVTIIIVLSILGLLLIYMVITLVEPILKREICTPKRENSG HYNKNISGKDCDCLHVVEPNPVAGDVBAYCLACECKYERSS VTIKVTIIIVLSILGLLLIYMVITLVEPILKREICTPKRENSG POERSQQQDDIBELETTAVGMSNDGRFIKFDITRGGSFKTYV KGLDTETTVEVAVACLQDOKKLTSERSRPKYQGRWKLQVQEQ RKSVPDRHVULS  6 PSTPAAVPGSAPPEPHREETVTATATSQVAQQPPAAAPGEGQAV AGPAPSTVPSSTSKDRPVSGPSLVGSKEEPPPARSGSGGSAKE POERSQQQDDIELELTTAVGMSNDGRFIKEDLERGGSFKTYV KGLDTETTVEVAVACLQDOKKLTSERSRPKEXDERSWLAUGLOPHII VAFTDSAMPGSRYSIRGLHARAFPECTALEEDCOCHULAEGC LEMATSSYPYSSCONAQIVRRYTSGVKPASFDKVAIPPVKEII ECCTRGNKORKYSIRGLHARAFPECTALTSTGVAQQPPAAAPGEQAV AGPAPSTVPSSTSKDRPVSGPSLVGKREPPPPARSGGGGGSAKE POERSGQODDIELETTANGMSNDGRFIKEDELAGGSPKTYY ADAPSTVPSSTSKDRPVSGPSLVGKKEPPPPARSGGGGGS				WAGGPWPQGATLRLDPTVLDAGELANRTGSVPRFRLLEGPRHGR
AGDSLYLELMAQGYPAVASLDFATEPYNAARPYSVALLSYPEA ARTEAGKPESTPYTGERPMASSPEPAKGGFLSFLEAMMFSV IIDMCLVLLLLALLLLPLLFYLEKKRIKTGKBDVQVLTAKPRIGLA GDTETFEKVEPQQAIPLTAVPGQGPPGGGPDEGLOFCCTPNIP ALMINGYYW  S451  1 2274 RDSSEGGRTGTTGRFSACMDALKPPCLWRHERGKKKDRDSCGR KNSEPGSPHSLEALRDAARSGGLINFLLFYKNLFTFRIFLSPLDF KRISPGSPHSLEALRDAARSGGLINFLLFYKNLFTFRIFLSPLDF TPALICILTFGAAFFLWLTTROPVUPLLDLINDQSVGIEGGARK GVSQKNNDLTSCCFSDAKTMVEVPGGLAVSDNGPCLGYRKPNQ PYRHLSYKQVSDRAEYLGSCLLHKGYKSSPDGFVGIFAQNRFSW IISBLACTTYSMVAVELYTTLGPBAIVHTUNKADINGYCLGYRKPNQ PYRHLSYKQVSDRAEYLGSCLLHKGYKSSPDGFVGIFAQNRFSW IISBLACTTYSMVAVELYTTLGPBAIVHTUNKADINAVICOTPQ KALVLIGKNEKGFTPSLKVILIMDFPDDLKGRGEKSGISLISL YDABMLGKEHFRKVPPSSPEDLSVICTSTGTDPYKGMTTHON IVSNAAAFLKCVERAVETPPDDVALSTCHIMFRIVQAVYS CGARVGFFCGDIRLLADDMKTLKPTLPPAVPBLLMTFRIVQAVYS CGARVGFFCGDIRLLADDMKTLKPTLPPAVPBLLMTFRIVQAVYS CGRVVIVTGAAPMSTSVMTFFRAMGCQVYEAVGGTECTGGCT FTLFGDMTSGHVGVPLACNTYKLEDVADMNYTTVNNBGEVCIKG TNNPKGYLKAPEETSTSVMTFFRAMGCQVYEAVGGTECTGGCT FTLFGDMTSGHVGVPLACNTYKLEDVADMNYTTVNNBGEVCIKG KNIFKLAGGEVIAPEKIENIYNRSGPVLQIFHGESLRSSLVGV VVPDTOULPSFAAKLGVKSSFEELCOMVYRSALIEDKSLGKEKSLGKVE VVPDTOULPSFAAKLGVKSSFEELCOMVYRSALIEDKSLKGEK SGLKFFEQVKA.IFLHPEPFSIENGLITPTLKAKRGELSKYFRTQ IDSLYHIQD  S452  1833  1138 SKYPSLCLSISISISSSPSREPVAGAPGCGTAGPPAMATLWGGLLR LGSLLSISCCLALSVLLLAQLSDAAKNFEDVRKCCICPYKRNSG HYNNKITSKOCCCLHVVEPMPVGGPVBAYCLKCEKKVERESS VTIKVTIIIVLSILGLLLLAWVUTLTUFEILKRELFGHAQLIGS DDDIGDHQPFANAHDVLARSRSRANVLNKVEXQQRWKLQVQEQ RKSVFDRHVVLS  5453  111  1520 PSIFRAVPGSAPPEPHREETVTATATSQVAQQPFAAAAFGGQAV KGPAPSTVPSSTSKORPVSQPSLVGSKEEPPPARSGSGGSAKE PQEERSQQQDDIEBLETKAVGMSNDGRFLKFDIE GRGSFKTVY KGLDTETTVSVANCKLLORKLAFTPEI HRDLKCONLFITEGFGSVKIGD LGMATTSSPYPSSCONAAQIVRRVTSGVKRASFDKVAIPPSKKIIV RSWCGLLKGLEPPKTSPTSVTSGTKKREGRQI.  ECKTRONKORRYS INCLUMAR FPGETGYRLAEDEDGGVALL RSWCFSTVSSTSKORRYS STOLMHAFPGGETGWLAEDEDGGVAAPGGGAVKAAPGFSTVYSACKGKTVALVFTGRFSFFDLERNVPEDVAQEMVESG YVCEGDHKTMAKAIKRYKONRALEFSFFDLERNVPEDVAQEMVESG YVCEGDHKTMAKAIKRORSLIKKRREGRQI.  FSIPANVPGSAPPBBHREETVTATATSGVAQOPPAAAAPGGAV APPASTVPSSTSKORPVSGYSLVGKKEPPPARSGSGGGSA	1	1		VVRVPRARTEPGGSQLVEQFTQODLEDGRLGLEVGRPEGRAPGD
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KALVLIGNVEKGFTPSLKVI ILMDPFDDDLKQRGEKSGIEILSI. YDARNLGKEHFRKPVPPSPEDLSVICFTSGTTGDPKGAMTHQN IVSNAAAFLKCVERAYETTPDDVAISYLDLAHMFERIVQAVVYS CGARVGFFQGDIRLLADDMKTLKDTLFPAVPRLINRIYDKVQNE AKTPLKKFLLKLAVOSKFKELQKGIIRHDSFMDKLIFAKIQDSL GGRVRVIVTGAAPMSTSVMTFFRAAMGCQVYEAYQTECTGGCT FTLPGDWTSGHVGYPLACNYVKLEDVADMNYFTVNNEGEVCIKG TNVFKGYLKDPEKTQEALDSDGWLHTGDIGRMLPMGTLKIJDRK KNIFKLAQGEYIAPEKTENIYNRSQPVLQIFVHGESLRSSLVGV VVPDTDVLPSFAAKLGVKGSFEELCQNQVVREAILEDLQKIGKE SGLKTFEQVKAIFLHPBEFSIENGLLTPTLKAKRGELSKYFRTQ IDSLYBHIQD  S452  1833  1138  SRVPSLCLSLSLSLSFSREPVAGAPGCGTAGPPAMATLWGGLLR LGSLLSLSCLALSVLLLAQLSDAAKNFEDVRCKCICPPYKENSG HIYNKNISQKDCDCLHVPPMPVRGPDVEAYCLRCECKYEERSS VTIKVTIIYLSILGLLLLYMVYLTLVEPILKRRLFGHAQLIQS DDDIGGHQPFANAHDVLARSRSRANVLNKVEYAQQRWKLQVQEQ RKSVFDRHVVLS  5453  111  1520  PSIPAAVPQSAPPEPHREETVTATATSQVAQQPPAAAAPGEQAV AGPAPSTVPSSTSKDRPVSQPSLVGSKEEPPPARSGSGGGSAKE PQEERSQQDDIELELTKAVGMSMDGRFLKFDIEIGRGSFKTYY KGLDTETTVEVAWCELQDRKLTKSBRQRFKEEPBRLKGLQHDMI VRFYDSWESTVKGKKCIVLVTELMTSGTLKTYLKRFKVMKIKVL RSWCRQILKGLQPHTTTPPJIHRDLKCDNIFITGPTGSVKIGD LGLATLKRASFAKSVIGTPPFMAPBMYEEKYDESVDVVAFGMCM LEMATSEYPYSECQNAAQIYRRVTSGVKPASFDKVAIPEVKEII EGCIRQNKDERYSIRDLLWHAFFQEETGVRVELABEDDGEKIAI KLWLRIEDIKKLKGKYKDNEAIEFSFDLERNVPEDVAQEMVESG YVCEGDHKTMAKAIKDRVSLIKKRREGRQL*  111  1520  PSIPAAVPGSAPPEPHREETVTATATSQVAQQPPAAAAPGEQAV AGPAPSTVPSSTSKDRPVSQPSLVGSKEEPPPARSGSGGSAKE POEERSQQQDDIEBLETKAVGMSNDGRFLKFDIEIGRGSFKTYY POEERSQQQDDIEBLETKAVGMSNDGRFPLKFDIEIGRGSFKTYY		{		PIRMLSYKQVSDRAEYLGSCLLHKGYKSSPDQFVGIFAQNRPEW
YDARNIGKEHFRKPVPPSPELSVICFTSGTTGDPKGAMITHQN IVSNAAAFLKCVEHAYEPTPDDVAISYLPLAHMFERIVOQWYYS CGARVGFFQGDIRLLADDMKTLKPTLFPAVPRLLNRIYDKVQNE AKTPLKKFLLKLAVSSKFKELQKGIIRHDSFWDKLIFAKIQDSL GGRVRIVTGAAPMSTSVMTFFRAMGCQVYEAYGGTECTGGCT FTLPGDWTSGHVGVPLACNYVKLEDVADMNYFTVNNEGEVCIKG TNVPKGYLKDPEKTQEALDSDGWLHTGDIGRNLPNGTLKIIDRK KNIFKLAQGEYIAPEKTENIYNRSQPVLQIFVHGESLRSSLVGV VVPDTDVLPSFAAKLGVKGSFEELCQNQVVREAILEDLQKIGKE SGLKTFEQVKAIFLHPEPFSIENGLLTPTLKAKRGELSKYFRTQ IDSLYBHIQD SRVPSLCLSLSLSSPSREPVAGAPGCGTAGPPAMATLWGGLLR LGSLSLSCLALSVLLLAQLSDAAKNFEDVRCKCICPPYKENSG HIYNKNISQKDCDCLHVVEPMPVRGPDVPAYCLRCECKYEERSS VTIKVTIIIYLSIIGLLLLYMVYLTLVEPILKRRLFGHAQLIQS DDDIGDHQPFANAHDVLARSRSRANVLNKVEYAQQRWKLQVQEQ RKSVPDRHVVLS S453 111 1520 PSIFAAVPQSAPPEPHREETVTATATSQVAQQPFAAAAPGEQAV AGPAPSTVPSSTSKDRPVSQPSLUGSKEEPPPARGSGGGSAKE PQEERSQQDDIEELETKAVGMSNDGRFLKFDIETGRGSFKTVY KGLDTETTVEVAWCELQDRKLTKSERGFKEEAEMLKGLQHDNI VRFYDSWESTVKGKKCIVLVTELMTSGTLKTYLKRFKVMKIKVL RSWCRQILKGLQFLHTRTPPIIHRDLKCDNIFITGPTGSVKIGD LGLATLKRASFAKSVIGTPEFMAPEMYEEKYDESUDVYAFGMCM LEMATSEYPYSECQNAAQIYRRVTSGVKPASFDKVAIPEVKEII EGCIRQNKDERYSIKDLLWHAFFQEETGVRVELAEEDDGEKIAI KLWIRIEDIKKLKKKYKUELERSPLERSVPDVAAAAPGEQAV VCEGDHKTMAKAIKDRVSLIKKKRERGQL*  111 1520 PSIPAAVPGSAPPEPHREETVTATATSGVAQQPPAAAAPGEGAV AGPAPSTVPSSTSKDRPVSQPSLUGSKEEPPPARSGSGGGSAKE PQEERSQQQDDIEELETKAVGMSNDGRFLKFDIETGRGSPKTYY PGEERSQQQDDIEELETKAVGMSNDGRFLKFDIETGRGSPKTYY PGEERSQQQDDIEELETKAVGMSNDGRFLKFDIETGRGSPKTYY	1	1		IISELACYTYSMVAVPLYDTLGPEAIVHIVNKADIAMVICDTPQ
IUSNAAAPLKCUEHAYEPTPDUVAISYLDLAHMFERIVQAVVYS CGARVGFFQGDIRLLADDMKTLKPTLFPAVPRLLNRIYDKVQNE AXTPLKKFLLKLAUSSKFKELQKGIIRHDSFMDKLIFAKYQDSL GGRVRYLVTGAAPMSTSVMTPFRAAMGCQVYEAYGQTECTGGCT FTLPGDWTSGHVGVPLACMYVKLEDVADMMYFTVNNEGEVCIKG TNVPKGYLKDPEKTGBALDSDGMLHTGDIGRHLPNGTLKXIDRK KNIFKLAQGEYIAPEKIENIYNRSQPVLQIFVHGESLRSSLVGV VVDDTDVLPSFRAKLGVKGSFEELCQNQVVREAILEDLQKIGKE SGLKTFEQVKAIFLHPEPFSIENGLLTPTLKAKRGEL9KYPRTQ IDSLYEHIQD  5452  1833  1138  SRVPSLCLSLSJSJSPSREPVAGAPGCGTAGPPAMATLWGGLLR LGSLLSLSCLALSVLLLAQLSDAAKNFEDVRCKCICPPYKENSG HTYNKNISQKDCDCLHVVEPMPVRGPDVEAYCLRCECKYEERS VTIKVTIIIVLSILGLLLLYMVYLTLVEPILKRRLFGHAQLIQS DDDIGDHQPFANAHDVLARSRSRANVLNKVEYAQQRWKLQVQEQ RKSVPDRHVVLS  5453  111  1520  PSIFAAVPQSAPPEPHREETVTATATSQVAQQPPAAAAPGEQAV AGPAPSTVPSSTSKDRPVSQPSLVGSKEEPPPARSGSGGSAKE PQEERSQQQDDIEELETKAVGMSNDGRFLKFDIEIGRGSFKTVY KGLDTETTVEVAWCELQDRKLTKSERQRFKEEARMLKGLQHDNI VRFYDSWESTVKGKKCIVLVTELMTSGTLKTYLKRFKVMKIKVL RSWCRQILKGLQPLHTRTPPIIHRDLKCDNIFITGPTGSVKIGD LGAPLKRASFARSVIGTPEFMAPEMYEEXPDESUVYAFRMCM LEMATSEYPYSECQNAAQIYRRVTSGVKPASFDKVAIPEVKEII ESCIRQNKDERYSIKDLLNHAFFQEETGVWELABEDDGEKTAI KLWIRIEDILKKLKGYNDAAIEFSFDLERNVPEDVAQEWVESG YVCEGDHKTMAKAIKDRVSLIKRKREQRQL*  5454  111  1520  PSIPAAVPQSAPPEHRBETVTATATSQVAQQPPAAAAPGEQAV AGPAPSTVPSSTSKDRPVSSLVGSKEEPPPARSGSGGGSAKE PQEERSQQQDDIEELETKAVGMNDGRFLKFDIEIGRGSFKTVY	ļ	l I		KALVLIGNVEKGFTPSLKVIILMDPFDDDLKQRGEKSGIEILSL
CGRVGFFQGDIRLLADDMKTLKPTLFPAVPRLLNRIYDKVQNE AKTPLKKFLLKLAVSSKFKELQKGIIRHDSFWDKLIFAKIQDSL GGRVRVIVTGAAPMSTSVMTPFRAAMGCQVYEAYQTECTGGCT FTLPGDMTSGHVGVPLACNYVKLEDVADMNYFTVNNEGEVCIKG TNVPKGYLKDPEKTQEALDSDGWLHTGDIGRWLPNGTTLKIIDRK KNIFKLAQGEYIAPEKIENIYNRSQPVLQIFVHGESLRSSLVGV VVPDTDVLPSFAAKLGVKGSFEELCONQVVREAILEDLQKIGKE SGLKTFEQVKAIFLHPEPFSIENGLLTPTLKAKRGELSKYPRTQ IDSLYEHIQD SRVPSLCLSLSLSLSJSFSREPVAGAPGCGTAGPPAMATLWGGLLR LGSLLSLSCLALSVLLLAQLSDAAKNFEDVRCKCICPPYKENSG HYYNKNISQKDCDCLHVVBPMPVRGPDVEAYCLRCECKYEERSS VTIKVTIIIYLSILGLLLLYMVYLTLVEPILKRRLFGHAQLIQS DDDIGHQPFANAHDVLARSRSRANVLNKVEYAQQRWKLQVQEQ RKSVFDRHVVLS  5453 111 1520 PSIFAAVPQSAPPEPHREETVTATATSQVAQQPPAAAAPGEQAV KGLDTETTVEVAWCELQDRKLTKSERQRFKEEAEMLKGLQHPNI VRFYDSWESTVKGKKCIVLVTELMTSGTLKTYLKRFKYWKIKVL RSWCRQILGCLQFLHTRTPPPIIHRDLKCDNIFITGPTGSVKIGD LGLATLKRASFAKSVIGTPERMAPEMYEEKYDESVDVYAFGMCM LEMATSEYPYSECONAAQIYRRVTSGVKPASFDKVAIPEVKEII EGCIRQNKDERYSIKDLLNHAFFQESTGWVELABEDDGEKTAI KLWLRIEDIKKLKGYKYNDNEITEFSFDLERNVPEDVAQEMVESG YVCEGDHKTMAKAIKDRVSLIKRKREQRQL*  5454 111 1520 PSIFAAVPQSAPPEPHREETVTATATSQVAQQPPAAAAPGEQAV AGPAPSTVPSSTSKDRPVSQDSLVGSKEPPPARSGSGGGSAKE PQEERSQQDDIELLETTATATTSQVAQQPPAAAAPGEQAV AGPAPSTVPSSTSKDRPVSQDSLVGSKEPPPARSGSGGGSAKE PQEERSQQDDIELELTKAVGMSNDGRFLKFDIEGRGSPKTVY PQEERSTURKKLKGYKYNDNEITEFSFDLERNVPEDVAQEMVESG PVCEGDHKTMAKAIKDRVSLIKRKREQRQL* PSIFAAVPQSAPPEPHREETVTATATSQVAQQPPAAAAPGEQAV AGPAPSTVPSSTSKDRPVSQDSLVGSKEPPPARSGSGGGSAKE PQEERSQQQDDIEELETKAVGMSNDGRFLKFPIEIGRGSPKTVY	1	1		YDAENLGKEHFRKPVPPSPEDLSVICFTSGTTGDPKGAMITHQN
AKTPLKKFLLKLAVSSKPKELQKGIIRHDSFWDKLIFAKIQDSL GGRVRVIVTGAAPMSTSVMFFRAAMGCQVYEAYGQTECTGGCT FTLPGDWTSGHVGVPLACNYVKLEDVADMNYFTVNNEGEVCIKG TNVPKGYLKDPEKTQBALDSDGWLHTGDIGRWLDNGTLKIIDRK KNIFKLAQGEYIAPEKIENIYNRSQPVLQIFVHGESLRSSLVGV VVPDTDVLPSFAAKLGVKGSFEELCQNQVVREAILEDLQKIGKE SGLKTFQVKAIFLHPEPFSIENGLITPTLKAKKGGLSKYPRTQ IDSLYEHIQD SRVPSLCLSLSLSLSSSPSREPVAGAPGCGTAGPPAMATLWGGLLR HYNKNISQKDCDCLHVVEPMPVRGPDVEAYCLKCECKYEERSS VTIKVTIIIYLSILGLLLLYMVYLTLVEPILKRRLFGHAQLIQS DDDIGDHQPFANAHDVLARSRSRANVLNKVEYAQQRWKLQVQEQ RKSVFDRHVVLS  5453 111 1520 PSIPAAVPQSAPPEPHREETVTATATSQVAQQPPAAAAPGEQAV AGPAPSTVPSSTSKDRPVSQPSLVGSKEEPPPARSGSGGGSAKE PQEERSQQQDDIEELETKAVGMSNDGRFLKFDIEIGRGSFKTVY KGLDTETTTURAWCELQDRKLTKSERQRFKEEAEMLKGLQHBNI VRFYDSWESTVKGKKCIVLVTELMTSGTLKTYLKRFKVMKIKVL RSWCRQILKGLQFLHTRTPPIIHRDLKCDNIFITGPTGSVKIGD LGLATLKRASFAKSVIGTPEFMAPEMYEEKYDESVDVYAFGMCM LEMATSEYPYSECONAAQIYRRVTSGVKPASFDKVAIPEVKEII EGCIRQNKDERYSIKDLINHAFFQEETGVRVELABEDDGEKIAI KLWLRIEDIKKLKGKYKDNEAIEPSFDLERNVPEDVAQEMVESG YVCEGDHKTMAKAIKDRVSLIKRREQRQL*  111 1520 PSIPAAVPGSAPPBPHREETVTATATTSGVAQQPPAAAAPGEQAV AGPAPSTVPSSTSKDRPVSQPSLVGSKEEPPPARSGSGGGSAKE PSIPAAVPGSAPPBPHREETVTATATTSGVAQQPPAAAAPGEQAV AGPAPSTVPSSTSKDRPVSQPSLVGSKEEPPPARSGSGGGSAKE PSIPAAVPGSAPPBPHREETVTATATTSGVAQQPPAAAAPGEQAV AGPAPSTVPSSTSKDRPVSQPSLVGSKEEPPPARSGSGGGSAKE PSIPAAVPGSAPPBPHREETVTATATTSGVAQCPPAAAAPGEQAV AGPAPSTVPSSTSKDRPVSQPSLVGSKEEPPPARSGSGGGSAKE PQEERSQQQDDIEELETTKAVGMSNDGRFLKFPIEIGRGSFKTVY	1	į l		IVSNAAAFLKCVEHAYEPTPDDVAISYLPLAHMFERIVQAVVYS
GGRVIVITGAAPMSTSVMTFFRAAMGCQVYEAYGGTECTGGCT FTLPGDWTSGHVGVPLACMYVKLEDVADMYFTVMNEGEVCIKG TTNVPKGYLKDPEKTOBALDSDGWLHTGDIGRWLDNGTKKIDRK KNIFKLAQGEYIAPEKIENIYNRSQFVLQIFVHGESLRSSLVGV VVPDTDVLPSFAAKLGUKGSFEELCONQVVREAILEDLQKIGKE SGLKTFEQVKAIFLHPEPFSIENGLLTPTLKAKRGELSKYFRTQ 105LYEHIQD SAVPSLCLSLSLSLSPSREPVAGAPGCGTAGPPAMATLWGGLLR LGSLLSLSCLALSVLLLAQLSDAAKNFEDVRCKCICPPYKENSG HIYNKNISQKDCDCLHVVEPMPVRGPDVEAYCLRCECKYERRS VTIKVTIIIVLSILGLLLLYMVYLTLVEPILKRRLFGHAQLIQS DDDIGDHQPFANAHDVLARSRSRANVLNKVEYAQQRWKLQVOEQ RKSVFDRHVVLS  5453 111 1520 PSIFAAVPQSAPPEPHREETVTATATSQVAQQPPAAAAPGRQAV AGPAPSTVPSSTSKDRPVSGPSLVGSKEEPPPARSGSGGSAKE PQEERSQQQDDIEELETKAVGMSNDGRFLKFDIEIGRGSFKTVY KGLDTETTVEVAWCELQDRKLTKSBRQRFKEEAEMLKGLQHDNI VRFYDSWESTVKGKKCIVLVTELMTSGTLKTYLKRFKVMKKVVL RSWCRQILKGLQFLHTRTPPIIHRDLKCDNIFITGPTGSVKIGD LGLATLKRASFAKSVIGTPEFMAPEMYEEKYDESVDVYAFGMCM LEMATSEYPYSECONAAQIYRRVTSGVKPASFDKVAIPEVKEII EGCIRQNKDERYSIKDLLNHAFFQEETGVRVELABEDDGEKIAI KLWLBIEDIKKLKGKYKDNBAIEFSFDLERNVPEDVSQEMVESG YVCEGDHKTMAKAIKDRVSLIKRKREQRQL*  111 1520 PSIPAAVPGSAPPBPHREETVTATATSGVAQQPPAAAAPGEQAV AGPAPSTVPSSTSKDRPVSQFSLVGSKEEPPPARSGSGGGSAKE PQEERSQQQDDIEELETKAVGMSNDGRFLKFDIEIGRGSFKTVY	1			CGARVGFFQGDIRLLADDMKTLKPTLFPAVPRLLNRIYDKVQNE
GGRVIVITGAAPMSTSVMTFFRAAMGCQVYEAYGGTECTGGCT FTLPGDWTSGHVGVPLACMYVKLEDVADMYFTVMNEGEVCIKG TTNVPKGYLKDPEKTOBALDSDGWLHTGDIGRWLDNGTKKIDRK KNIFKLAQGEYIAPEKIENIYNRSQFVLQIFVHGESLRSSLVGV VVPDTDVLPSFAAKLGUKGSFEELCONQVVREAILEDLQKIGKE SGLKTFEQVKAIFLHPEPFSIENGLLTPTLKAKRGELSKYFRTQ 105LYEHIQD SAVPSLCLSLSLSLSPSREPVAGAPGCGTAGPPAMATLWGGLLR LGSLLSLSCLALSVLLLAQLSDAAKNFEDVRCKCICPPYKENSG HIYNKNISQKDCDCLHVVEPMPVRGPDVEAYCLRCECKYERRS VTIKVTIIIVLSILGLLLLYMVYLTLVEPILKRRLFGHAQLIQS DDDIGDHQPFANAHDVLARSRSRANVLNKVEYAQQRWKLQVOEQ RKSVFDRHVVLS  5453 111 1520 PSIFAAVPQSAPPEPHREETVTATATSQVAQQPPAAAAPGRQAV AGPAPSTVPSSTSKDRPVSGPSLVGSKEEPPPARSGSGGSAKE PQEERSQQQDDIEELETKAVGMSNDGRFLKFDIEIGRGSFKTVY KGLDTETTVEVAWCELQDRKLTKSBRQRFKEEAEMLKGLQHDNI VRFYDSWESTVKGKKCIVLVTELMTSGTLKTYLKRFKVMKKVVL RSWCRQILKGLQFLHTRTPPIIHRDLKCDNIFITGPTGSVKIGD LGLATLKRASFAKSVIGTPEFMAPEMYEEKYDESVDVYAFGMCM LEMATSEYPYSECONAAQIYRRVTSGVKPASFDKVAIPEVKEII EGCIRQNKDERYSIKDLLNHAFFQEETGVRVELABEDDGEKIAI KLWLBIEDIKKLKGKYKDNBAIEFSFDLERNVPEDVSQEMVESG YVCEGDHKTMAKAIKDRVSLIKRKREQRQL*  111 1520 PSIPAAVPGSAPPBPHREETVTATATSGVAQQPPAAAAPGEQAV AGPAPSTVPSSTSKDRPVSQFSLVGSKEEPPPARSGSGGGSAKE PQEERSQQQDDIEELETKAVGMSNDGRFLKFDIEIGRGSFKTVY		ŀ		AKTPLKKFLLKLAVSSKFKELQKGIIRHDSFWDKLIFAKIQDSL
FTLPGDMTSGHVGVPLACNYVKLEDVADMNYFTVNNEGEVCIKG TNVPKGYLKDPEKTGBALDSDGMLHTGDIGRMLPNGTIKIIDRK KNIFKLAQGEYJAPEKIENIYNRSQPVLQIFVHGESLRSSLVGV VVPDTDVLPSFAAKLGVKGSFEELCQNQVVREAILEDLQKIGKE SGLKTFEQVKAIFLHPEPFSIENGLLTPTLKAKRGELSKYPRTQ IDSLYEHLQD  SRVPSLCLSLSISISPSREPVAGAPGCGTAGPPAMATLWGGLLR LGSLLSLSCLALSVLLLAQLSDAKNFEDVRCKCICPPYKENSG HIYNKNISQKDCDCLHVVEPMPVRGPDVEAYCLRCECKYEERSS VTIKVTIIIYLSILGLLLLYMVYLTLVEPILKRRLFGHAQLIQS DDDIGDHQPFANAHDVLARSRSRANVLNKVEYAQQRWKLQVQEQ RKSVPDRHVVLS  FSIPAAVPQSAPFEPHREETVTATATSQVAQQPPAAAAPGRQAV AGPAPSTVPSSTSKDRPVSQPSLVGSKEEPPPARSGSGGGSAKE PQEERSQQDDIEELETKAVGMSNDGRFLKFDIEIGRGSFKTVY KGLDTETTVEVAWCEBLQDRKLTKSERQRFKEEAEMLKGLQHPNI VRFYDSWESTVKGKKCIVLVTELMTSGTLKTYLKRPKVMKIKVL RSWCRQILKGLQFLHTRTPPIIHRDLKCDNIFITGPTGSVKIGD LGLATLKRASFAKSVIGTPEFMAPEMYEEKYDESVDVYAFGMCM LEMATSEYPYSECQNAAQIYRRVTSGVKPASFDKVAIPEVKEII EGCIRQNKDERYSIRDLLNHAFFQEETGVRVELABEDDGEKIAI KLWLRIEDIKKLKGKYKDNEAIEFSFDLERNVPEDVAQEMVESG YVCEGDHKTMAKAIKDRVSLIKRKREQRQL*  5454  111 1520 PSIPAAVPQSAPPEHREETVTATATSQVAQQPPAAAAPGEQAV AGPAPSTVPSSTSKDRPVSQPSLVGSKEEPPPARSGSGGGSAKE PQEERSQQQDDIEELETKAYGMSNDGRFLKFDIEIGRGSFKTVY PSIPAAVPGSAPPEHREETVTATATSQVAQQPPAAAAPGEQAV AGPAPSTVPSSTSKDRPVSQPSLVGSKEEPPPARSGSGGGSAKE PQEERSQQQDDIEELETKAYGMSNDGRFLKFDIEIGRGSFKTVY		]	•	GGRVRVIVTGAAPMSTSVMTFFRAAMGCQVYEAYGOTECTGGCT
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VRFYDSWESTVKGKKCIVLVTELMTSGTLKTYLKRFKVMKIKVL RSWCRQILKGLQFLHTRTPPIIHRDLKCONIFITGPTGSVKIGD LGLATLKRASFAKSVIGTPEFMAPEMYEEKYDESVDVYAFGMCM LEMATSEYPYSECQNAAQIYRRVTSGVKPASFDKVAIPEVKEII EGCIRQNKDERYSIKDLLNHAFFQEETGVVELABEDDGEKIAI KLWLRIEDIKKLKGKYKDNEAIEFSFDLERNVPEDVAQEMVESG YVCEGDHKTMAKAIKDRVSLIKRKREQRQL* 111 1520 PSIPAAVPQSAPPBPHREETVTATATSQVAQQPPAAAAPGEQAV AGPAPSTVPSSTSKDRPVSQPSLVGSKEEPPPARSGSGGGSAKE PQEERSQQQDDIEELETKAVGMSNDGRFLKFDIEIGRGSFKTYY	1 1		1	KGLDTETTVEVAWCELQDRKLTKSERQRFKEEAEMLKGLQHPNI
RSWCRQILKGLQFLHTRTPPIIHRDLKCDNIFITGPTGSVKIGD LGLATLKRASFAKSVIGTPEFMAPEMYEEKYDESVDVYAFGMCM LEMATSEYPYSECQNAAQIYRRVTSGVKPASFDKVAIPEVKEII EGCIRQNKDERYSIKDLLNHAFFQEETGVRVELABEDDGEKIAI KLWLRIEDIKKLKGKYKDNEAIEFSFDLERNVPEDVAQEMVESG YVCEGDHKTMAKAIKDRVSLIKKRREQRQL* PSIPAAVPQSAPPBPHRBETVTATATSQVAQQPPAAAAPGEQAV AGPAPSTVPSSTSKDRPVSQPSLVGSKEEPPPARSGSGGSAKE PQEERSQQQDDIEELETKAVGMSNDGRFLKFPIEIGRGSFKTYY				VRFYDSWESTVKGKKCIVLVTELMTSGTLKTYLKRFKVMKIKVL
LGLATLKRASFAKSVIGTPEFMAPEMYEEKYDESVDVYAFGMCM LEMATSEYPYSECQNAAQIYRRVTSGVKPASFDKVAIPEVKEII EGCIRQNKDERYSIKDLLNHAFFQEETGVRVELABEDDGEKIAI KLWLRIEDIKKLKGKYKDNEAIEFSFDLERNVPEDVAQEMVESG YVCEGDHKTMAKAIKDRVSLIKKRREQRQL* PSIPAAVPQSAPPBPHRBETVTATATSQVAQQPPAAAAPGEQAV AGPAPSTVPSSTSKDRPVSQPSLVGSKEEPPPARSGSGGSAKE PQEERSQQQDDIEELETKAVGMSNDGRFLKFPIEIGRGSFKTYY	( !		!	RSWCRQILKGLQFLHTRTPPIIHRDLKCDNIFITGPTGSVKIGD
LEMATSEYPYSECQNAAQIYRRVTSGVKPASFDKVAIPEVKEII EGCIRQNKDERYSIKDLLNHAFFQEETGVRVELABEDDGEKIAI KLWLRIEDIKKLKGKYKDNBAIEFSFDLERNVPRDVAQEMVESG YVCEGDHKTMAKAIKDRVSLIKKRREQRQL*  111 1520 PSIPAAVPQSAPPBPHRBETVTATATSQVAQQPPAAAAPGEQAV AGPAPSTVPSSTSKDRPVSQPSLVGSKEEPPPARSGSGGGSAKE PQEERSQQQDDIEELETKAVGMSNDGRFLKFDIEIGRGSFKTYY	j		ſ	LGLATLKRASFAKSVIGTPEFMAPEMYEEKYDESVDVYAFGMCM
EGCIRQNKDERYSIKDLLNHAFFQEETGVRVELABEDDGEKIAI KLWLRIEDIKKLKGKYKDNERIEFSFDLERNVPEDVAQEMVESG YVCEGDHKTMAKAIKDRVSLIKRKREQRQL*  5454 111 1520 PSIPARVPQSAPPBPHRBETVTATATSQVAQQPPAAAAPGEQAV AGPAPSTVPSSTSKDRPVSQPSLVGSKEEPPPARSGSGGGSAKE PQEERSQQQDDIEELETKAVGMSNDGRFLKFDIEIGRGSFKTYY	ļ Ē		1	LEMATSEYPYSECQNAAOIYRRVTSGVKPASFDKVATDEWKPTT
KLWLRIEDIKKLKGKYKDNEAIEFSFDLERNVPEDVAQEMVESG YVCEGDHKTMAKAI KDRVSLIKRKREQRQL*  111 1530 PSIPAAVPQSAPPBPHREETVTATATSQVAQQPPAAAAPGEQAV AGPAPSTVPSSTSKDRPVSQPSLVGSKEEPPPARSGSGGGSAKE PQEERSQQQDDIEELETKAVGMSNDGRFLKFDIEIGRGSFKTYY	}	1	l	EGCIRONKDERYSIKDLLNHAFFOEETGVRUELAREDDGRUTAT
5454 111 1520 PSIPAAVPQSAPPBPHRBETVTATATSQVAQQPPAAAAPGEQAV AGPAPSTVPSSTSKDRPVSQPSLVGSKEEPPPARSGSGGGSAKE PQEERSQQQDDIEELETKAVGMSNDGRFLKFDIEIGRGSFKTVY	ļ ļ	ļ	!	KLWLRIEDIKKLKGKYKDNEA I EFGFDI. FDNUDEDVAOFMURGO
111 1520 PSIPAAVPQSAPPEPHREETVTATATSQVAQQPPAAAAPGEQAV AGPAPSTVPSSTSKDRPVSQPSLVGSKEEPPPARSGSGGGSAKE PQEERSQQQDDIEELETKAVGMSNDGRFLKFDIEIGRGSFKTVY	l _	1	}	YVCEGDHKTMAKAIKDRUSI,TKPKPPPOPOL.
AGPAPSTVPSSTSKDRPVSQPSLVGSKEEPPPARSGSGGGSAKE PQEERSQQQDDIEELETKAVGMSNDGRFLKFDIEIGRGSFKTVY	5454	111	1520	DST DAAVDOSA DDB DUDD DD MITTON MAN MOONTA A A DOS
PQEERSQQQDDIEELETKAVGMSNDGRFLKFDIEIGRGSFKTVY				AGDADETUDEGTEVDDDUGGDGI
KGLDTETTVEVAWCELQDRKLTKSERQRFKEEAEMLKGLQHPNI		1	j	POPERSONORDIERY
AGLUTETTVEVAMCELQDRKLTKSERQRFKEEAEMLKGLQHPNI	1	]		PVEEKSQUQDDIEELETKAVGMSNDGRFLKFDIEIGRGSFKTVY
	<del>ا ۔ ا</del>			NODDIE I I VEVANCELQDRKLTKSERQRFKEEAEMLKGLQHPNI

SEQ	Predicted	Predicted end	Tamino poid
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, R=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
}	corresponding	to first	LaLeucine, Mamethionine, NaAsparagine,
l	to first	amino acid	P-Proline, Q=Glutamine, R=Arginine,
ì	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
- [	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
	<del></del>	<del> </del>	VRFYDSWESTVKGKKCIVLVTBLMTSGTLKTYLKRFKVMKIKVL
(	<b>∤</b> ·	1	RSWCRQILKGLQFLHTRTPPIIHRDLKCDNIFITGPTGSVKIGD
1			LGLATLKRASFAKSVIGTPEFMAPEMYEEKYDESVDVYAFGMCM
1	1	1	LEMATSEYPYSECQNAAQIYRRVTSGVKPASFDKVAIPEVKEII
,	Į.	1	EGCIRONKDERYSIKDLLNHAFFQEETGVRVELAEEDDGEKIAI
i i		1	KLWLRIEDIKKLKGKYKDNEAIEFSFDLERNVPEDVAQEMVESG
1	1	1	YVCEGDHKTMAKAIKDRVSLIKRKREQRQL*
5455	1359	377	LTMVSPATRKSLPKVKAMDFITSTAILPLLFGCLGVFGLFRLLQ
4	1		WVRGKAYLRNAVVVITGATSGLGKECAKVFYAAGAKLVLCGRNG
]	j		GALEELIRELTASHATKVQTHKPYLVTFDLTDSGAIVAAAAEIL
-		[	-QCFGYVDILVNNAGISYRGTIMDTTVDVDKRVMETNYFGPVALT
1	1	}	KALLPSMIKRROGHIVAISSIQGKMSIPFRSAYAASKHATQAFF
			DCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDTT
1	1		TAQGRSPVEVAQDVLAAVGKKKKDVILADLLPSLAVYLRTLAPG
			LFFSLMASRARKERKSKNS
5456	2	2332	CGAGLVAAGAVLVLYPASRAGERTRVPGSPAPSSLPLHSPGACG
}			TEVDMDPQRSPLLEVKGNIELKRPLIKAPSQLPLSGSRLKRRPD
			QMEDGLEPEKKRTRGLGATTKITTSHPRVPSLTTVPQTQGQTTA
1		•	QKVSKKTGPRCSTAIATGLKNQKPVPAVPVQKSGTSGVPPMAGG
<u>,</u>			KKPSKRPAWDLKGQLCDLNAELKRCRERTQTLDQENQQLQDQLR
1 1			DAQQQVKALGTERTTLEGHLAKVQAQAEQGQQELKNLRACVLEL
· 1			EERLSTQEGLVQELQKKQVELQEERRGLMSQLEEKERRLQTSEA
-			ALSSSQAEVASLRQETVAQAALLTEREERLHGLEMERRRLHNQL
1			QELKGNIRVFCRVRPVLPGEPTPPPGLLLFPSGPGGPSDPPTRL
			SLSRSDERRGTLSGAPAPPTRHDFSFDRVFPPGSGQDEVFEBIA
1			MLVQSALDGYPVCIFAYGQTGSGKTFTMEGGPGGDPQLEGLIPR
1			ALRHLFSVAQELSGQGWTYSFVASYVEIYNETVRDLLATGTRKG
1 1	•		QGGECEIRRAGPGSEELTVTNARYVPVSCEKEVDALLHLARONR
1 1			AVARTAQNERSSRSHSVFQLQISGEHSSRGLQCGAPLSLVDLAG
1 1			SERLDPGLALGPGERERLRETQAINSSLSTLGLVIMALSNKESH
1 1			VPYRNSKLTYLLQNSLGGSAKMLMFVNISPLEENVSESLNSLRF
1			ASKVEPSVLFGTAQSNRKWKTDPDLCVCVCVCVCVCVCVCVCVCVCVP
5457			MSMYRVRGGRVAGGCFIGWRAPCPRAIK
343/	2	1540	DDFVERRRWTRTTCLVRSPPHVPVCGHACSWNGGSLDPLKGTPA
1 1			LLRSAERLMRKVKKLRLDKENTGSWRSFSLNSEGAERMATTGTP
ł 1			TADRGDAAATDDPAARFQVQKHSWDGLRSIIHGSRKYSGLIVNK
	ł		APHDFQFVQKTDESGPHSHRLYYLGMPYGSRENSLLYSEIPKKV
1 1			RKEALLLLSWKOMLDHFQATPHHGVYSREBELLRERKRLGVFGI
] ]	}		TSYDFHSESGLFLFQASNSLFHCRDGGKNGFMVSPGPGCVSPMK
1 1	1		PLEIKTQCSGPRMDPKICPADPAFFSFINNSDLWVANIETGEER
1 1	j		RLTFCHQGLSNVLDDPKSAGVATFVIQEEFDRFTGYWWCPTASW
j 1			EGSEGLKTLRILYEEVDESEVEVIHVPSPALEERKTDSYRYPRT
t i	ł	i	GSKNPKIALKLAEFQTDSQGKIVSTQEKELVQPFSSLFPKVEYI
]			ARAGWTRDGKYAWAMFLDRPQQWLQLVLLPPALFIPSTENEEQA
5458	6642	4022	ASLCQSCPQECPAVCGVRGGHQRLDQCS
	****	7042	FVPGLREPQWEPAQPSATMSAPSEEEYARLVMEAQPEWLRAEV
t l			KRLSHELAETTREKIQAAEYGLAVLEEKHQLKLQFEELEVDYEA
1 1		1	IRSEMEQLKEAFGQAHTNHKKVAADGESREESLIQESASKEQYY
}		İ	VRKVLELQTELKQLRNVLTNTQSENERLASVAQBLKEINQNVEI
1 1	(	1	QRGRLRDDIKEYKFREARLLQDYSELEEENISLQKQVSVLRQNQ
j j			VEFEGLKHEIKRLEEETEYLNSQLEDAIRLKEISERQLEEALET
	1	ł	LKTEREQKNSLRKELSHYMSINDSFYTSHLHVSLDGLKFSDDAA
	}		EPNNDAEALVNGFEHGGLAKLPLDNKTSTPKKEGLAPPSPSLVS
			DLLSELNISEIQKLKQQLMQMEREKAGLLATLQDTQKQLEHTRG
1	1		SLSEQQEXVTRLTENLSALRRLQASKERQTALDNEKDRDSHEDG
l J	ĺ		DYYEVDINGPEILACKYHVAVAEAGELREQLKALRSTHEAREAQ
1	Į	1	HABEKGRYEAEGQALTEKVSLLEKASRQDRELLARLEKELKKVS
	ļ	j	DVAGETQGSLSVAQDELVTFSEELANLYHHVCMCNNETPNRVML
ļ <b>!</b>	1		DYYREGOGGAGRTSPGGRTSPEARGRRSPILLPKGLLAPEAGRA
	ł	1	DGGTGDSSPSPGSSLPSPLSDPRRBPMNIYNLIAIIRDQIKHLQ
	<del></del>	<u></u>	AAVDRTTELSRORIASQELGPAVDKDKEALMEEILKLKSLLSTK

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine
[	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine.
{	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine.
	to first .	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid residue of	residue of amino acid	S=Serine, T=Threonine, V=Valine,
ļ	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	sedacuce	Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
		<del> </del>	REQITTLRTV:KANKQTAEVALANLKSKYENEKAMVTETMMKLR
1			NELKALKEDAATFSSLRAMFATRCDEYITQLDEMQRQLAAAEDE
ĺ			KKTLNSLLRMAIQQKLALTQRLELLELDHEQTRRGRAKAAPKTK
L	}	·	PATPSVSHTCACASDRAEGTGLANQVFCSEKHSIYCD
5459	316	1262	RGGHRLSGMASNFNDIVKQGYVRIRSRRLGIYQRCWLVFKKASS
Ì		}	KGPKRLEKFSDERAAYFRCYHKVTELNNVKNVARLPKSTKKHAI
ļ			GIYFNDDTSKTFACESDLEADEWCKVLQMECVGTRINDISLGEP
	1		DLLATGVEREQSERFNVYLMPSPNLGCYMGECALOITYEYICLW
1	ł		DVQNPRVKLISWPLSALRRYGRDTTWFTFEAGRMCETGEGLFIF
Į.	İ		QTRDGEAIYQKVHSAALAIAEQHERLLQSVKNSMLQMKMSERAA
			SLSTMVPLPRSAYWQHITRQHSTGQLYRLQDVSSPLKLHRTETF
5460	45	2097	PAYRSEH
	13	2097	RPGCRAGELSTGSRARERVRNRVSAPCGQDSRRCDPEVLRGRSP
1			GLGLAEMPSCGACTCGAAAVRLITSSLASAQRGISGGRIHMSVL GRLGTFETQILQRAPLRSFIETPAYFASKDGISKDGSGDGNKKS
ı			ASEGSSKKSGSGNSGKGGNQLRCPKCGDLCTHVETFVSSTRFVK
1			CEKCHHFFVVLSEADSKKSIIKEPESAAEAVKLAFQQKPPPPPK
			KIYNYLDKYVVGQSFAKKVLSVAVYNHYKRIYNNIPANLRQQAE
			VEKQTSLTPRELEIRRREDEYRFTKLLQIAGISPHGNALGASMO
(			QQVNQQIPQEKRGGEVLDSSHDDIKLEKSNILLLGPTGSGKTLL
,			AQTLAKCLDVPFAICDCTTLTQAGYVGEDIESVIAKLLQDANYN
1			VEKAQQGIVFLDEVDKIGSVPGIHQLRDVGGEGVQQGLLKLLEG
l i			TIVNVPEKNSRKLRGETVQVDTTNILFVASGAFNGLDRIISRRK
1			NEKYLGFGTPSNLGKGRRAAAAADLANRSGESNTHQDIEEKDRL
1		_	LRHVEARDLIEFGMIPEFVGRLPVVVPLHSLDEKTLVQILTEPR
)		·	NAVIPQYQALFSMDKCELNVTEDALKAIARLALERKTGARGLRS IMEKLLLEPMFEVPNSDIVCVEVDKEVVEGKKEPGYIRAPTKES
1 1			SEEEYDSGVEEEGWPRQADAANS
5461	1481	160	INPPPPPKSPCGRARKWRRRRRPGAPEAAVMELPSGPGPERLFD
]			SHRLPGDCFLLLVLLLYAPVGFCLLVLRLFLGIHVFLVSCALPD
1			SVLRRFVVRTMCAVLGLVARQEDSGLRDHSVRVLISNHVTPFDH
1 1	ļ		NIVNLLTTCSTPLLNSPPSFVCWSRGFMEMNGRGELVESLKRFC
] [	ŀ		ASTRLPPTPLLLFPEEEATNGREGLLRFSSWPFSIQDVVQPLTL
1 1			QVQRPLVSVTVSDASWVSELLWSLFVPFTVYQVRWLRPVHRQLG
}	İ		EANBEFALRVQQLVAKELGQTGTRLTPADKAEHMKRQRHPRLRP
	1		QSAQSSFPPSPGPSPDVQLATLAQRVKEVLPHVPLGVIQRDLAK
1 1			TGCVDLTITNLLEGAVAFMPEDITKGTQSLPTASASKFPSSGPV TPQPTALTFAKSSWARQESLQERKQALYEYARRRFTERRAQEAD
5462	663	3353	KIKERQMSANNSPPSAQKSVLPTAIPAVLPAASPCSSPKTGLSA
1 1	ì		RLSNGSFSAPSLTNSRGSVHTVSFLLQIGLTRESVTIEAQELSL
Į ļ	}		SAVKDLVCSIVYQKFPECGFFGMYDKILLFRHDMNSENILQLIT
] [			SADEIHEGDLVEVVLSALATVEDFQIRPHTLYVHSYKAPTFCDY
1	1		CGEMLWGLVRQGLKCEGCGLNYHKRCAFKIPNNCSGVRKRRLSN
J t			VSLFGPGLSVPRPLQPEYVALPSEESHVHOEPSKRIPSWSGRPI
		Į	WMEKMVMCRVKVPHTFAVHSYTRPTICQYCKRLLKGLFRQGMQC
			KDCKFNCHKRCASKVPRDCLGEVTFNGEPSSLGTDTDIPMDIDN
		į	NDINSDSSRGLDDTEEPSPPEDKMFFLDPSDLDVERDEEAVKTI
	1	l	SPSTSNNIPLMRVVQSIKHTKRKSSTMVKEGWMVHYTSRDNLRK
			RHYWRLDSKCLTLFQNESGSKYYKEIPLSEILRISSPRDFTNIS QGSNPHCFEIITDTMVYFVGENNGDSSHNPVLAATGVGLDVAQS
			WEKAIRQALMPVTPQASVCTSPGQGKDHKDLSTSISVSNCQIQE
	)	ļ	NVDISTVYQIFADEVLGSGQFGIVYGGKHRKTGRDVAIKVIDKM
Ì	Į.	İ	RFPTKQESQLRNEVAILQNLHHPGIVNLECMFETPERVFVVMEK
- 1	1	Ì	LHGDMLEMILSSEKSRLPERITKFMVTQILVALRNLHFKNIVHC
	l		DLKPENVLLASAEPFPQVKLCDFGFARIIGEKSFRESVVGTPAY
	1	İ	LAPEVLRSKGYNRSLDMWSVGVIIYVSLSGTFPFNEDEDINDOI
1	1	}	QNAAFMYPPNPWREISGEAIDLINNLLQVKMRKRYSVDKSLSHP
	. }		WLQDYQTWLDLREFETRIGERYITHESDDARWEIHAYTHNLVYP
5463	237		KHPIMAPNPDDMEEDP
5403	231	1012	LLSVTMTTSRCSHLPEVLPDCTSSAAPVVKTVEDCGSLVNGQPQ
			YVMQVSAKDGQLLSTVVRTLATQSPFNDRPMCRICHEGSSQEDL

SEO	Predicted	( Barada - 1 - 1	
ID	beginning	Predicted end	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location		Glutamic Acid, F=Phenylalanine, G=Glycine,
1	corresponding	corresponding to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
İ	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
}	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i	sequence	sequence	Codon, /-possible nucleotide deletion,
ļ	- Judguecc	<del> </del>	\=possible nucleotide insertion)
ļ	}		LSPCECTGTLGTIHRSCLEHWLSSSNTSYCELCHFRFAVERKPR
<b>.</b>	ĺ		PLVEWLRNPGPQHEKRTLFGDMVCFLFITPLATISGWLCLRGAV
	ļ	1	DHLHFSSRLEAVGLIALTVALFTIYLFWTLVSFRYHCRLYNEWR
5464	195		RTNQRVILLIPKSVNVPSNQPSLLGLHSVKRNSKETVV
3401	135	677	SPSMNPRKKVDLKLIIVGAIGVGKTSLLHQYVHKTFYEEYQTTL
}		ł	GASILSKIIILGDTTLKLQIWDTGGQERVRSMVSTFYKGSDGCI
1			LAFDVTDLESFEALDIWRGDVLAKIVPMEQSYPMVLLGNKIDLA
5465			DRKYQSILENHLTESIKLSPDQSRSRCC
3463	5278	3348	KGDPREFIRVHREALECDYVSAHLHEWIDLIFGYKQQGPAAVEA
ı		į	VNVFHHLFYEGQVDIYNINDPLKETATIGFINNFGQIPKQLFKK
i			PHPPKRVRSRLNGDNAGISVLPGSTSDKIFFHHLDNLRPSLTPV
ł .	1	i	KELKEPVGQIVCTDKGILAVEQNKVLIPPTWNKTFAWGYADLSC
1	j		RLGTYESDKAMTVYECLSEWGQILCAICPNPKLVITGGTSTVVC
			VWEMGTSKEKAKTVTLKQALLGHTDTVTCATASLAYHIIVSGSR
1	1		DRTCIIWDLNKLSFLTQLRGHRAPVSALCINELTGDIVSCAGTY
J	1		IHVWSINGNPIVSVNTFTGRSQQIICCCMSEMNEWDTONVIVTG
			HSDGVVRFWRMEFLQVPETFAPEPAEVLEMQEDCPEAQIGQEAQ
1			DEDSSDSRADEQSISQDPKDTPSQPSSTSHRPRAASCRATAAWC
1			TDSGSDDSRRWSDQLSLDEXDGFIFVNYSEGQTRAHLOGPLSHP
			HPNPIEVRNYSRLKPGYRWERQLVFRSKLTMHTAFDRKDNAHFA
Ì			EVTALGISKDHSRILVGDSRGRVFSWSVSDQPGRSAADHWVKDE
1 .	,		GGDSCSGCSVRFSLTERRHHCRNCGQLFCQKCSRFQSEIKRLKI
5466			SSPVRVCQNCYYNLQHERGSEDGPRNC
5466	3	992	HACAHASAHASGRLVRWWRKRRSVMGIQTSPVLLASLGVGLVTL
1			LGLAVGSYLVRRSRRPQVTLLDPNEKYLLRLLDKTTVSHNTKRF
1			RFALPTAHHTLGLPVGKHIYLSTRIDGSLVIRPYTPVTSDEDOG
1			YVDLVIKVYLKGVHPKFPEGGKMSQYLDSLKVGDVVEFRGPSGL
1			LTYTGKGHFNIQPNKKSPPEPRVAKKLGMIAGGTGITPMLOLIR
ļ .		·	AILKVPEDPTQCFLLFANQTEKDIILREDLEELQARYPNRFKLW
í i			FTLDHPPKDWAYSKGFVTADMIREHLPAPGDDVLVLLCGPPPMV
H			QLACHPNLDKLGYSQKMRFTY
5467	2103	4	GEALRYGTRGCRRDLPDPQARIFIQKKDLEEDESVTAAHLKSRG
1			RSPRKIDQFCNSSNMVHGSVTFRDVAIDFSOBEWECLOPDORTI,
1 1	1		YRDVMLENYSHLISLAGSSISKPDVITLLEQBKEPWMVVRKETS
]			RRYPDLELKYGPEKVSPENDTSEVNLPKQVIKQISTTLGIEAFY
1 1	ĺ		FRNDSEYRQFEGLQGYQEGNINQKMISYEKLPTHTPHASLICHT
1 1	1		HKPYECKECGKYFSCGSNLIQHQSIHTGEKPYKCKECGKAFOLH
1			IQLTRHQKFHTGEKTFECKECGKAFNLPTQLNRHKNIHTVKKLF
1 1			ECKECGKSFNRSSNLTQHQSIHAGVKPYOCKECGKAFNRGSNLT
i i	ł		QHQKIHSNEKPFVCKECGMAFRYHYQLIEHCQIHTGEKPFECKE
1 1			CGKAFTLLTKLVRHQKIHTGEKPFECRECGKAFSLLNOLNRHKN
	Į		IHTGEKPFECKECGKSFNRSSNLVQHQSIHAGIKPYECKECGKG
1			FNRGAHLIQHQKIHSNEKPFVCRECEMAFRYHCQLIEHSRIHTG
[			DKPFECQDCGKAFNRGSSLVQHQSIHTGEKPYECKECGKAFRLY
1			LQLSQHQKTHTGEKPFECKECGKFFRRGSNLNOHRSIHTGKKPF
1 1			ECKECGKAFRLHMHLIRHQKLHTGEKPFECKECGKAFRLHMQLI
			RHOKLHTGEKPFECKECGKVFSLPTQLNRHKNIHTGEKAS
5468	225	2976	SFLTDLFQSLAQLENLCKQLYETTDTTTRLQAEKALVEFTNSPD
1	İ	İ	CLSKCQLLLERGSSSYSQLLAATCLTKLVSRTNNPLPLEQRIDI
	1	J	RNYVLNYLATRPKLATFVTQALIQLYARITKLGWFDCQKDDYVF
	1		RNAITDVTRFLQDSVEYCIIGVTILSQLTNEINQVSATAFLIEA
	1		DTTHPLTKHRKIASSFRDSSLFDIFTLSCNLLKQASGKNLNLND
	1		ESQHGLLMQLLKLTHNCLNFDFIGTSTDESSDDLCTVQIPTSWR
1	1	į	SAFLDSSTLQLSTIGRCEYEKTCALLVQLFDQSAQSYQELLQSA
	1	1	SASPMDIAVQEGRLTWLVYIIGAVIGGRVSFASTDEQDAMDGEL
1		J	VCRVLQLMNLTDSRLAQAGNEKLELAMLSFFEQFRKIYIGDQVQ
ŀ		1	KSSKLYRRLSEVLGLNDETMVLSVFIGKIITNLKYWGRCEPITS
i	<u> </u>	l	KTLOLLNDLSIGYSSVRKLVKLSAVQFMLNNHTSEHFSFLGINN
i			QSNLTDMRCRTTFYTALGRLLMVDLGEDEDQYEQFMLPLTAAFE
1			AVAQMFSTNSFNBQEAKRTLVGLVRDLRGIAFAFNAKTSFMMLF
		ĺ	EWIYPSYMPILQRAIELWYHDPACTTPVLKLMAELVHNRSQRLQ
	<del></del>	<u></u>	

SEQ	Predicted	Predicted end	Dmino pold second second
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ł	location	corresponding	H-Histidine, I-Isoleucine, K-Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	1	\=possible nucleotide insertion)
			FDVSSPNGILLFRETSKMITNYGNRILTLGEVPKDQVYALKLKG
ļ.			ISICFSMLKAALSGSYVNFGVFRLYGDDALDNALQTFIKLLLSI
			PHSDLLDYPKLSQSYYSLLEVLTODHMNFIASLEPHVIMYTLSS
ł	1	}	ISEGLTALDTMVCTGCCSCLDHIVTYLFKOLSRSTKKRTTPLNO
ļ			ESDRFLHIMQQHPEMIQQMLSTVLNIIIFEDCRNOWSMSRPLLG
ŀ			LILLNEKYFSDLRNSIVNSQPPEKQQAMHLCFENLMEGIERNLL
			TKNKDRFTQNLSAFRREVNDSMKNSTYGVNSNDMMS
5469	134	2653	DQEFETSLVPWHLPMGWLCSGLLFPVSCLVLLQVASSGNMKVLQ
ł	1		EPTCVSDYMSISTCEWKMNGPTNCSTELRLLYOLVFLLSEAHTC
[	(		VPENNGGAGCVCHLLMDDVVSADNYTLDLWAGQOLLWKGSFKPS
i	ì		EHVKPRAPGNLTVHTNVSDTLLLTNSNPYPPDNYLYNHLTYAVN
1	1		IWSENDPADFRIYNVTYLEPSLRIAASTLKSGISYRARVRAWAQ
			CYNTTWSEWSPSTKWHNSYREPFEQHLLLGVSVSCIVILAVCLL
[			CYVSITKIKKEWWDQIPNPARSRLVAIIIQDAQGSQWEKRSRGQ
ì			EPAKCPHWKNCLTKLLPCFLEHNMKRDEDPHKAAKEMPFQGSGK
J			SAWCPVEISKTVLWPESISVVRCVELPEAPVECEEEEEVEEEKG
{			SFCASPESSRDDFQEGREGIVARLTESLFLDLLGEENGGFCQQD
Ĭ			MGESCLLPPSGSTSAHMPWDEFPSAGPKEAPPWGKEQPLHLEPS
ì	}		PPASPTQSPDNLTCTETPLVIAGNPAYRSPSNSLSQSPCPRELG
j			PDPLLARHLEEVEPEMPCVPQLSEPTTVPQPEPETWEQILRRNV
			LQHGAAAAPVSAPTSGYQEFVHAVEQGGTQASAVVGLGPPGEAG
1			YKAFSSLLASSAVSPEKCGFGASSGEEGYKDFQDLIPGCPGDPA PVPVPLFTFGLDREPPRSPQSSHLPSSSPEHLGLEPGEKVEDMP
1			KPPLPQEQATDPLVDSLGSGIVYSALTCHLCGHLKQCHGQEDGG
			QTPVMASPCCGCCCGDRASPPTTPLRAPDPSPGGVPLEASLCPA
			SLAPSGISEKSKSSSFHPAPGNAQSSSQTPKIVNFVSVGPTYM
1 1	1		RVS
5470	17	1418	TACRIRTSLNRGIAAVKRDAVEMLASYGLAYSLMKFFTGPMSDF
1			KNVGLVFVNSKRDRTKAVLCMVVAGAIAAVFHTLIAYSDLGYYI
1			INKLHHVDESVGSKTRRAFLYLAAFPFMDAMAWTHAGILLKHKY
1			SFLVGCASISDVIAQVVFVAILLHSHLECREPLLIPILSLYMGA
1 '	j		LVRCTTLCLGYYKNIHDIIPDRSGPELGGDATIRKMLSFWWPLA
1 1			LILATQRISRPIVNLFVSRDLGGSSAATEAVAILTATYPVGHMP
	1		YGWLTEIRAVYPAFDKNNPSNKLVSTSNTVTAAHIKKFTFVCMA
1 1	}		LSLTLCFVMFWTPNVSEKILIDIIGVDFAFAELCVVPLRIFSFF
)	•		PVPVTVRAHLTGWLMTLKKTFVLAPSSVLRIIVLIASLVVLPYL
			GVHGATLGVGSLLAGFVGESTMDAIAACYVYRKQKKKMENESAT
5471	1000		EGEDSAMTOMPPTEEVTDIVEMREENE
54/1	1868	658	RSSAPPGPORAAAATAAAAAGVEMAAAAAQGGGGGEPRRTEGV
1 1	ļ	· ·	GPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAYDHVR
1 1			KTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILR
	ł		ASTLEAMRDVYIVQDLMETDLYKLLKSQQLSNDHICYFLYQILR
1			GLKYIHSANVLHRDLKPSNLLINTTCDLKICDFGLARIADPEHD
]		i	HTGFLTEYVATRWYRAPEINLNSKGYTKSIDIWSVGCILAEMLS
! !			NRPIFPGKHYLDQLNHILGILGSPSQEDLNCIINMKARNYLQSL
1	}		PSKTKVAWAKLFPKSDSKALDLLDRMLTFNPNKRITVEEALAHP
	ļ		YLEQYYDPTDEPVAEEPFTFAMELDDLPKERLKELIFQETARFQ PGVLEAP
5472	1469	753	
		, , , ,	LYVMARYLSDEEVAVSIDRLCKANGRSPSIPFGTVRIPGRARVR DPQALWIFGYGSLVWRPDFAYSDSRVGFVRGYSRRFWQGDTFHR
	ļ		GSDKMPGRVVTLLEDHEGCTWGVAYQVQGEQVSKALKYLNVREA
			VLGGYDTKEVTFYPQDAPDQPLKALAYVATPQNPGYLGPAPEEA
			IATQILACRGFSGHNLEYLLRVRDVMQLCGPQAQDEHLAAIVDA
	1		VGTMLPCFCPTEQALALV
5473	3	2119	FMNVKLLIQDLEDIEQRVPVMDAQYKIITKTAHLITKESPQEEG
]	ļ		KEMFATMSKLKEQLTKVKECYSPLLYESQQLLIPLBELEKQMTS
	}		FYDSLGKINEIITVLEREAQSSALFKQKHQELLACQENCKKTLT
' I		1	LIEKGSQSVQKFVTLSNVLKHFDQTRLQRQIADIHVAFQSMVKK
-		ļ	TGDWKKHVETNSRLMKKFEESRAELEKVLRIAQEGLEEKGDPEE
}			LLRRHTEFFSQLDQRVLNAFLKACDELTDILPEGEGGGLORAUR
			KLHKQWKDLQGEAPYHLLHLKIDVEKNRFLASAEECRTELDRET

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	1	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
[		corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine.
	amino acid	residuc of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence	_	\=possible nucleotide insertion)
			KLMPQEGSEKIIKEHRVFFSDKGPHHLCEKRLQLIBELCVKLPV
· ·			RDPVRDTPGTCHVTLKELRAAIDSTYRKLMEDPDKWKDYTSRFS
İ		{	EPSCHICTMETOL VOLVORA TRESPONDENCE DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DEL CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DEL CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DEL CONTRETA DE LA CONTRETA DE LA CONTRETA DEL CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DEL CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DEL CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRET
i	i	Ì	EFSSWISTNETQLKGIKGEAIDTANHGEVKRAVEEIRNGVTKRG
1	}	}	ETLSWLKSRLKVLTEVSSENEAQKQGDELAKLSSSFKALVTLLS
	ł		EVEKMLSNFGDCVQYKEIVKNSLEELISGSKEVQEQABKILDTE
i			NLFEAQQLLLHHQQKTKRISAKKRDVQQQIAQAQQGEGGLPDRG
ļ	}	]	HEELRKLESTLDGLERSRERQERRIQVTLRKWERFETNKETVVR
	[		YLFQTGSSHERFLSFSSLESLSSELEQTKEFSKRTESIAVQAEN
1	Ĭ		LVKEASEIPLGPQNKQLLQQQAKSIKEQVKKLEDTLEBEYVIDK
			S
5474	2	780	TPDVRQLQASRRGIAVASWCSPRWFAGEEMAFVKSGWLLRQSTI
			LKRWKKNWFDLWSDGHLIYYDDQTRQNIEDKVHMPMDCINIRTG
1			QECRDTQPPDGKSKDCMLQIVCRDGKTISLCAESTDDCLAWKFT
-			LQDSRTNTAYVGSAVMTDETSVVSSPPPYTAYAAPAPEVGRTLS
1			LOGAVGYCDYGGAYDDGTGYTTAYAAAAAAAADEVGRTLS
			LQQAYGYGPYGGAYPPGTQVVYAANGQAYAVPYQYPYAGLYGQQ
5475	2	506	PANQVIIRERYRDNDSDLALGMLAGAATGMALGSLFWVF
	<b>'</b> 1	306	ARGWLESLSLTCQTTPPPSSPCLLHSPZTFIHTMPPNLTGYYRF
1 1			VSQKNMEDYLQALNISLAVRKIALLLKPDKEIEHQGNHMTVRTL
	·		STFRNYTVQFDVGVEFEEDLRSVDGRKCQTIVTWEEEHLVCVQK
5476			GEVPNRGWRHWLEGEMLYLELTARDAVCEQVPRKVR
34/6	192	1457	SDSMSLLDCFCTSRTQVESLRPEKQSETSIHQYLVDEPTLSWSR
1 1			PSTRASEVLCSTNVSHYELQVEIGRGFDNLTSVHLARHTPTGTL
1			VTIKITNLENCNEERLKALQKAVILSHFFRHPNITTYWTVFTVG
1			SWLWVISPFMAYGSASQLLRTYFPEGMSETLIRNILFGAVRGLN
1 1			YLHQNGCIHRSIKASHILISGDGLVTLSGLSHLHSLVKHGQRHR
] ]			AVYDFPQFSTSVQPWLSPELLRQDLHGYNVKSDIYSVGITACEL
1	1		ASGOVPFQDMHRTQMLLQKLKGPPYSPLDISIFPQSESRMKNSQ
	· · ·	•	SCALLECT CECAT ACCULATION TO SERVICE SCALLES
	1		SGVDSGIGESVLVSSGTHTVNSDRLHTPSSKTFSPAFFSLVQLC
1 1	<i>'</i>	•	LQQDPEKRPSASSLLSHVFFKQMKEESQDSILSLLPPAYNKPSI
5477	3	1044	SLPPVLPWTEPECDFPDEKDSYWEF
	· · · · · · · · · · · · · · · · · · ·	1033	RGNSRLRYSHEDELQLPRLPELFETGRQLLDEVEVATEPAGSRI
1 1	{		VQEKVFKGLDLLEKAAEMLSQLDLFSRNEDLEEIASTDLKYLLV
1 1	1		PAFQGALTMKQVNPSKRLDHLQRAREHFINYLTQCHCYHVAEFE
1 ]	ŀ		LPKTMNNSAENHTANSSMAYPSLVAMASQRQAKIQRYKQKKELE
]			HRLSAMKSAVESGOADDERVREYYLLHLORWIDISLEETESTDO
			EIKILRERDSSREASTSNSSRQERPPVKPFILTRNMAQAKVFGA
ļ j			GYPSLPTMTVSDWYEQHRKYGALPDOGIAKAAPREFRKAAOOOF
L			EQEEKEEEDDEQTLHRAREWDDWKDTHPRGYGNRQNMG
5478	2	835	KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT
1	j		VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK
j l			LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW
į f	i		DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL
ļ l	ł:		MEGRILLYTLHCHQGPATTVAFSRTGEYFASGGSDEQVMVWKSNF
] 1	1		DIGDHGEVTKUDDDDATIACOMONTONIONIONIONIONIONIONIONIONIONIONIONIONIO
[	1	1	DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC
5479	2	835	LENQQLIMQRATP
į l	-	633	KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT
	Í	1	VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK
	1		LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW
			DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDI.
		ł	MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDEOVMVWKSNF
		l	DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC
			LENQQLIMQRATP
5480	444	1952	LSLTSRMEEAELVKGRLQAITDKRKIQEEISQKRLKIEEDKLKH
1			QHLKKKALREKWLLDGISSGKEQEEMKKQNQQDQHQIQVLEQSI
]	1		LRLEKEIQDLEKAELQISTKEEAILKKLKSIERTTEDIIRSVKV
l l			PPEPDAEPCIEDTVANIED BY BY CHERT TEDI IRSVKV
- 1	1	1	EREERAEESIEDIYANIPDLPKSYIPSRLRKEINEEKEDDEONR
	İ	1	KALYAMEIKVEKDLKTGESTVLSSIPLPSDDFKGTGIKVYDDGQ
1		1	KSYYAVSSNHSAAYNGTDGLAPVEVEELLRQASERNSKSPTEYH
i	1	1	EPVYANPFYRPTTPQRETVTPGPNFQERIKIKTNGLGIGVNESI
			HNMGNGLSEERGNNFNHISPIPPVPHPRSVIQOAEEKLHTPQKR

SEQ	Predicted	Predicted end	I hmino poid
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, R=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
[	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
-	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
l	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
ŀ	sequence	-	\=possible nucleotide insertion)
			LMTPWEESNVMQDKDAPSPKPRLSPRETIFGKSEHQNSSPTCQE
ſ	1	}	DEEDVRYNIVHSLPPDINDTEPVTMIFMGYQQAEDSEEDKKFLT
		j	GYDGIIHAELVVIDDEEEEDEGEAEKPSYHPIAPHSQVYQPAKP
		}	TPLPRKRSEASPHEKHKS
5481	3	1422	NSPGSVCLCQCVCPSLLHCLPPLLLLLLLLLLLLHESPQPPALRV
1	]	}	VATSSDRNFMNKHQKPVLTGQRFKTRKRDEKEKFEPTVFRDTLV
			QGLNEAGDDLEAVAKFLDSTGSRLDYRRYADTLFDILVAGSMLA
i	1		PGGTRIDDGDKTKMTNHCVFSANEDHETIRNYAQVFNKLIRRYK
1			YLEKAFEDEMKKLLLFLKAFSETEOTKLAMLSGILLGNGTLPAT
i	!		ILTSLFTDSLVKEGIAASFAVKLFKAWMAEKDANSVTSSLRKAN
1			LDXRLLELPPVNRQSVDHFAKYFTDAGLKELSDFLRVOOSLGTR
]	]		KELQKELQERLSQECPIKEVVLYVKEEMKRNDLPETAVIGLLWT
			CIMNAVEWNKKEELVAEQALKHLKQYAPLLAVFSSOGOSELILL
1			QKVQEYCYDNIHFMKAFQKIVVLFYKADVLSEEAILKWYKEAHV
5482	3.465		akgksvfldqmkkfvewlqnabeesesegeen
3402	1492	528	THVVMTGMCYAPHQVLSYINGVTTSKPGVSLVYSMPSRNLSLRL
1	'		EGLQEKDSGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPS
] :	ļ.		CRLQGVPHVGANVTLSCQSPRSKPAVQYQWDRQLPSFQTFFAPA
			LDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLEVSTGP
1			GAAVVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDA
}			IAPRTLPWPKSSDTISKNGTLSSVTSARALRPPHGPPRPGALTP
1 1			TPSLSSQALPSPRLPTTDGAHPQPISPIPGGVSSSGLSRMGAVP VMVPAQSQAGSLV
5483	1	788	FFFFKGCRAGRGNESDYRKLEEMHQRFLVSERSKDDLQLRLTRA
	·	, ,,,,	ENRIKQLETDSSEEISRYQEMIQKLQNVLESERENCGLVSEQRL
			KLQQENKQLRKETESLRKIALEAQKKAKVKISTMEHEFSIKERG
1 1			FEVOLREMEDSNRNSIVELRHLLATQQKAANRWKEETKKLTESA
	j		RIRINNLKSELSROKLHTQELLSQLEMANEKVAENEKLILEHOE
			KANRLORRLSQAEERAASASQOLSVITVQRRKAASLMNLENI
5484	3	1997	IMADMEDLFGSDADSEAERKDSDSGSDSDSDOENAASGSNASGS
1 1			ESDQDERGDSGQPSNKELFGDDSEDEGASHHSGSDNHSERSDNR
[ ]	ľ		SEASERSDHEDNDPSDVDQHSGSEAPNDDEDEGHRSDGGSHHSE
1 1	1		AEGSEKAHSDDEKWGREDKSDQSDDEKIQNSDDEERAQGSDEDK
1 1	į		LQNSDDDEKMQNTDDEERPQLSDDERQQLSEEEXANSDDERPVA
1 1	1		SDNDDEKQNSDDEEQPQLSDEEKMQNSDDERPQASDEEHRHSDD
1 1	1		EEEQDHKSESARGSDSEDEVLRMKRKNAIASDSEADSDTEVPKD
1 1			NSGTMDLFGGADDISSGSDGEDKPPTPGQPVDENGLPQDQQEEE
1. 1			PIPETRIEVEIPKVNTDLGNDLYFVKLPNFLSVEPRPFDPQYYE
1			DEFEDEEMLDEEGRTRLKLKVENTIRWRIRRDEEGNEIKESNAR
1 1			IVKWSDGSMSLHLGNEVFDVYKAPLQGDHNHLFIRQGTGLQGQA
}			VFKTKLTFRPHSTDSATHRKMTLSLADRCSKTQKIRILPMAGRD PECQRTEMIKKEEERLRASIRRESQQRRMREKQHQRGLSASYLE
1 1	1		PDRYDEEEEGEESISLAAIKNRYKGGIREERARIYSSDSDEGSE
} }	1	į	EDKAQRLLKAKKLTSDEVRPNLFNSRGLSCTQEPTALNEELTDQ
			AGTN
5485	161	1074	KRKILSSMMDSEAHEKRPPILTSSKQDISPHITNVGEMKHYLCG
	1	1	CCAAFNNVAITFPIQKVLFRQQLYGIKTRDAILQLRRDGFRNLY
1			RGILPPLMQKTTTLALMFGLYEDLSCLLHKHVSAPEFATSGVAA
1	Į.	{	VLAGTTEAIFTPLERVQTLLQDHKHHDKFTNTYQAFKALKCHGI
	1	j	GEYYRGLVPILFRNGLSNVLPFGLRGPIKEHLPTATTHSAHLVN
			DFICGGLLGAMLGFLFFPINVVKTRIQSQIGGEFOSFPKVFQKI
F405			WLERDRKLINLFRGAHLNYHRSLISWGIINATYEFLLKVI
5486	1404	142	IPGSTISWSPAAARGLSVCRCCRLHPASAMDLFGDLPEPERSPR
			PAAGKEAQKGPLLFDDLPPASSTDSGSGGPLLFDDLPPASSGDS
1		i	GSLATSISQMVKTEGKGAKRKTSEEEKNGSEELVEKKVCKASSV
·		J	IFGLKGYVAERKGEREEMQDAHVILNDITEECRPPSSLITRVSY
į			FAVFDGHGGIRASKFAAQNLHONLIRKFPKGDVISVEKTVKRCI.
		1	LDTFKHTDEEFLKQASSQKPAWKDGSTATCVLAVDNILYIANLG
		1	DSRAILCRYNEBSQKHAALSLSKEHNPTQYEERMRIQKAGGNVR
	<u>-</u> -		DGRVLGVLEVSRSIGDGQYKRCGVTSVPDIRRCQLTPNDRFILL

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location		
		corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
Í	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
}	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence	-	\=possible nucleotide insertion)
	1		ACDGLFKVFTPBEAVNFILSCLEDEKIQTREGKSAADARYEAAC
1			NRLANKAVQRGSADNVTVMVVRIGH
5487	535	182	AVSLEQIRGLQTPAPVPLPLQPCPSNCDMERVTLALLLLAGLTA
	i		LEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGK
1		į	CKCKSSQKQHSPVPEKAIPLITPGSATTC
5488	1072	259	AMAASGEPQRQWQEEVAAVVVVGSCMTDLVSLTSRLPKTGETIH
1 3400	10/2	239	
1			GHKFFIGFGGKGANQCVQAARLGAMTSMVCKVGKDSFGNDYIEN
	i		LKQNDISTEFTYQTKDAATGTASIIVNNEGQNIIVIVAGANLLL
1	(		NTEDLRAAANVISRAKVMVCQLEITPATSLEALTMARRSGVKTL
}			FNPAPAIADLDPQFYTLSDVFCCNESEAEILTGLTVGSAADAGE
			AALVLLKRGCQVVIITLGAEGCVVLSQTEPEPKHIPTEKVKAVD
	L		TTVSFKI
5489	81	893	GKGPVAAFIDQSNIFLTDPKIFLGQWREEPKMPLLLLGETEPLK
1	1		LERDCRSPVEPWAAASPDLALACLCHCQDLSSGAFPNRGVLGGV
1	1		LFPTVEMVIKVFVATSSGSIAIRKKQQEVVGFLEANKIDFKELD
1	1		IAGDEDNRRWMRENVPGEKKPQNGIPLPPQIFNEEQYCGDFDSF
{			FSAKEENIIYSFLGLAPPPDSKGSEKAEEGGETEAOKEGSEDVG
}			NLPEAQEKNEEEGETATBETEEIAMEGAEGEAEEEEETAEGEEP
1			GEDEDS
5490	81	003	
3430	9.1	893	GKGPVAAFIDQSNIFLTDPKIFLGQWREEPKMPLLLLGETEPLK
i			LERDCRSPVERWAAASPDLALACLCHCQDLSSGAFPNRGVLGGV
1	,		LFPTVEMVIKVFVATSSGSIAIRKKQQBVVGFLEANKIDFKELD
1			IAGDEDNRRWMRENVPGBKKPQNGIPLPPQIFNEEQYCGDFDSF
1	ĺ		FSAKEENIIYSFLGLAPPPDSKGSEKAEEGGETEAQKEGSEDVG
	J .		NLPBAQEKNEBEGETATEETEEIAMEGAEGEAEEEEETAEGEEP
i			GEDBDS
5491	204	1194	GSAPRLSLGPTGAQARDPDWWARPPSRPYTQSKEDRPDTEGRSE
			QGDMASSFLPAGAITGDSGGELSSGDDSGEVEFPHSPEIEETSC
			LAELFEKAAAHLQGLIQVASREQLLYLYARYKQVKVGNCNTPKP
		ŀ	SFFDFEGKQKWBAWKALGDSSPSQAMQEYIAVVKKLDPGWNPQI
1 .			PEKKGKEANTGFGGPVISSLYHEETIREEDKNIFDYCRENNIDH
1	!		ITKAIKSKNVDVNVKDEEGRALLHWACDRGHKELVTVLLOHRAD
1			INCODNEGOTALHYASACEFLDIVELLLQSGADPTLRDQDGCLP
			l
5492	-	1000	EEVTGCKTVSLVLQRHTTGKA
1 3474	3	1896	ASKNPLSAVCTTGIMSSLAVRDPAMDRSLRSVFVGNIPYEATEE
[	ĺ		QLKDIFSEVGSVVSFRLVYDRETGKPKGYGFCEYQDQETALSAM
1			RNLNGREFSGRALRVDNAASEKNKEELKSLGPAAPIIDSPYGDP
1			IDPEDAPESITRAVASLPPEQMFELMKQMKLCVQNSHQEARNML
1	†		LQNPQLAYALLQAQVVMRIMDPEIALKILHRKIHVTPLIPGKSQ
j l			SVSVSGPGPGPGPGLCPGPNVLLNQQNPPAPQPQHLARRPVKDI
1			PPLMQTPIQGGIPAPGPIPAAVPGAGPGSLTPGGAMQPQLGMPG
1			VGPVPLERGQVQMSDPRAPIPRGPVTPGGLPPRGLLGDAPNDPR
]	1		GGTLLSVTGEVEPRGYLGPPHQGPPMHHASGHDTRGPSSHEMRG
	. <b>i</b>		GPLGDPRLLIGEPRGPMIDQRGLPMDGRGGRDSRAMETRAMETE
į į	·		VLETRVMERRGMETCAMETRGMEARGMDARGLEMRGPVPSSRGP
1 1			MTGGIQGPGPINIGAGGPPQGPRQVPGISGVGNPGAGMQGTGIQ
			GTGMQGAGIQGGGMQGAGIQGVSIQGGGIQGGGIQGASKQGGSQ
] !			
} I			PSSFSPGQSQVTPQDQEKAALIMQVLQLTADQIAMLPPEQRQSI LILKEQIOKSTGAS
5493	<del></del> ,		
65.50	1	1876	RAPMMTKAVPEEPRKPGRLTQALNSPLTWEHVWICVPGGTPDCL
, ,			TDTFRVKRPHLRRSASNGHVPGTPVYREKEDMYDEIIELKKSLH
]			VQKSDVDLMRTKLRRLEEENSRKDRQIEQLLDPSRGTDFVRTLA
]	Ī		EKRPDASWVINGLKQRILKLEQQCKEKDGTISKLQTDMKTTNLE
}	ł		EMRIAMETYYEEVHRLQTLLASSETTGKKPLGEKKTGAKRQKKM
<b> </b>			GSALLSLSRSVQELTEENQSLKEDLDRVLSTSPTISKTQGYVEW
( l	1		SKPRLLRRIVELEKKLSVMESSKSHAAEPVRSHPPACLASSSAL
j	ļ		HROPRODRNKDHERLRGAVRDLKEERTALQEQLLORDLEVKOLL
į į	1	İ	QAKADLEKBLECAREGEEERREREVLREEIQTLTSKLQELQEM
	į	ļ	
	i	ì	KKEEKEDCPEVPHKAQELPAPTPSSRHCEQDWPPDSSBEGLPRP
] !	1		RSPCSDGRRDAAARVLQAQWKVYKHKKKKAVLDEAAVVLQAAFR

SEQ	Predicted	Predicted end	Amino acid goment containing
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, R=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
- [	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valinc,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
j	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	1	\=possible nucleotide insertion)
1		1	GHLTRTKLLASKAHGSEPPSVPGLPDQSSPVPRVPSPIAQATGS
1	1	ļ	PVQEEAIVIIQSALRAHLARARHSATGKRTTTAASTRRRSASAT
i			HGDASSPPFLAALPDPSPSGPQAVAPLPGDDVNSDDSDDIVIAP
			SLPTKNFPV
5494	71	536	RSKAKIGTPTREVPSTDMKVRRESSSSLTHRPAPSPATPRLLGT
ł			RRVLLGVSEGTGCADAMELVLVFLCSLLAPMVLASAAEKEKEMD
			PFHYDYQTLRIGGLVFAVVLFSVGILLILSRRCKCSFNQKPRAP
	<u> </u>		GDEEAQVENLITANATEPQKAEN
5495	273	2168	DSLLLIQVDTMPFTLHLRSRLPSAIRSLILQKKPNIRNTSSMAG
i			ELRPASLVVLPRSLAPAFERFCQVNTGPLPLLGOSEPEKWMLPP
ł			QGAISETRMGHPQFWKYEFGACTGSLASLEOYSEOLKDMVAFFI.
l l	j		GCSFSLEEALEKAGLPRRDPAGHSQAGAYKTTVPCVTHAGFCCP
	·		LVVTMRPIPKDKLEGLVRACCSLGGEQGQPVHMGDPELLGIKEL
1	}		SKPAYGDAMVCPPGEVPVFWPSPLTSLGAVSSCETPLAFASIPG
}			CTVMTDLKDAKAPPGCLTPERIPEVHHISQDPLHYSIASVSASQ
}	!		KIRELESMIGIDPGNRGIGHLLCKDELLKASLSLSHARSVLITT
	1		GFPTHFNHEPPEETDGPPGAVALVAFLQALEKEVAIIVDQRAWN
1	ļ		LHQKIVEDAVEQGVLKTQIPILTYQGGSVEAAQAFLCKNGDPQT
			PRFDHLVAIERAGRAADGNYYNARKMNIKHLVDPIDDLFLAAKK
1			IFGISSTGVGDGGNELGMGKVKEAVRRHIRHGDVIACDVEADPA
1			VIAGVSNWGGYALACALYILYSCAVHSQYLRKAVGPSRAPGDQA
1	·		WTQALPSVIKEEKMLGILVQHKVRSGVSGIVGMEVDGLPFHNTH
5496	3	2408	AEMIQKLVDVTTAQV
1	_	2400	QDTKMHEIYKGNITPQLNKNTLKTSAATDVWAVYFSQFWIDYEG
	j		MKSGKGRPISPVDSFPLSIWICQPTRYAESQKEPQTCNQVSLNT
1	İ		SQSESSDLAGRLKRKKLLKEYYSTESEPLTNGGQKPSSSDTFFR FSPSSSEADIHLLVHVHKHVSMQINHYQYLLLLFLHESLILLSE
i i			NLRKDVEAVTGSPASQTSICIGILLRSAELALLLHPVDQANTLK
1 1	].		SPVSESVSPVVPDYLPTENGDFLSSKRKQISRDINRIRSVTVNH
1 1			MSDKRSMSVDLSHIPLKDPLLFKSASDTNLQKGISFMDYLSDKH
	1		LGKISEDESSGLVYKSGSGEIGSETSDKKDSFYTDSSSVLNYRE
1			DSNILSFDSDGNQNILSSTLTSKGNETIESIFKAEDLLPEAASL
			SENLDISKEETPPVRTLKSQSSLSGKPKERCPPNLAPLCVSYKN
1	1		MKRSSSQMSLDTISLDSMILEEQLLESDGSDSHMFLEKGNKKNS
1 1			TINYRGTAESVNAGANLQNYGETSPDAISTNSEGAQENHDDLMS
		•	VVVFKITGVNGEIDIRGEDTEICLQVNQVTPDQLGNISLRHYLC
1 1			NRPVGSDQKAVIHSKSSPEISLRFESGPGAVIHSLLAEKNGFLO
1 1			CHIKNFSTEFLTSSLMNIQHFLEDETVATVMPMKIOVSNTKINI.
] ]			KDDSPRSSTVSLEPAPVTVHIDHLVVERSDDGSFHIRDSHMINT
]		İ	GNDLKENVKSDSVLLTSGKYDLKKORSVTOATOTSPGVPWPSOS
(	ľ		ANFPEFSFDFTREQLMEENESLKQELAKAKMALAEAHLEKDALL
5497	1821		HHIKKMTVE
/	4021	3308	SISKLLKRRSNIDAYLLSNSCAFFAPRLFSLASQIIREQQSPNV
1	ĺ	'	CFIYKYSGFPSLECQCHFVSPHSSCYINFFSFPPPFFVCFQLSN
1 1		4.5	GFSHYSLSSESHVGPTGAGLFPHCLPASRLLPRVTSVHLPDYAH
1 1	`		YYTIGPGMFPSSQIPSWKDWAKPGPYDQPLVNTLQRRKEKREPD
1		j	PNGGGPTTASGPPAAAEEAQRPRSMTVSAATRPGBEMEACEELA
1 1		ł	LALSRGLQLDTQRSSRDSLQCSSGYSTQTTTPCCSEDTIPSQVS
[ [	}	J	DYDYFSVSGDQEADQQEFDKSSTIPRNSDISQSYRRMFQAKRPA
i ,		Į	STAGLPTTLGPAMVTPGVATIRRTPSTKPSVRRGTIGAGPIPIK
[		ł	TPVIPVKTPTVPDLPGVLPAPPDGPEERGEHSPESPSVGEGPQG VTSMPSSMWSGQASVNPPLPGPKPSIPEEHRQAIPBSEAEDQER
		1	FDDSATUSDCOLDEGDDADI CDDDEGDGADI CDDDEGDGADI CDDDGADI CDDDGADI CDDDGADI CDDDGADI CDDDGADI CDDDGADI CDDDGADI CDDDGADI CDDDGADI CDDDGADI CDDDGADI CDDDGADI CDDDGADI CDDDGADI CDDDGADI CDDDGADI CDDDGADI CDDDGADI CDDDGADI CDDDGADI CDDDGADI CDDDGADI CDDDGADI CDDDGADI CDDDGADI CDDDGADI CDDDGADI CDDDGADI CDDDGADI CDDDGADI CDDGADI CDDDGADI  CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI CDDGADI C
			EPPSATVSPGQIPESDPADLSPRDTPQGEDMLNAIRRGVKLKKT TTNDRSAPRFS
5498	2434		ILTHQE1FTGEXPCECGKASIQMSHLSQQKIYSGENPFACKVCG
	!		KVFSHKSNLTEHEHFHTREKPFECNECGKAFSQKQYVIKHQNTH
j	1		TGEKLFECNECGKSFSQKENLLTHQKIHTGEKPFECKDCGKAFI
•	į	1	QKSNLIRHQRTHTGEKPFVCKECGKTFSGKSNLTEHEKIHIGEK
1	1	1	PFKCSECGTAFGQKKYLIKHQNIHTGEKPYECNECGKAFSQRTS
- }		j	LIVHVRIHSGDKPYECNVCGKAFSOSSSLTVHVRSHTGEKPYGC
			NECGKAFSQFSTLALHLRIHTGKKPYQCSECGKAFSQKSHHIRH

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G-Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
}	corresponding	to first	L-Leucine, M-Methionine, N-Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine.
	amino acid	residue of	S=Serine, T=Threonine, V=Valine.
	residuc of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Ston
· [	amino acid	sequence	Codon, /=possible nucleotide deletion
<b>-</b>	sequence		\=possible nucleotide insertion)
5499			QKIHTH
3499	324	926	GFGQIGRGHKITTYPFSPRKSGRKGMAQSQGWVKRYIKAFCKGF
1	ł		FVAVPVAVTFLDRVACVARVEGASMQPSLNPGGSQSSDVVLLNH
1		j	WKVRNFEVHRGDIVSLVSPKNPEQKIIKRVIALEGDIVRTIGHK
}		1	NRYVKVPRGHIWVEGDHHGHSFDSNSFGPVSLGLLHAHATHILW
5500	1978	1286	PPERWQKLESVLPPERLPVQREEE
		}	KPDWRLQNLPPRLYLWRSSRFGFGHLKKRLQMDFKIEHTWDGFP VKHBPVFIRLNPGDRGVMMDISAPFFRDPPAPLGEPGKPFNELW
			DYEVVEAPFLNDITEQYLEVELCPHGQHLVLLLSGRRNVWKQEL
		1	PLSFRVSRGETKWEGKAYLPWSYFPPNVTKFNSFAIHGSKDKRS
1	1	l	YEALYPVPQHBLQQQQKPDFHCLEYFKSFNFNTLLGEEWKQPES
L			DLWLIEKCDI
5501	2927	2226	CRPPVSARVAPGHQGAVGGSGRRPARVEVVDAAARPSSRPFSLP
1	1		AAIMLALISRLLDWFRSLFWKEEMELTLVGLOYSGKTTFVNVIA
ļ			SGQFSEDMIPTVGFNMRKVTKGNVTIKIWDIGGOPRFRSMWERY
		[	CRGVNAIVYMIDAADREKIEASRNELHNLLDKPOLOGIPVLVLG
1		}	NKRDLPNALDEKQLIEKMNLSAIQDREICCYSISCKEKDNIDIT
5502	<u> </u>		LQWLIQHSKSRRS
3302	3	824	NSAFPVWVPERTALLTCPLGAAPGSSREAPGIAGPPNSTAMSKL
1			GKFFKGGGSSKSRAAPSPQEALVRLRETEEMLGKKQEYLENRIQ
1	)		REIALAKKHGTQNKRAALQALKRKKRFEKQLTQIDGTLSTIEFQ
1			REALENSHTNTEVLRNMGFAAKAMKSVHENMDLNKIDDLMQEIT
1			EQQDIAQEISEAFSQRVGFGDDFDEDELMAELEELEQEELNKKM
)			TNIRLPNVPSSSLPAQPNRKPGMSSTARRSRAASSQRAEEEDDD IKQLAAWAT
5503	216.	654	KGVRRGRVRSDSEDSHLGYFKMSFLLPKLTSKKEVDQAIKSTA
İ			EKVLVLRFGRDEDPVCLQLDDILSKTSSDLSKMAAIYLVDVDQT
ļ			AVYTQYFDISYIPSTVFFFNGQHMKVDYGGEDPALRSIKAVRRT
	<u> </u>		SPAGTLGBKPVNS
5504	58	3563	QLSFSFQAPVTFDDITVYLLQEEWVLLSQQQKELCGSNKLVAPL
ì	1		GPTVANPELFRKFGRGPEPWLGSVQGQRSLLEHHPGKKOMGYMG
1			EMEVQGPTRESGQSLPPQKKAYLSHLSTGSGHIEGDWAGRNRKI.
1	[		LKPRSIQKSWFVQFPWLIMNEEQTALFCSACREYPSIRDKRSRL
ł	}		IEGYTGPFKVETLKYHAKSKAHMFCVNALAARDPIWAARFRSIR
j .	[		DPPGDVLASPEPLFTADCPIFYPPGPLGGFDSMAELLPSSRAEL
[	[		EDPGGDGAIPAMYLDCISDLRQKEITDGIHSSSDINILYNDAVE
1 1	}	ļ	SCIQDPSAEGLSEEVPVVFEELPVVFEDVAVYFTREEWGMLDKR
		Ì	QKELYRDVMRMNYELLASLGPAAAKPDLISKLERRAAPMIKDPN GPKWGKGRPPGNKKMVAVREADTQASAADSALLPGSPVEARASC
			CSSSICEEGDGPRRIKRTYRPRSIQRSWFGQFPWLVIDPKETKL
1 1	·		FCSACIERPNLHDKSSRLVRGYTGPFKVETLKYHEVSKAHRLCV
)			NTVEIKEDTPHTALVPEISSDLMANMEHFFNAAYSIAYHSRPLN
	l i	•	DFEKILQLLQSTGTVILGKYRNRTACTQFIKYISETLKREILBD
	ľ		VRNSPCVSVLLDSSTDASEQACVGIYIRYFKOMEVKESYTTIAD
[ ]			LYSETADGYFETIVSALDELDIPFRKPGWVVGLGTDGSAMLSCR
		1	GGLVEKFQEVIPQLLPVHCVAHRLHLAVVDACGSIDLVKKCDRH
		i	IRTVFKFYQSSNKRLNELQEGAAPLEOBIIRLKDLNAVRWVASR
			RRTLHALLVSWPALARHLQRVAEAGGOIGHRAKGMLKLMRGFHF
		j	VKFCHFLLDFLSIYRPLSEVCQKEIVLITEVNATLGRAYVALES
[. <b>.</b>		1	LRHQAGPKEEEFNASFKDGRLHGICLDKLEVAEQRFQADRERTV
	]		LTGIEYLQQRFDADRPPQLKNMEVFDTMAWPSGIELASFGNDDI
			LNLARYFECSLPTGYSEEALLEEWLGLKTIAQHLPPSMLCKNAL
I	1	Į.	AQHCRFPLLSKLMAVVVCVPISTSCCERGFKAMNRIRTDERTKL
		i i	
	1	ľ	SNEVLNMLMMTAVNGVAVTEYDPQPAIQHWYLTSSGRRFSHVYT
			CAQVPARSPASARLRKEEMGALYVEEPRTOKPPII.PSPEAAFIT.
5505	3312	_	CAQVPARSPASARLRKEEMGALYVEEPRTQKPPILPSREAAEVL KDCIMEPPERLLYPHTSQEAPGMS
5505	3312	1219	CAQVPARSPASARLRKEEMGALYVEEPRTQKPPILPSREAAEVL KDCIMEPPERLLYPHTSQEAPGMS NCSPRSLSAAKMSNRNNNKLPSNLPOLONLIKRDPPAYTEEPLO
5505	3312	1219	CAQVPARSPASARLRKEEMGALYVEEPRTQKPPILPSREAAEVL KDCIMEPPERLLYPHTSQEAPGMS NCSPRSLSAAKMSNRNNNKLPSNLPQLQNLIKRDPPAYIEEFLQ QYNHYKSNVEIFKLQPNKPSKELAELVMFMAOISHCYPEYLSNF
5505	3312	1219	CAQVPARSPASARLRKEEMGALYVEEPRTQKPPILPSREAAEVL KDCIMEPPERLLYPHTSQEAPGMS NCSPRSLSAAKMSNRNNNKLPSNLPOLONLIKRDPPAYTEEPLO

Second   Predicted   Predicted end   Indication   Coloration   Coloration   Corresponding   Corresponding   Corresponding   Coloration   Corresponding   Corresponding   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Coloration   Col	SEQ	Predicted	Predicted end	I bring gold gorgest control -
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Cocresponding   to first   amino acid   cocresponding   to first   amino acid   cocresponding   to first   amino acid   cocresponding   to first   cocresponding   to first   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding   cocresponding	NO:	nucleotide	4	Glutamic Acid. F=Phenylalanine, GeGlycine
Leleucine, M-Methionine, N-Asparagine, popular damino acid residue of amino acid sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Seque	l.	location	corresponding	H=Histidine. I=Isoleucine. Kalvsine
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amino acid creidue of amino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequen	Ţ		amino acid	P-Proline, Q-Glutamine, R-Arginine,
##STYPTOSIANE X-DUKKNOWN, *=Stop amino acid sequence  ##STYPTOSIANE, X-DUKKNOWN, *=Stop Codon, *possible nucleotide deletion,	1			S=Serine, T=Threonine, V=Valine,
anino acid sequence    Codon, /=possible nucleotide deletion,    -possible nucleotide destrion    YMMLROSNATARAMSLOVHELVERTKINDAUTYNITACESK     YKLUAALTFELGEDEKGOSISSESDOGFTARDLUVQYATO	1		amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
YTMLRUSHATTAKKELDVITELYRRINKINDAUTVITTACESK VYKLUVALITFELGEDERKODESKEDEDGSTARDLUVOTATO KKSSKHKKKLEKAMRVILKHRKKKKEVFFFSALILIBOPODFA BELLKULGECCREFFEVOMMENNISKUNG HELLELINTYPTOLOR FLOPHOREVTKILLEAAOASHHLVPPEI IGSLUMTVANNPYTIK SIGGEVTVOITAIR SITTARCILAMTEVIDENTHENDAVM MSARTLIHLETTLNDQULOKKPRGKYTEAS IEARVQEYGSLOJK DVIPGRAVLEVEKERIANDEDGEMESTISLEBEDADGERIJOVOH SODEGOGISKKINSHMERERKAKAAAISTSRVLTQEDFOKTEM AOMEKSLDAAPGKOSKRVTISIDSBEPGRELILSUDELELIKK FRSDKETELATAMAGKTDREFFVEKKTKTNFFSSSTNEKKKOK NOMMRYSGOWYRSKNSKSFREKOLABOLALLKKKKRIKK FRSDKETELATAMAGKTDREFFVEKKTKTNFFSSSTNEKKKOK NOMMRYSGOWYRSKNSKSFREKOLABOLALLKKKKRIKK FRSDKETELATAMAGKTDREFFVEKKTKTNFFSSSTNEKKKOK NOMMRYSGOWYRSKNSKSFREKOLABOLALLKKKRIKK FRSDKETELATAMAGKTDREFFVEKKTKTNFFSSSTNEKKKOK NOMMRYSGOWYRSKNSKSFREKOLABOLALLKKKRIKK FRSDKETELATAMAGKTDREFFVEKKTAMAGKASFWOOT LLVYPRRINTLEGGETPORTOLAFOLATION FROM THE STARTE TO THE STARTE TO THE STARTE THE STARTE TO THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE STARTE THE	i		sequence	Codon, /=possible nucleotide deletion.
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PAARTTPMOQALKLIPCATGLOVS/LITROVLOREWTRS YGATA TSPGERFTDSOFLVLWARNEVALLIVAGCULCKOPREGRAPYRY SFASLSNVLSSWCOYEALKFVSFTOVLAKASKVIFVMLMKKLV SRRSYEHWEYLTATLISIGYENEVISSOFPRESPATTLSCLIL LAGYIAFDSFTSNWODALFAYKNSSVQMMFCVFFSFCTFVGSL LEQGALLECTRFMGRHESFPAHALLISICSACOGLFIFYTTGOF GAAVFTIITMTLQAFATLLSCLIVGHTVYGGLGVAVVFAALL LRVYARGRIKAGRKKAVPVESPYQKV  S507 3704 1271 PROTRCRPAGRASRRARRFPFCGPAAFGSLEIGGFGTAAGKK VAVADVQFQPMFFHQDOLOVLLVFTKEDNOCNGFCRACEKAGFK CTVYKEAQAVLACFLDKHHDIIIIHHRPRRQLDAZALCRSIRSS KJSSNTVIGVVRRVDEELSWMPPISTTRYVVENNINACY NELLQLEFGEVRSQLKLRACNSVFTALENSEDAFIG VANDAPFTTMOYGSGELIGKELGEVFTRYVENNINACY NELLQLEFGEVRSQLKLRACNSVFTALENSEDAFIG GKEWQGIYYAKKKNGDNIQONVKIIPVIGGGKIRHVSIRVC MGNNKAEKISBCVQSDTHTDNOTGKHXDRKKGSLDVKAVASRAT EVSSQRRHSSNARTHSHTIAPITVININAQESSFMPYTER LDRVLSILKTTELYSPQFGAKDDPHANDLVGGLWSDGLRRLSS NEYVLSTKNTOMVSSNITIFISLDDVFTARAMMNESPYMPDFI PELEAATHNRPLIVIGLKMFARRGICEFLHGSESTLRSWLQIIE ANYHSSNPYHRSTHSADVLHATAYFLSKRRIKETHLPDTDEVAAL LAATHIDVDHGGRTNSFFLCNAGSELALIYMDTAVLESHAALAF QLITGDDKCNIFKMERNDYRTLRGGIIDMVATATMTHFBHYN KCADVSNPCRFLQVCIEWAARISBFYSGTDERKQOGLPVVMPV FDRNTGSIFSKOJGFIDVYFTGGLGLEGGTVGSCOGLHEKFW FPYKNTSVFTRKSJGFIDVYFTGGLGLEGGTVGSCOGLHEKFW EFYKADWCVWPAAQFVNFLFVPPQFRVTYINGLTLGWDTYLSYL KYRSVPUTLPPPGCVALDTAD  5509 1238 619 RKSRCONALSASGFAAAAATMVRKLKFHEQKLLKQVDFLNNE VTDRILHBLRVLRRYRLQGREDYTRYNQLSRAVERLARRLRDLP ERQPFVWYDSSKIKRHLYENDERDPDLEA  LEPVYLLKLRNAQHIQAAVAPVQGHVRVQPDVVTDPAFLVTRSM EPPTYWDYSSKIKRHLYENDERDPDFLLBA AGGERQPPPDSSERAPPATONFIIPKKELHTVPDMGKKRSQAY AGGERQPPPDSSERAPPATONFIIPKKEHTVPDMGKKRSQAY AGGERQPPPDSSERAPPATONFIIPKKEHTVPDMGKKRSQAY AGGERQPPPDSSERAPPATONFIIPKKEHTVPDMGKKRSQAY AGGERQPPPDSSERAPPATONFIIPKKEHTVPDMGKKRSQAY AGGERQPPPDSSERAPPATONFIIPKKEHTVPDMGKKRSQAY AGGERQPPPDSSERAPPATONFIIPKKEHTVPDMGKKRSQAY AGGERQPPPDSSERAPPATONFIIPKKEHTVPDMGKKRSQAY AGGERQPPPDSSERAPPATONFIIPKKEHTVPDMGKKRSQAY AGGERQPPPDSSERAPPATONFIIPKAGCLEKFYDTHLAADAV EVAVLKSVONSTRILDFWIGCHUKACHLURTURDLELEFTIFUKT GFFAHLSGOLMNISAVYPEGSKSVNOGLHAVRGELCEKFYDIGHF GFFAHSKOLMNISAVYPEGSKSVNOGLHAVRACLECKFYDIGHF				LLVQYFRRKNYLETGRGLCFPLVKACVFGNEPKASDEVPLADDT
SPGERFTDSQTAULMINRULALIVAGLSCVUCKOPRIGAPMYRY   SFASISSAVISSMCQVSALKFVSFTPUCKASKVIPFWIMMGKLV    SRRYEHWEYLTATLISIGVSMPLLSSGPEPRSSPATTLSCIIL   LAGYIAFDSFTSNMCDALFAYNNSSVQMMFCVWFFSCLFTVGSL    LEQGALLECTRTMGRHSEPAAHALLISIGSAGQLFIFYTTGGF    GAAVFTIIMTLRQAFAILLSCLLYGHTVTVVGGLGVAVVFAALL    LRVYARGRIKQRGKKAVVFVSSPVQKV    SSO7   3704   1271   PROTRERPAGRASRERREPPCFGPAAFGSLEIGGFGTAAGKK    VANADVQFOPMFHQDOLOVLLWFTKEDNCONFCRACEKAGFK    VANADVQFOPMFHQDOLOVLLWFTKEDNCONFCRACEKAGFK    VANADVQFOPMFHQDOLOVLLWFTKEDNCONFCRACEKAGFK    VANADVGFOPMFHQDOLOVLLWFTKEDNCONFCRACEKAGFK    VANADVGFOPMFHQDOLOVLLWFTKEDNCONFCRACEKAGFK    VANADVGFOPMFHQDOLOVLLWFTKEDNCONFCRACEKAGFK    VANADVGFOPMFHQDOLOVLWFTKEDNCONFCRACEKAGFK    VANADVGFOPMFHQDOLOVLWFTKEDNCONFCRACEKAGFK    VANADVGFOPMFHQDOLOVFTCHENDTOLOVLWFTKEDNCONFCRACEKAGFK    VANADVGFOPMFHQDOLOVLWFTKEDNCONFCRACEKAGFK    VANADVGFOPMFHQDOLOVLWFTKEDNCONFCRACEKAGFK    VANADVGFOPMFHQDOLOVLWFTKEDNCONFCRACEKAGFK    VANADAFETTMOVGGGKLACASUMFISAGET SAGGTATISTEDRIO     VANDAFETTMOVGGGKLACASUMFISAGET SAGGTATISTEDRIO     VANDAFETTMOVGGGKLACASUMFISAGET SAGGTATISTEDRIO     VANDAFETTMOVGGGKLACASUMFISAGET SAGGTATISTEDRIO     VANDAFETTMOVGGGKLACASUMFISAGET SAGGTATISTEDRIO     VANDAFETTMOVGGGKLACASUMFISAGET SAGGTATISTEDRIO     VANDAFETTMOVGGGKLACASUMFISAGET SAGGTATISTEDRIO     VANDAFETTMOVGGGKLACASUMFISAGET SAGGTATISTEDRIO     VANDAFETTMOVGGGKLACASUMFISAGET SAGGTATISTEDRIO     VANDAFETTMOVGGKLACASUMFISAGET SAGGTATISTEDRIO     VANDAFETTMOVGGKLACASUMFISAGET SAGGTATISTEDRIO     VANDAFETTMOVGGKLACASUMFISAGET SAGGTATISTEDRIO     VANDAFETTMOVGGKLACASUMFISAGET SAGGTATISTEDRIO     VANDAFETTMOVGGKACASUMFISAGET SAGGTATISTEDRIO     VANDAFETTMOVGGKACASUMFISAGET SAGGTATISTEDRIO     VANDAFETTMOVGGKACASUMFISAGEN SAGGTATISTEDRIO     VANDAFETTMOVGGKACASUMFISAGET SAGGTATISTEDRIO     VANDAFETTMOVGGKACASUMFISAGET SAGGTATISTEDRIO     VANDAFETTMOVGAMAVAFVQGHVVARGELCEKIFVATORD     VANDAFETTMOVGAMAVAFVARLDERENDHOLRAN     VANDAFETTMOVGAMAVAFVARLDERENDHOLRAN     VANDAFETTMOVGAMAVAFVARLDERENDHOLRAN     VANDAFETTMOVGAMAVAFVARLDERENDHOLR				EAAETTPMWQALKLLFCATGLOVSYLTWGVLOERVMTRSYGATA
SFASLSNVLSSNCOYEALKFVSFPTTVLAKASKVIPVMLMGKLU SRRSYEMEVLTATLISIGUSMPLLSSPPRSSPATTISGLIL LAGYLAPDSFTSNWODALFAYKMSSVQMMFGVNFFSCLFTVGSL LEQGALLEGTRFMGRHSEFAAHALLISTCSACGLFIFYTTGSL LEQGALLEGTRFMGRHSEFAAHALLISTCSACGLFIFYTTGSL LEQGALLEGTRFMGRHSEFAAHALLISTCSACGLFIFYTTGSG GAAVFTIINTERQAFAILLSCLLYGHTVTVVGGLGVAVVFAALL LRVVARGRIKAGRKKAVPVESPVQKV  PROTREGERAGASGRARREPPETGFAAFASLEIGGFGTAAGKK CTVTKEAGAVLACFLDKHDDIIIIDHRNPRQLDBAALCRSITSSA KLSENTVIVGVVRRVDREELSWMPFISAGFTRRYVENNIMACV NELLQLEFGEVRSQLKLRACNSVFTALENSEDALIITSEDBFIG YANDAFSTTMOYGSGELIGKELGEVP INEKKADLLDITINSCIRI GKEWGGIYYAKKKNGDNIQONVKIIPVIGGGKIRHYVSIIRVC MGNNKABKTISEVOSGHTDNOTGKHNOTKGSLRIVSGIRVASRAT EVSSQRRHSSMARIHSMTIEAFITVINIINAAQESSFMPVTER LDRVLBILKTTELVSPQFGAKDDPHANDLUGGLWSDGLRRLSG NETVLISTKTTOMYSSNITITISLDDV FARMMENSPMPFIE FELEAATHNRPLIVLGLKMFARFGICEFLICGSSTIRSWLQIIE ANNHSSNISADVLHATAYPLERARMENESTWPDFI FELEAATHNRPLIVLGLKMFARFGICEFLICGSSTIRSWLQIIT ANNHSSNISADVLHATAYPLERIKETLDP DEVAAL LAATIHDUDHPGRTNSFLCNAGSELAILYNDTAVLESHHAALAF QLITGDBKCNIFRMEENDYRTLRGGIIDMVLATETMTHEHEHIN KCADVSNPCRFLQVCIEWAARISEPYSGOTDEBKQGGLPVMPV FDRNTGSIPKSQISFIDVFITMFDAWDAPULPDLMQHLDNNF KYWKGLDEMKLRNLRPPPB  S500 1151 691 LISUPSRRSASHFAVGCSNGFFLHYWYLSLDRLPPABGLRGFFN VLKKVLVDQLVASPLLGVWYFLGGLGEGOTVGSSCOELHEKW EFYKADWCVWBPAAQFVNFLFVUPGGRRVTYINGLILGWDTYLSYL KYRSVPETUPPGCVALDTTAD  SKRSGCONALSASGPAAAAAIMVRKLKFHEQKLLKQVDFLNWE EPVEXDLWSSKIKHLUENDENDDDHOLMYCHDRWID DFTDWYDSSKIKHULENDENDDDHOLMYCHDRWID EPPUVUPSSKIKHULENDENDDDHOLMYCHDFUTORM ACGERQPPPDSSERAPPATONFIIPKKEHTVPDOMGWKRSQAY ACGERQPPPDSSERAPPATONFIIPKKEHTVPDOMGWKRSQAY ACGERQPPPDSSERAPPATONFIIPKKEHTVPDOMGWKRSQAY ACGERQPPPDSSERAPPATONFIIPKKEHTVPDOMGWKRSQAY ACGERQPPPDSSERAPPATONFIIPKKEHTVPDOMGWKRSQAY ACGERQPPPDSSERAPPATONFIIPKKEHTVPDOMGWKRSQAY ACGERQPPPDSSERAPPATONFIIPKKEHTVPDOMGWKRSQAY ACGERQPPPDSSERAPPATONFIIPKKEHTVPDOMGWKRSQAY ACGERQPPPDSSERAPPATONFIIPKAGCCLKIGVLRVDDQ LAIVFKVFNRYLEVMRKLQKTYRWERASGGVMGLDDFGLPFI WGSSGLIDHPYLEPRIFUDEKANNENKNYGELCEKFYPUGHF	1			TSPGERFTDSQFLVLMNRVLALIVAGLSCVLCKOPRHGAPMYRY
SRRSYEMBEVLTATLISIGUSMPILLSGEPERSPARTILSGLIL LAGYIAFDSTSMWODALFAYKMSVOMMPGUMPFECLFTUGSL LEQGALLEGTRFMGRHSEFAAHALLLSICACGQLFIFYTIGGE GARVFTITHTLRQAFAILLSICLLYGHTVUVGGLGVAVVFAALL LRVYARGRIKARGRKAVPVESPUKV  5507 3704 1271 PRGTRRCR+PAGRASRRARRPPCFGFAAPGSLEIGGFGTAAGKK VAVAUVQFGPMR*HOOOLQVLLVFTKEDNQCNGFCRACEKAGFK CTVTKEAQAVLACFLDKHHDIIIIDKHNPRQLDAZALCRSIRSS KISENTVIUGVVRRVDREELSUMPFISAGFTRRYVENDNIMACV NELLQLEFGEVRSQLKLARCNSVFLABUSDDAIITSBDRFIG YAMPAFFTTMGYGGGELIGKELGBVPINBKKADLLDTINSCIRI GEMQGIYVAKKKNGNIQONVKIIPVIGGGGKIRHVVSIIRVC NGNNKAEKISECVQSDTHTDNQTGKHKDRRKGSLDVKAVASRAT EVSSQRRHSSMARIHSMTIEAPTIKVINIINAAQESSMPVTER LDRVLBILITTELTSPOFGAKDDPHANDLVGGLMSGLGKLGS NEYVLSTKNTONVSSNIITPISLDDVPPRIARAMSNEEYMDPDI FELEAATHRPLIITJGLMFARFGICEFLHCSESTLRSWLQIIE ANYHSSNPYHNSTHSADVLHATAFYLSKERIKETLDPIDBVAAL IAATHBUVDHGGRTNSFLCNAGSELAILKNDTAVLESHHAALAF QLTGGDKCNIFKMRRRDNYRTLRGQIIDMVLATHRTKHEHTNN KYNSINKELATLEENGBTDKNOGVINTHLRTPENRTLIKRMLI KCADVSNPCRPLQYCIEWAARISEEYFSQTDEBKQQLEVYMPV FRRNTCSIPKSQISFIDYFTDMFDAMDAFVDLPDLMQHHDNNF KYMKGLDEMKLRNLRPPPB  5508 1151 691 LSSVFSRSSMFMSWGCSMGFFLHYWYLSLDRLPPABGLRGPPN VLKKULVDQLUASPLLGVUMPYFLGJGCLEGQTVGESCQELREKFW EFYKADMCVWPAAGFVNFLFVPPQRRVTYINGLTAGMTYLSYL KYRSPVPLTPBGCVALDITAD  5509 1238 619 RKSRGCONLSSSGFAAAAAINWRKLKFHEGKLLKQVDFLNME VTDHLHLBLRVLLRFYPLQREDYTRYNQLSRAVRELARRLRDLP ERDQFRVRASAALDKLYALGGUPPTGSSELCDFVTASSFCRR LPTVLLKLRMAQHLQAAVAFVEGGIRVGEPDVTDPSFCRR LPTVLKLRMAQHLQAAVAFVEGGIRVGERGLAASGSAPGRSKM AEGERQPPPUNSSKIKKHVLEYNEERDFDLEA PAGAHLSSGSSEPLVEFGRGVGARVKGERGLQASGSAPGRSKM AEGERGPPPUNSSKIKKHVLEYNEERDFDLEA PAGAHLSSGSSEPLVEFGRGVGARVKGERGLAASGSAPGRSKM AEGERGPPPDSSERAPPATONIIEKKLTURDRVID ETPPUDQPSRRGNAVATWWAKLDERABNLVATVUPHLAAAVP EVAVILVBSSVIKKHVLEYNERBDFALECLCKIGVURVDDQ IALVFKVPNRYLEVMRKLQKTYRMEPAGSQGVWGLDDFQFIPFI WGSSQLIDHPYLEBRHSVDENKVNQCLIRMYMAGECLEFFFICHKT GFFAEMSNQLMNISSVEKNGCLIRMYMAGECLEFFFICHKT GFFAEMSNQLMNISSVEKNGCLIRMYMAGECLEFFFICHKT GFFAEMSNQLMNISSVEKNGCLIRMYMAGECLEFFFICHKT GFFAEMSNQLMNISSVEKNGCLIRMYMAGECLEFFFICHKT	ļ	1		SFASLSNVLSSWCQYEALKFVSFPTQVLAKASKVIPVMLMGKLV
LEQGALLEGTFFMGRHSFFAHALLLSLCAGGQLFIFYTIGQF GAGAPTITIMTLRQAPATILLSCLLUGHTVTVVGGLGVAVVFAALL LRVVARGRLKQRGKKAVPUESPVQKV  5507  3704  1271  PROTRECEPAGRASERRARERPECFGPAAGSELGGFGTAAGKK VAVAVOVGFQMRH-PDOLQVLLUVTKEDNOCNG-CRACE KAGFK CTVTKEAQAVLACFLDKHHDIIIDHRNPRQLDASALCESITES KISENTVIVUVVRVDEELSVMPFISAGFTRRYVENPNIMACY NELLQLEFGEVRSQLKLRACNSVFTALENSROAISITSEDRFIQ YANDAFFITMGVGSGELIGKELGEVFINEKKADLLDTINSCIRI GERQGGYTYAKKNOENIQONVIIIPVIGGGKIRHVYSIIRVC NEGNKABEKISECVQSDTHTDNOTIGKHKJRRKGSLDVKAVASRAT EVSSQRRHSSMARIHSMTIEAPITKVIINAGESSPMEVTER LDRVLBILRTTELYSPQFGAKDDDPHANDLVGGLUSDGLRELGG NEYVLSTKNTQNVSSNIITPISLDDVPPHARAMENEYVNDFDI FELEAATHNRPLIVIGLEMPARFGICEFLHCSESTLASMQOITE ANYHSSNPYHRSTHSADVLHATAYFLSKERIKETLDPIDEVAAL LAATHDVDHPGETNSFLCXAGSELAILVNDTAVLESHHAALAF QLTTGDDKCNIFKMMERNDVRTLRQGILDMVLATEMTKHEHVN KPANSINKELATLEENGETDKNQSVINTHLRTPENRTLIKRMLI KCADVSMPCPRLDVGIERARAISERYSGTDERQQGLPVVMPV FDRNTCSIPKSQISFIDYFITDMFDAMDAFVULPIMCHEDHAHLANF KYMKGLDEMKLRNLRPPBR  5508  1151  691  LSSVESRESSMFAYGCSMGDFLHWYLSLDRLPFABGLRGPPN VLKKVLVDQLVASPLLGWWFLGELGCLEGQTVGESCQELREKFW EFYKADMCVWPAAQFVNFLFVPPQFRVTYINGLTLGWDTYLSYL KYRSVPLTPPGCVALDTRAD  5509  1238  619  RKSRGCONALSASGPAAAAAIMVRKLKFHEQKLLKQVDFLNNE VTHNLHLERVLIRRYRLQREDYTHQLSRAVELLARRILDHP ERDQFRVRASAALLDKLYALGLVPTRGSLELCDFVTASSFCRR LPTVLUKURNSKIKKHVLEYNEREDDFLEA AGEGROPPPDSSERAPPATQNFITPKKELKOLLGGAGGSGAPGRSKM AEGERQPPPUNSSKIKKHVLEYNEREDDFLEA AGERQPPPDSSERAPPATQNFITPKKELKURDDVATDAFFLYTRSM EPFYVWDSSKIKKHVLEYNEREDDFLEA AGERQPPPDSSERAPPATQNFITPKKELKURDDVATDAFFLYTRSM EPFYVWDSSKIKKHVLEYNEREDDFLEA AGERQPPPDSSERAPPATQNFITPKKELKURDDVATDAFFLYTRSM EPFYVWDSSKIKKHVLEYNEREDDFLEA AGERQPPPDSSERAPPATQNFITPKKELKURLDDRVTD ETPPUDQPSRRGNAYNTWYAKLDEBABNLVATVUPTHLAAAVP EVANTALKSVONSTRIDVTGHEEAAPALCCLCKGVURVDDQ LATVFKVPNRYLEWMRKLQKTYRMEPAGSQGVWGLDDFQFLPFI WGSSQLIDHPYLEWRKLQKTYRMEPAGSQGVWGLDDFQFLPFI WGSSQLIDHPYLEWRKLQKTYRMEPAGSQGVWGLDDFQFLPFI WGSSQLIDHPYLEWRKLQKTYRMEPAGSQGVAGLDDFQFLPFI WGSSQLIDHPYLEWRKLQKTYRMERGRGGUNGLDDFQFLPFI WGSSQLIDHPYLEWRKLQKNENNTHDTWHFECILFTIEMKT GFFAEMSNQLWNISSUKNOGLIRMYKAGELEKFPVIQHF	[			SRRSYEHWEYLTATLISIGVSMFLLSSGPEPRSSPATTLSGLIL
GAAVFTIIMTLRQAFAILISCLIVGHTYTVVGGLGVAVVFAALL LRVVARGRIKQRGKKAVPUESPVGKV  5507  3704  1271  PRGTRCRFAGRASRRARRPFCFGFAAPGSLEIGGFGTAAGKK VAVADVQFGPMRPHQDQLQVLLVFYKEDNQCMGFCRACEKAGFK VAVADVQFGPMRPHQDQLQVLLVFYKEDNQCMGFCRACEKAGFK KUSENTVIVGVVRRVDREELSVMPFISAGFTRRYVENPIMACY NELLQLEFGEVRSQLKLRACNSVFTALENSEDAIEITSEDRFIQ YAMPAFFTTMGYQSGELIGKELGBVPINEKKADLDTINSCIRI GKEMQGIYYAKKKNGDNIQANVKIIPVIQGGKIRHVYRSIIRVC NGNNKARKISBCVGSDTHTADDGHKNDRKKGSLDVKAVASRAT EVSSQRRHSSMARIHSMTIEAPITKVINIINAAQESSPMPVTEA LDRVLEILRTTELYSPQRGAKDDPHAANDLVGGLMSDGLRRLSG NEYVLETKNTQNVSSNITPISLDDVPPRIARAMENEEYMDPDI FELEAATHNRPLIYLGLMFARFGICEFLHCSESTLRSWLQIIE ANYHSSNPYHNSTHSADVLHATAYFICKERIKETLDPIDEVAAL IAATIHDVDHPGRTNSFLCNAGSELAILYNDTAVLESHHAALAF QLTTGDDKCNIFRNMERNDYRTLRGGIIDMVLATEMKHEHVN KPNNSINKPLATLEENGETDKNQGVINTMLRTPENRTLIKKMLI KCADVSNPCRFLQYCIEMAARISEEYFSQTDEEKQGGLPVVMPV FDRNTCSIPKSQISFIDVFITMFDAMDAFVDLPDIMGHLDNNF KYNKGLDEMKLRNLPPPB  5508  1151  691  LSSVFSRSASMFAVGCSMGFFLHYWYLSLDRLFFABGLRGFPN VLKKVLVDQLVASPLLGWYFLGLGCLEGGTVGESCQELREKFW KYRSPYPLTPPGCVALDTRAD  SYNGLDEMKLNLPPPGGRVTYINGLILGMDTYLSYL KYRSPYPLTPPGCVALDTRAD  5509  1238  619  RKSRGCQNALSASGPAAAAAAIMVRKLKFHEQKLLKQVDFLNWE VTDHALHELRVLRRYRLQRREDYTRYNQLSRAVRELARRILRDLP ERPOPRVRASAALLDKLJAALGLVPTRGSLELCDFVTASSFCRR LPPVLLKLRMAQHLQAAVAPVEQGHVVRVPDDVVTDPAFLVTRSM EDFYTWDSKIKRHVLEYNEERDDFDLEA  5510  96  1195  PAGAHLSSGSSEPLVEFGRGRVGARVKGERGLQASGAAPGRSKM ACGERGPPDSSEERPAPATOPL KKELLTVDDMCKWKRSQAY ADYIGFILTUNEGVKGKKLTFEYRVSEAIEKLVALLNTLDRRID ETPVDQPSRGNKAYRTWYAKLDERAPADFLCCLKGIVLRVDDQ IAIVSKVPNRYLEWMRKLQKTYRMEPAGSQGVWGLDDFQFLPFI WGSSQLIDHPYLEPRHEVDEKAVNEHKLDVATVUPTHLAAAVP EVAVYLKESVONSTRIDYGTGHEAPAFLCCLCKGIVLRVDDQ IAIVSKVPNRYLEWMRKLQKTYRMEPAGSQGVWGLDDFQFLPFI WGSSQLIDHPYLEPRHEVDEKAVNEHKLDVMTLECILETIEMCT GFFAEHSNQLMNISAVPSBKSKVNGGLIRMYKAELEKEFPVIQHF	1			LAGYIAFDSFTSNWQDALFAYKMSSVQMMFGVNFFSCLFTVGSL
LRVYARGRIKQRGKKAVPUSPYQKY  PRGTRRCRPAGRASRRARRPPCPGPAAPGSLEIGGFGTAAGKK VAVADVQFGPMRPHQDOLQVILVFTKEDNQCNGFCRACEKAGFK CTVTKEAQAVIACFLDKHHDIIIIDHSPRQLDAZALCRSIRSS KISSINTVIVGVVRVENDELSVMPFISAGFTRRYVENPNIMACY NELLQLEFGEVRSQLKLRACNSVFTALBNSBDAIEITSEDFTQ YANDAFFTTMGYQSGELIGKELGBYPINEKKADLIDTINSCIRI GKEMGGIYYAKKKIGDINQONVKIIPVIQGGKIRTHVSIIRVC MGNNKASKISBCVQSDTHTDNQTGKHKORRKGSLDVKAVASRAT EVSSQRRHSSMARIHSMTIEAPITKVININAAGESSPMPVTEA LDRVLSILKTTELIYSPQFGAKDDPHANDLVGGUMSDLRRLSG NEYVLSTKNTONVSSNIITPISLDDVPRIARAMENEEYWDFDI FELEAATHNRFLIYLGLKMFARFGICEFINCSSTIRSWLQIIE ANYHSSNPYHNSTHSADVLHATAYPLSKERIKETLDPIDEVALL IAATIHDVDHFGRTNSFLCNAGSELAILYNDTAVLBSHHAALAF QLTTGDDKCNIPKMBENDYRTLCQIIDWAMATAYPLSKERIKETLDPIDEVALL IAATIHDVDHFGRTNSFLCNAGSELAILYNDTAVLBSHHAALAF QLTGDDKCNIPKMBENDYRTLCQIIDWAMATAYPLSKERIKETLDPIDEVALL IAATIHDVDHFGRTNSFLCNAGSELAILYNDTAVLBSHHAALAF QLTGDDKCNIPKMSENDYRTLGVGIDDHAMDAFVDLPDIMQHLDNNF KPVNSINKELATLEENGSTDKNQEVINTMLRTEPRNTLIKRMII KCADVSNPCRPLQYCIEWAARISESYSGOTDERGQGLPVMPV FDRNTCSIPKSQISFIDYBITDMDADAFVDLPDIMQHLDNNF KYWKGLDEMKLRNLRPPPB  5508  1151 691 LSSVFSRSSASMFAVGCSMGFFLHYWYLSLDRLPPAAGLRGFPN VLKKVLVDQLVASPLLGWYFLGLGCLEGQTVGESCQELREKFW EFYKADWCVWPAAQFVNFLFVPPQFRVTYINGITLSWDTYLSYL KYRSEVPLIPPGCVALDTRAD  RKSRGGONALSASGSPAAAAAAIMWRKLKFHEQKILKQVDFLNWE VTDHNLHELRVLRRYRLQRREDYTRYNQLSRAVRELARRIRDLP ERDQFRVASAAALLDKLYALGLUPTRGSLELCDFVTASSFCRR LPTVVLLKLRMAGHLQAAVAFVEQGHVEVGPDVVTDPAFLVTRSM EDFVTWDSSKIKRRYLEYNEERDDFDLEA ASGERQPPPDSSEEPPPATOMF IPKKEIHTVPDMGKWRSQAY ADYIGFILTLEEGVRGKUTFEYRVSEAIEKLVALLNTLDRWID EFYPVDQPSRFGNKAYRTWYAKLDEREERLVATVVPTHLAAAVP BEAAHLSSGSSEPPLEFFGREGRGRGGAGGASGAFGRSKM AGGERQPPPDSSEEPPPATOMF IPKKEIHTVPDMGKWRSQAY ADYIGFILTLEEGVRGKUTFEYRVSEAIEKLVATLLNTLDRWID ETPVVLKSSVONSTRIDYGTGHEAAFAAFLCCLCKGGULVDDQ IAIVYKVPNRYLEWMRKLQKTYRMEPAGSQCWGLDDFQFLPFI WGSSQLIDHPYLEPRHFVDEKAVNEHHKUMTLECILETIEMTT GFFAEHSNQLMNISAVPSMSKVROGLINMYKLECLEKFPVLGHF		j		LEQGALLEGTRFMGRHSEFAAHALLLSICSACGQLFIFYTIGQF
PROTRECEPAGRASERARERPPCOPPAAPGSLEIGGFGTAAGKK VAVADVQFGPMRFHQDQLQVLLVFTKEDDNCCNGFCRCEKAGEK CTVTKEAQAVLACFLDKHHDIIIDHNPRQLDAFALCRSIRSS KLSENTUIVGVURRVDREELSVMPFISAGFTRRYVENPNIMACY NELLQLEFGEWGSQLKLRACNSVFTALENSEDAIETTSEDRFIQ YANPAFETTMGYQSGELIGKELGEVPINEKKADLLDTINSCIRI GKEWGGIYYAKKNGDNIQQNVKIIPVIGGGGKIRHVSIIRVC NGNNKAEKISECVQSDHTHONGTGKHCDRKGSIDVKANASRAT EVSSQRRHSSMARHSMTIEAPITKVINIINAAQESSPMPVTEA LDRVLEILRTTELYSPQFGAKDDDFRANDLVGGLMSDGLRRLSG NEYVLSTKNTQMVSSNITTISLDDVPPRIRARMENEEWMDFDI FELEAATHNRPLIYLGLKMPARFGICEFLICGESTIRSWLQIIE ANYHSSNPYINSTHSADVLHATAYFLSKERIKETLDPIDEVAAL IAATIHDVDHPGRTNSFLCNAGSELAILVMDTAVLESHHAALAF QLTTGDDKCNIFRKMGENDYNTURQGIIDMVLATEMTKHFEHYN KFUNSINKPLATLEENGETDKOVINTURTEPENTLIKRWLI KCADVSNPCRPLQYCIEWAARISEEYFSQTDEEKQOGJPVVMPV FDRNTCSIPKSGISFIDYFITDMFDAWDAFVDLPDLMOHLDNNF KYMKGLDEMKLRNLRPPPB  S508 1151 691 LSSVFSRSASMPAVGCSMGDFLHYWYLSLDRLPPABGLRGFPN VLKKVLVDQLVASPLLGVWYFJGLGCGCTVGESCGLREEKFW EFYKADWCWPPAAQFVNEIFVPPQFRVTYINGLITLGWDTYLSYL KYRSPVPLTPPGCVALDTRAD  \$509 1238 619 RKSRGCQNALSASGPAAAAANWKKLKFHEQKLLKQVDFLNWE VTCHHALHELRVLERYRLQREDYTTYNQLSRAVRELARRLRDLP ERDQFRVRASAALLDKLYALGRUPYTGSLELCDFVTASSFCRR LPTVLLKLRMAGHLQAAVAPCGHVRVGPDVVTDPAFLVTRSM EDFYTWDSSKIKRHVLEYNEERDDFDLEA  \$510 96 1195 PAGAHLSSGSSEPLVEPGRGRVGAKVKGRGGLQASGSAPGRSKM AGGERQPPDSSGEAPPAROMGLQAAVAPCBGRGCQASGSAPGRSKM EDFYTWDSSKIKRHVLEYNEERDDFDLEA  \$520 AGGERQPPPDSSGEAPPAROMGREDNIAVTVYPTHLAAAVP BAGAHLSSGSSEPLVEPGRGRVGAKVKGRGGLQASGSAPGRSKM AGGERQPPPDSSGEAPPAROMGREDNIAVTVYPTHLAAAVP BAGAHLSSGSSEPLVEPGRGRVGAKVKGRGGLQASGSAPGRSKM EDFYTWDSSKIKRHVLEYNEERDDFDLEA  \$5510 PAGAHLSSGSSEPLVEPGRGRVGAKVKGRGGLQASGSAPGRSKM EDFYTWDSSKIKRHVLEYNEERDDFDLEA  \$521 BAGAHLSSGSSEPLVEPGRGRVGAKVKGRGGLQASGSAPGRSKM BCCCPPPDGPSRCMAYRTMYAKLDERBERNLVATVYPTHLAAAVP BCANYLKESVGNSTRIDGVGTGHBAAFAAPLCCLKCIGULTVDQ IAIVFKVFNRYLEVMRKLCKTYRMEPAGSQGVWGLDDFQFLPFI WGSQLLDHPYLEPRHFVDEKAVNGCLIKNPYKAECLEKFPVYQHF	-	•		GAAVFTIIMTLRQAFAILLSCLLYGHTVTVVGGLGVAVVFAALL
VAVADVOPGEMRERIQDIQUILUFTKEDNOCNGFCRACE KAGEK CTVTKEAQAVLACELDKHHDIIIIDHNPRQLDABALCRSIRSS KISENTVIVGVQVRVVREELSVMPFISAGFTRRYVENPNIMACY NELLQLEFGEVRSQLKLRACNSVETALENSEDALZITSEDRFIQ YANDAFETTMGYQSGELIGKELGEVPINEKKADLLDTINSCIRI GKEMGGIYYAKKNGDNIQQOWKIIPVIGQGKIRHVYSIIRVC NGNNKAEKISECVQSDTHTDNQTGKHKXPRKGSLIDVKAVASRAT EVSSQRRHSSMARIHSHTIEAPTIKVININAQGESSPMPVTEA LDRVUEILKTELYSPQFGAKDDPHANDLVGGIMSDGKRLSG NEYVLSTKNTQNMYSSNITTPISLDDVPPRIARAMENEEYWDFDI FELEAATHNRPLIYLGLKMFARRGIEGFLHCESSTLRSHLQIIE ANYHSSNPYHNSTHSADVLHATAYFISKERIKSTLDSHDEVAAL IAATIHDVDHFGRTNSFLCNAGSELAILYNDTAVLESHHAALAP QLTTGDDKCNIFKNMERNDYRTLRGGIIDMVLATEMTKHFEHNN KFVNSINKELATLEENSETDKOEVINTHLRTFENRTLIKRMII KCADVSNPCRPLQYCIEWAARISEEYFSQTDEEKQQGLPVVMPV FDRNTCSIPKSQISFIDYSTTDMGDAWDAFVDLPDIMQHLDNNF KYWKGLDEMKLRNLRPPPB  5508 1151 691 LSSVFSRSSSMFAVGCSMGPFLHYWYLSLDRLPPABGLRGFPN VLKKVLVDQLUXASPLLGAWYFLGLGCLEGQTVGESCQELREKFW EFYKADWCVWPAAQFVNFLFVPPQFRVTYINGLTLGWDFTLSYL KYRSPVPLTPPGCVALDTRAD  75509 1238 619 RKSRGCONALSAGSAAAAANVRKLKFHEGKLLKQVDFLNME VTDHNLHELRVLRRYRLQRREDYTRYNQLSRAVRELARRIRDLP ERDQFRVRASAALLDKLYALGLVPTRGSLELCDFVTASSFCRR VTDHNLHELRVLRRYRLQRREDYTRYNGLSRAVRELARRIRDLP ERDQFRVRASAALLDKLYALGLVPTRGSLELCDFVTASSFCRR UPTVLLKLRMAGALQAVAPVEGGHVVGOPVTDPAFLVTRSM EDFVTMVDSSKIKRHVLEYNEERDDFDLEA ARGERQPPPDSSEAPPARONFIIPKKELKTVDMGKKKNGAY ADYIGFILTLNEGVKGKKLTFFYRVSEAIEKLVALLNTLDRWID EPPAVDSSKIKRHVLEYNEERDDFDLEA ARGERQPPPDSSEAPPARONFIIPKKELKTVDDMGKKKRSQAY ADYIGFILTLNEGVKGKKLTFFYRVSEAIEKLVALLNTLDRWID ETPEVDGPSRFGNKAYRTWYAALDEBEAELVAATUVPTHLAAAVP EVAVYLKESVGNSTRIDYSTGHEAAFAAFLCCLCKIGULTWDDQ IAIVFKVPRRYLEVMRKLCKTYRMPAAGSQGVWGLDDFQFLPFI WGSQLLDHPYLEVRRKLQKTYRMPAAGSQGVWGLDDFQFLPFI WGSQLLDHPYLEVRRKLQKTYRMPAAGSQGVWGLDDFQFLPFI WGSQLLDHPYLEVRRKLQKTYRMPAAGSQGVWGLDDFQFLPFI WGSQLLDHPYLEVRRKLQKTYRMPAGGGCLGKEFTVUTHF	5502	3704		LRVYARGRLKQRGKKAVPVESPVQKV
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NELLOLEFGURSOLKLRACNSUFTALENSEDALETSBDRFIQ YANDAFBTTMGYQSGELIGKUPINEKKADLLDTINSCIRI GKEWQGIYYAKKKNDDNIQOWKKIPVIQGGKIRHYSIIRVC NGNNKABKISECVQSDTHFDNQTGKHKDRKKGSLDVKAVASRAT EVSSQRRHSSMARIHSMTIEAPITKVINIINAAQESSPMPVTEA LDRVLEILRTTELYSPQFGAKDDDPHANDLVGGLMSDGLRRLSG NEYVLSTKNTQNVSSNIITPISLDDVPPRIARAMENEEYWDFDI FELEAATHNRPLIYLGLKMFARFGICEFLHCSESTLRSWLQIIE ANYHSSNPYHNSTHSADVHATAYPISKERIKETLDPIDEVAAL IAATIHDVDHFGRTNSFLCNAGSELAILYNDTAVLESHHAALAF QLTIGDUKCNIFKMERNDYRTLRQGIIDMVLATEMTKHFEHVN KPONSINKPLATLEENGENIONGEVINTWLRTPENRILKRMLI KCADVSNPCRPLQYCIEWAARISEEYFSQTDEEKQQGLFVVMFV FDRNTCSIPRSQISFIDYFTTDMFDAWDAFVDLPDLMQHLDNNF KYWKGLDEMKRINLRPPEN TYMKGLDEMKRINLRPPEN  5508  1151 691 LSSVFSRRSASMFAVGCSMGPFLHYWYLSLDRLFPASGLRGPFN VLKKVLVDQLVASFLLGVWYFLGLGCEGQTVGESCQELREKFW EFFKADMCVWPAAQFVNFLFVPQGRVTYINGLTLGWDTYLSYL KYRSPVPLTPPGCVALDTRAD  5509 1238 619 RKSRGCONALSASGPAAAAAIMVRKLKFHEQKLLKQVDFLNWE ERDQFRVRASAALLDKLYALGLVPTRGSLELCDFVTASSFCRRR LPTVLLKLRMAQHLQAAVAFVEQGHVRVGPDVVTDPAFLVTRSM EERDQFRVRASAALLDKLYALGLVPTRGSLELCDFVTASSFCRRR LPTVLLKLRMAQHLQAAVAFVEQGHVRVGPDVVTDPAFLVTRSM EDFVUWDSSKIKRHVLEYNEERDDFDLEA AEGERQPPPDSSEAPPATQNFIIPKKEIHTVPDMGKWKRSQAY ADYIGFILITLNEGVKGKKLTFEYRVSEAIEKLVALLMTLDRWID ETPPDVDOPSFGNKAYRTWYAKLDERERENLVATVVPTHLAAAVP EVAVYLKESVGNSTRIDYGTGHERAAFAAFLCCLCKIGVLRVDDQ IAIVFKVFMRYLEVMKKLQKTYRMEPAGSQGVMGLDDFQFLPFI WGSSQLIDHPYLEPRHFVDEKAVNENHKDYMFLECILFITEMKT GFFABHSNQLMNISAYPSWSKVMQGLIRMYKAECLEEKFPVIQHF	1 1			KISENTVI VOVVDDVDDEFI SVMDET SACETED VVDNIMA SV
YANPAFETTMGYQGELIGKELGBYPINEKKADLLDTINSCIRI GKEWQGIYYAKKKNGDNIQQNVKIJPVIGQGGKIRHYVSIIRVC NGNKABKISBCVQSDTHTDNOTGKHKDRRKGSLDVKAVASRAT EVSSQRRHSSMARIHSMTIEAPITKVINIINAAQESSPMPVTEA LDRVLEILRTTELYSPQFGAKDDPHANDLUGGLMSDGIRRISG NEPYLSTKNTOMVSSNIJTPISLDDVPPRIARMENEEYWDPDI FELEAATHNRPLIYIGLKMFARFGICEFLHCSESTLRSWLQTIE ANYHSSNPYHNSTHSADVLHATAYFLSKERIKETLDPIDEVAAL IAATIHDVDHPGRTNSFLCNAGSELAILYNDTAVLESHHAALAF QLTIGDDKCNIFKAMERNDYRTLRQGIIDMVLATEMTKHFEHVN KPVNSINKPLATLEENGETDKNQEVINTMLRTPENRTLIKRMLI KCADVSNPCRPLQYCIEWAARISEEYFSGTDEEKQQGLPVVMPV FDRNTCSIPKSQISFIDVFITDMFDAWDAFVDLPDLMQHLDNNF KYWKGLDEMKLRNLRPPPB  5508  1151 691 LSSVFSRRSASMFAVGCSMGPFLHYWYLSLDRLFPASGLRGFPN VLKKVLVDQLVASPLLGVWYFIGLGCLEGQTVGESCQELREKFW EFYKADWCVWPAAQFVNSLFVPPQGRVTYINGLTGWDTYLSYL KYKSPVPLTPPGCVALDTRAD  5509 1238 619 RKSRGCQNALSASGPAAAAAATMVRKLKFHEQKLLKQVDFLNWE VTDHNLHELRVLRYRYLQREDYTRYNQLSRAVRELARRIKDLP ERDQFRVRASAALLDKLYALGLVPTRGSLELCDFVTASSFCRRR LPTVLLKLRMAQHLQAVAFVEQGHVVGPDVVTDPAFLVTRSM EDPVTWVDSKIKKHVLQAVAFVEQGHVVGPDVVTDPAFLVTRSM EDPVTWDSKIKRHVLQAVAFVEGGRGRGGGGGGGGGGRSKM AGGERQPPPDSSERAPPATQNFIIPKEILLTNDWID AGGERQPPPDSSBEAPPATQNFIIPKKEIHTVPDMGKWKRSQAY ADYIGFILTLNEGVKGKKLTTERVSEAIEKUJALLNTLDRWID ETTPPUDQPSRFGNKAYRTWYAKLDERAENLVATVYPHLAAAVP EVAVYLKESVGNSTRIDYGTGHEAAFAAFLCCLCKIGVLRVDDQ IAIVFKVFNRYLEVMRKLQKTYRMEPAGSQGWGLDDFGFLPFI WGSSQLIDHPYLEPRHFVDEKAVNENHKDYMFLECILFITEMKT GFFABHSNQLWNISAVPSWSKVNQGLIRNYKABCLEKFFVIQHF	J ·	j		NELLOLEFGEVESOLKI. PACNEVETAL ENGEDATETTERDETO
GKEMGGIYYAKKNGDNIQQNVKIIPVIGQGGKIRHYVSIIRVC NGNNKAEKISBCVQSDTHTDNQTGKHKDRRKGSLDVKAVASRAT EVSSQRRHSSMARIHSMTIEAPITKVINIINAAQESSPMPYTEA LDRVLEILRTTELYSPQFGAKDDDPHANDLVGGLMSDGLRRLSG NEYVLSTKNTQMVSSNIITPISLDDVPPRIARAMENEEYWDPDI FELEAATHNRPLIYLGLKMFARGGICFHLGESETIRSWLQIIE ANYHSSNPYHNSTHSADVLHATAYFLSKERIKETLDPIDEVAAL IAATIHDVDHPGRTNSFLCNAGSELAILYNDTAVLESHHAALAF QLTTGDDKCNIFKNMENDYRTLRQGIIDMVLATEMTKHFEHVN KPVNSINKPLATLEENGETDKNQEVINTMLRTPENRTLIKRMLI KCADVSNPCRPLQYCIEWAARISEEYFSQTDEEKQQGLPVVMPV FDRNTCSIPKSQISFIDYSTIDMFDAWDAFVLPDLMQHLDNNF KYWKGLDEMKLRNLRPPB  S508  1151 691 LSSVFSRSASMFAVGCSNGPFLHYWYLSLDRLPPASGLRGFPN VLKKVLVDQLVASPLLGWUFJLGGCLEGGTVGESCQELRKFW EFYKADWCVMPAAQFVNTLFVPPQFRVTYINGLTLGWDTYLSYL KYRSPVPLTPPGCVALDTRAD  5509 1238 619 RKSRGCQNALSASGPAAAAAATMVRKLKFHEQKLLKQVDFLNWE VTDHNLHELRVLRRYRQNELGWREDYTRYNQLSRAVRELARRLRDLP ERDQFRVRASAALLBKLYALGLVPTRGSLELCDFVTASSFCRRR LPTVLLKLRNAQHLQAAVAFVRGGHVRVGPDVVTDPAFLVTRSM EDFVTWVDSSKIKRHVLEYNBERDDFDLEA  5510 96 1195 PÄGÄHLSSGSSEPLVEFGRGRVGARVKGERGLQASGSAPGRSKM AEGERQPPPDSSEEAPPATQNFIIPKKEIHTVPDMGKWKRSQAY ADYIGFILTUNEGVKGKKITFFYRVSEAIEKLVALLNTLDRWID ETPPVDOPSRFGNKAYATWAKLDEBAENLVATVVPTHLAAAVP EVAVYLKESVGNSTRIDYGTGHEAAFAAPLCCLCKIGVLRVDDQ IAIVFKVFNRYLEVMRKLQKTYRMPAGSGGWGLDDFQLPFI WGSSQLIDHPYLEPRHFVDEKAVNENHKDYMFLECILFITEMKT GFPABHSNQLWNISAVPSWSKVNQGLIRNYKABCLEKFPVJQHF	<b>!</b>	1		YANPAFETTMGYOSGELIGKELGKVPINEKKADILDTINGCIDT
NGNKAEKISECVQSDTHTDNQTGKHKJRRKGSLDVKAVASRAT EVSSQRRHSSMARIHSMTIEAPITKVINIINAAQESSPMPVTEA LDRVLEILRTTELJYSPQFGAKDDPHANDLVGGLMSDGLRRLSG NEYVLSTKNTOMVSSNIITPISLDDVPPRIARAMENEEYWDFDI FELEAATHNRFLIYLGLLKMFARFGICEFLHCSESTLRSWLQIIE ANYHSSNPYHNSTHSADVLHATAYPISKERIKETLDPIDEVAAL IAATIHDVDHFGRTNSFLCNAGSELAILYNDTAVLESHHAALAF QLTIGDDKCNIFKNMERNDYRTLRGGIIDMVLATEMTKHFEHVN KPVNSINKPLATLEENGETDKNQEVINTMLRTFENRTLIKRMLI KCADVSNPCRPLQYCIEWAARISEEYFSGTDEEKQQGLPVVMPV FDRNTCSIPKSQISFIDYFITDMFDAWDAFVDLPDLMQHLDNNF KYWKGLDEMKLRNLRPPPB S508 1151 691 LSSVFSRRSASMFAVGCSMGPFLHYWYLSLDRLFPABGLRGFPN VLKKVLVDQLVASPLLGVWYFLGLGCLEGQTVGESCQELREKFW EFYKADMCVWPPAQFVNFLFVPPQFRVTYINGLTLGWDTYLSYL KYRSPVPLTPPGCVALDTRAD  5509 1238 619 RKSRGCONALSASGPAAAAAIMVRKLKFHEQKLLKQVDFLNWE ERDQFRVRASAALDKLYALGLVPTRGSLELCDFVTASSFCRR LPTVLLKLRMAQHLQAAVAFVEQGHVWGPDVVTDPAFLVTRSM EPFVTWVDSSKIKRRVLEYNEERDDFDLEA  5510 96 1195 PAGAHLSSGSSEPLVEFGRGRVGARVKGERGLQASGSAPGRSKM AGGEROPPPDSSBEAPPATONFIIPKKEIHTVPDMGKWKRSQAY ADYIGFILTILNEGVKGKKKLTFEYRVSEAIEKLVALLINTLDRWID ETPPVDQPSRRGNKAYRTWYAKLDEERENLVATLVDTWLDAAVP EVAVYLKESVGNSTRIDYGTGHEAAFAAFLCCLCKIGVLRVDDQ IAIVFKVFNRYLEVMRKLQKTYRMEPAGSQGVWGLDDFGFLPFI WGSSQLIDDHPYLEPRHFVUDEKAVNENHKDYMFLECILFITEMKT GPFAEHSNQLWNISAVPSWSKVMQGLIRMYKABCLEKFFPVIQHF	1 1	ł		GKEWQGIYYAKKKNGDNIQONVKIIPVIGOGGKIRHYVSTIRVC
EVSSQRRHSSMARIHSMTIEAPITKVINIINAAQESSPMPVTEA LDRVLEILRTTELYSPQFGAKDDDPHANDLVGGLMSDGLRRISG NEYVLSTKNTONYSSNITPISLDVPPRIARAMENEEYWDPDI FELEAATHNRPLIYLGLKMFARFGICEFLHCSESTLRSWLQIIE ANYHSSNPYHNSTHSADVLHATAYFLSKERIKETLDPIDEVAAL IAATIHDVDHPGRTNSFLCNAGSELAILYNDTAVLESHHAALAF QLTTGDDKCNIFKNMERNDYRTLRQGIIDMVLATEMTKHFEHVN KPVNSINKPLATLEENGETDKNQEVINTMLRTPENRTLIKKMLI KCADVSNPCRPLQYCIEWAARISEEYSGTDEEKQQGLPVVMPV FDRNTCSIPKSQISFIDYFITDMFDAWDAFVDLPDIMQHLDNNF KYWKGLDEMKLRNLRPPPB  S508 1151 691 LSSVFSRSASMFAVGCSMGPFLHYWYLSLDRLFPABGLRGFPN VLKKVLVDQLVASPLLGWYFLGIGCLEGQTVGESCQELREKFW EFYKADWCVWPAAQFVNFLFVPPGFRVTYINGLTLGWDTYLSYL KYRSPVPLIPPGCVALDTRAD VTCHNLHELRVLRRYRLQRREDYTRYNQLSRAVRELARRLRDLP ERDQFRVRASAALDKLYALGLVPTRGSLELCDFVTASSFCRRR LPTVLLKLRMAQHLQAAVAFVEQGHVRVGPDVVTDPAFLVTRSM EDFVTWVDSSKIKRHVLEYNEERDDFDLEA  5510 96 1195 PAGAHLSSGSSEPLVEFGRGVGARVKGERGLQASGSAPGRSKM AEGERQPPPDSSEEAPPATOMFIIPKEIHTVPDMGKWKRSQAY ADYIGFILTLNEGVKGKKLTFEYRVSEAIEKLVALLNTLDRWID ETPPVDQPSRFGNKAYRTWYSKLDEERAENLVATVVPTHLAAAVP EVAVYLKESVGNSTRIDYGTGHEAAFAAFLCCLCKIGVLRVDDQ IAIVFKVFNRYLEVWRKLQKTYRMEPAGSGGVWGLDDFGFLPFI WGSSQLIDHPYLLEPHFVDEKAVNENHKDYMFLECILFITEMKT GPFAEHSNQLWNISAVPSWSKVNQGLIRNYKAECLEKFPVIQKF	] }	}		NGNNKAEKISBCVQSDTHTDNQTGKHKDRRKGSLDVKAVASRAT
LDRVLEILRTTELYSPQRGAKDDDPHANDLVGGLMSDGLRRLSG NEYVLSTKNTQNVSSNIITPISLDDVPPRIARAMENEYWDPDI FELEAATHNRPLIYIGLKMFARRGICEFHCSESTLRSWLQIIE ANYHSSNPYHNSTHSADVLHATAYFLSKERIKETLDPIDEVAAL IAATIHDVDHPGRTNSFLCNAGSELAILYNDTAVLESHHAALAF QLTTGDDKCNIFKNMERNDYRTLRQGIIDMVLATEMTKHFEHVN KPVNSINRPLATLEENGETDKNQEVINTMLRTPENRTLIKRMLI KCADVSNPCRPLQYCIEWAARISEEYFSQTDEEKQQGLPVVMPV FDRNTCSIPKSQISFIDYFITDMFDAWDAFVDLPDIMQHLDNNF KYWKGLDEMKLRNLRPPPB  5508 1151 691 LSSVFSRSASMFAVGCSMGPFLHYWYLSLDRLFPABGLRGPPN VLKKVLVDQLVASPLLGVWYFLGLGCLEGQTVGESCQELREKFW EFYKADWCVWPAAQFVMFLFVPPQFRVTYINGLTLGWDTYLSYL KYRSPVPLTPPGCVALDTRAD  5509 1238 619 RKSRGCQNALSASGPAAAAAAIMVRKLKFHEQKLLKQVDFLNWE VTDHNLHELRVLRRYRLQRREDYTRYNQLSRAVRELARRLRDLP ERDQFRVRASAALLDKLYALGLVPTRGSLELCDFVTASSFCRRR LPTVLLKLRMAQHLQAAVAFVEQGHVRVGPDVVTDPAFLVTRSM EDFVTWVDSSKIKRHVLEYMEERDDFDLEA  5510 96 1195 PAGAHLSSGSSEPLVEPGRGVGARVKGERGLQASGSAPGRSKM ABGERQPPPDSSEEAPPATOMFIIPKEIHTVPDMGKWKRSQAY ADYIGFILTLNEGVKGKKLTFEYRVSEAIEKLVALLNTLDRWID ETPPVDQPSRFGNKAYRTWYSKLDEEFAENLVATVVPTHLAAAVP EVAVYLKESVGNSTRIDYGTGHEAAFAAFLCCLCKIGVLRVDDQ IAIVFKVFNRYLEVWRKLQKTYRMEPAGSGGVWGLDDFGFLPFI WGSSQLIDHPYLLEPHFVDEKAVNENHKDYMFLECILFITEMKT GPFAEHSNQLWNISAVPSWSKVNQGLIRNYKAECLEKFPVIQKF	1 1			EVSSQRRHSSMARIHSMTIEAPITKVINIINAAQESSPMPVTEA
FELEAATHNRPLIYLGLKMFARFGICEFLHCSESTLRSWLQIIE ANYHSSNPYHNSTHSADVLHATAYPLSKERIKETLDPIDEVAAL IAATIHDVDHPGRTNSFLCNAGSELAILYNDTAVLESHHAALAF QLTTGDDKCNIFKMMERNDYRTLRGGIIDMVLATEMTKHPEHVN KPVNSINKPLATLEENGETDKNQEVINTMLRTPENRTLIKRMLI KCADVSNPCRPLQVCIEWAARISEEYFSQTDEEKQQGLPVVMPV FDRNTCSIPKSQISFIDYPITDMFDAWDAFVDLPDLMQHLDNNF KYWKGLDEMKLRNLRPPPB  S508  1151  691  LSSVFSRRSASMFAVGCSMGPFLHYWYLSLDRLFPABGLRGFPN VLKKVLVDQLVASPLLGVWYPLGLGCLEGQTVGESCQELREKFW EFYKADWCVWPAAQFVNTLFVPPQFRVTYINGLTLGWDTYLSYL KYRSPVPLTPPGCVALDTRAD  7509  1238  619  RKSRGCQNALSASGPAAAAAINVRKLKFHEQKLLKQVDFLNWE ERDQFRVRASAALLDKLYALGLYPTRGSLELCDFVTASSFCRRR LPTVLLKLRMAQHLQAAVAFVEQGHVRVGPDVVTDPAFLVTRSM EPFVTWVDSKIKRHVLEYNEERDDFDLEA  5510  96  1195  PAGAHLSSGSSEPLVEPFGRGRVGARVKGERGLQASGSAPGRSKM AGEGROPPDSSEEAPPATONFIIPKEIHTVPDMGKWKRSQAY ADYIGFILTLNEGVKGKKLTFEYRVSEAIEKLVALLNTLDRWID ETPPVDQPSRFCNKAYRTWYAKLDEEAENLVATVVPTHLAAAVP EVAVYLKESVGNSTRIDYGTGHEAAFAAFLCCLCKIGVLRVDDQ IAIVFKVFNRYLEVMRKLQKTYRMEPAGSQGVWGLDDFGLIFFI WGSSQLIDHPYLEPRHFYDEKAVNENHKDYMFLECILFITEMKT GPFAEHSNQLWNISAVPSWSKVNQGLTRMYKABCLEKFPVIQHF	1 1	İ		LDRVLEILRTTELYSPQFGAKDDDPHANDLVGGLMSDGLRRLSG
ANYHSSNPYHNSTHSADVLHATAYFLSKER IKETLDPIDEVAAL  IAATIHDVDHPGRTNSFLCNAGSELAILYNDTAVLESHHAALAF QLTTGDKCKIFKKMERNDYRTLRQGI IDMVLATEMTKHFEHVN KPVNS INKPLATLEENGETDKNQEVINTMLRTE ENRTLIKRMLI KCADVSNPCRPLQYCIEWAARISEEYFSQTDEEKQQGLPVVMPV FDRNTCSIPKSQISFTDYFITDMFDAWDAFVDLPDLMQHLDNNF KYWKGLDEMKLRNLRPPPB  1151 691 LSSVFSRSASMFAVGCSMGPFLHYWYLSLDRLFPABGLRGFPN VLKKVLVDQLVASPLLGVWYFLGLGCLEGQTVGESCQELREKFW EFYKADWCVWPAAQFVNFLFVPPQFRVTYINGLTLGWDTYLSYL KYRSPVPLTPPGCVALDTRAD  5509 1238 619 RKSRGCQNALSASGPAAAAAAIMVRKLKFHEQKLLKQVDFLNWE ERDQFRVRASAALLDKLYALGLVPTRGSLELCDFVTASSFCRRR LPTVLLKLRMAQHLQAAVAFVEQGHVRVGPDVVTDPAFLVTRSM EDFVTWVDSSKIKRHVLEYNEERDDFDLEA  5510 96 1195 PAGAHLSSGSSEPJVEFGRGRVGARVKGERGLQASGSAPGRSKM AEGERQPPPDSSEEAPPATQNFIIPKKEIHTVPDMKKWKRSQAY ADYIGFILTLNEGVKGKKLTFEYRVSEAIEKLVALLNTLDRWID ETPPVDQPSRFGNKAYRTWYAKLDEEAENLVATVVPTHLAAAVP EVAVYLKESVGNSTRIDYGTGHEAAFAAFLCLCKKIGVLRVDDQ IAIVFKVFNRYLEVMRKLQKTYRMEPAGSQGVWGLDDFGFLPFI WGSSQLIDHPYLEPRHFVDEKAVNNGKLIRTLGEMKT GPFAEHSNQLWNISAVPSWSKVNGGLIRMYKAECLEKFPVLGHF	1 ]	. [		NEYVLSTKNTQMVSSNIITPISLDDVPPRIARAMENEEYWDFDI
IAATIHDVDHPGRTNSFLCNAGSELAILYNDTAVLESHHAALAF QLTTGDKCNIFKNMERNDYRTLRGGIIDMVLATEMTKHFEHVN KPVNSINKPLATLEENGETDKNQEVINTMLRTPENRTLIKRMLI KCADVSNPCRPLQYCIEMAARISEBYFSQTDEBKQQGLPVVMPV FDRNTCSIPKSQISFIDYFITDMFDAWDAFVDLPDLMQHLDNNF KYWKGLDEMKLRNLRPPPB  5508  1151  691  LSSVFSRSASMFAVGCSMGPFLHYWYLSLDRLFPASGLRGPPN VLKKVLVDQLVASPLLGVWYPLGLGCLEGQTVGESCQELREKFW EFYKADWCVWPAAQFVNFLFVPPQFRVTYINGLTLGWDTYLSYL KYRSPVPLTPPGCVALDTRAD  5509  1238  619  RKSRGCQNALSASGPAAAAATMVRKLKFHEQKLLKQVDFLNWE VTDHNLHELRVLRRYRLQRREDYTRYNQLSRAVRELARRLRDLP ERDQFRVRASAALLDKLYALGLVPTRGSLELCDFVTASSFCRRR LPTVLLKLRMAQHLQAAVAFVEGGHVRVGPDVVTDPAFLVTRSM EDFVTWVDSSKIKRHVLEYNEERDDFDLEA  5510  96  1195  PAGAHLSSGSSEPLVEFGRGRVGARVKGERGLQASGSAPGRSKM AEGERQPPPDSSBEAPPATQNFIIPKKEHTTVPDMGKWKRSQAY ADYIGFILTLNEGVKGKKLTFEYRVSEAIEKLVALLNTLDRWID ETPPVDQPSRFGNKAYRTWYAKLDBEAENLVATVVPTHLAAAVP EVAVYLKESVGNSTRIDYGTGHEAAFAAFLCCLCKIGVLRVDDQ IAIVFKVFNRYLEVMRKLQKTYRMEPAGSQGVWGLDDFQFLPFI WGSSQLIDHPYLEFRHFVDEKAVNENHKDYMFLECILFITEMKT GPFAEHSNQLWNISAVPSWSKVNQGLIRMYKAECLEKFPVIQHF	1 1	į		FELEAATHNRPLIYLGLKMFARFGICEFLHCSESTLRSWLQIIE
QLTTGDKCNIFKNMERNDYRTLRQGIIDMVLATEMTKHFEHVN KPYNSINKPLATLEENGETDKNQEVINTMLRTPENRTLIKRMLI KCADVSNPCRFLQYCIEWAARISEEYFSQTDEEKQQGLPVVMPV FDRNTCSIPKSQISFIDYFITDMFDAWDAFVDLPDLMQHLDNNF KYWKGLDEMKLRNLRPPPB  S508  1151 691 LSSVPSRRSASMFAVGCSMGPFLHYWYLSLDRLFPAEGLRGPPN VLKKVLVDQLVASPLLGTWYFLGLGCLEGQTVGESCQELREKFW EFYKADWCVWPAAQFVNFLFVPPQFRVTYINGLTLGWDTYLSYL KYRSPVPLTPPGCVALDTRAD  S509 1238 619 RKSRGCQNALSASGPAAAAAAIMVRKLKFHEQKLLKQVDFLNWE VTDHNLHELRVLRRYRLQRREDYTRYNQLSRAVRELARRLRDLP ERDQFRVRASAALLDKLYALGLVPTRGSLELCDFVTASSFCRRR LPTVLLKLRMAQHLQAAVAFVEQGHVRVGPDVVTDPAFLVTRSM EDFVTWVDSSKIKRHVLEYNEERDDFDLEA  5510 96 1195 PAGAHLSSGSSEPLVEFGRGRVGARVKGERGLQASGSAPGRSKM AEGERQPPPDSSEEAPPATQNFIIPKKETHTVPDMKWKRSQAY ADYIGFILTLNEGVKGKKLTFEYRVSEAIEKLVALLNTLDRWID ETPPVDQPSRFGNKAYRTWYAKLDEEAENLVATVVPTHLAAAVP EVAVYLKESVGNSTRIDYGTIGHEAAFAAFLCCLCKIGVLRVDDQ IAIVFKVFNRYLEVMRKLQKTYRMEPAGSQGVWGLDDFQFLPFI WGSSQLIDHPYLEFRHFVDEKAVNENHKDYMFLECILFITEMKT GPFAEHSNQLWNISAVPSWSKVNQGLIRMYKAECLEKFPVIQHF	1		l	ANYHSSNPYHNSTHSADVLHATAYFLSKERIKETLDPIDEVAAL
KPVNSINKPLATLEENGETDKNQEVINTMLRTPENRTLIKRMLI KCADVSNPCRPLQYCIEWAARISEBYFSQTDEBKQQGLPVVMPV FDRNTCSIPKSQISFIDYFITDMFDAWDAFVDLPDLMQHLDNNF KYWKGLDEMKLRNLRPPPB S508 1151 691 LSSVFSRSSASMFAVGCSMGPFLHYWYLSLDRLFPASGLRGPPN VLKKVLVDQLVASPLLGVWYFLGLGCLEGQTVGESCQELREKFW EFYKADWCVWPAAQFVNFLFVPPQFRVTYINGLTLGWDTYLSYL KYRSPVPLTPPGCVALDTRAD  5509 1238 619 RKSRGCQNALSASGPAAAAAIMVRKLKFHEQKLLKQVDFLNWE VTDHNLHELRVLRRYRLQRREDYTRYNQLSRAVRELARRLRDLP ERDQFRVRASAALLDKLYALGLVPTRGSLELCDFVTASSFCRRR LPTVLLKLRMAQHLQAAVAFVEQGHVRVGPDVVTDPAFLVTRSM EDFVTWVDSSKIKRHVLEYNEERDDFDLEA  5510 96 1195 PAGAHLSSGSSEPLVEPGRGRVGARVKGERGLQASGSAPGRSKM AEGERQPPPDSSBEAPPATQNFIIPKKEIHTVPDMGKWKRSQAY ADYIGFILTLNEGVKGKKLTFEYRVSEAIBKLVALLNTLDRWID ETPPVDQPSRFGNKAYRTWYAKLDEEDEBLVATVVPTHLAAAVP EVAVYLKESVGNSTRIDYGTGHEAAFAAFLCCLCKIGVLRVDDQ IAIVFKVFNRYLEVMRKLQKTYRMEPAGSQGVWGLDDFQFLPFI WGSSQLIDHPYLEFRHFVDEKAVNENHKDYMFLECILFITEMKT GPFAEHSNQLWNISAVPSWSKVNQGLIRMYKAECLEKFPVLQHF	.	•		LAATIHDVDHPGRTNSFLCNAGSELAILYNDTAVLESHHAALAF
KCADVSNPCRPLQYCIEWAAR ISBEYFSQTDEB KQQGLPVVMPV FDRNTCSI PRSQISFIDYFITDMFDAWDAFVDLPDLMQHLDNNF KYWKGLDEMKLRNLRPPPB LSSVFSRRSASMFAVGCSMGPFLHYWYLSLDRLFFABGLRGFPN VLKKVLVDQLVASPLLGWYYFLGIGCLEGQTVGESCQELREKFW EFYKADWCVWPAAQFVNFLFVPPQFRVTYINGLTLGWDTYLSYL KYRSPVPLTPPGCVALDTRAD  5509 1238 619 RKSRGCQNALSASGPAAAAAAIMVRKLKFHEQKLLKQVDFLNWE VTDHNLHELRVLRRYRLQREDYTRYNQLSRAVRELARRLRDLP ERDQFRVRASAALLDKLYALGLVPTRGSLELCDFVTASSFCRRR LPTVLLKLRMAQHLQAAVAFVEQGHVRVGPDVVTDPAFLVTRSM EDFVTWVDSSKIKRHVLEYNEERDDFDLEA AEGERQPPPDSSBEAPPATQNFIIPKKEIHTVPDMGKWKRSQAY ADYIGFILTLNEGVKGKKLTFEYRVSEAIEKLVALLNTLDRWID ETPPVDQPSRFGNKAYRTWYAKLDEEAEDLVATVVPTHLAAAVP EVAVYLKESVGNSTRIDYGTGHEAAFAAPLCCLCKIGVLRVDDQ IAIVFKVFNRYLEVMRKLQKTYRMEPAGSQGVWGLDDFQFLPFI WGSSQLIDHPYLEFRHFVDEKAVNENHKDYMFLECILFITEMKT GPFAEHSNQLWNISAVPSWSKVNQGLIRMYKAECLEKFPVLQHF			•	KENNE INKDI PATIBENGEMDINIANATANATANATANATANATANATANATANATANATA
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AEGERQPPPDSSBEAPPATQNFIIPKKEIHTVPDMGKWKRSQAY ADYIGFILTLNEGVKGKKLTFEYRVSEAIEKLVALLNTLDRWID ETPPVDQPSRFGNKAYRTWYAKLDEEAENLVATVVPTHLAAAVP EVAVYLKESVGNSTRIDYGTGHEAAFAAFLCCLCKIGVLRVDDQ IAIVFKVFNRYLEVMRKLQKTYRMEPAGSQGVWGLDDFQFLPFI WGSSQLIDHPYLEPRHFVDEKAVNENHKDYMFLECILFITEMKT GPFAEHSNQLWNISAVPSWSKVNQGLIRMYKAECLEKFPVIQHF	EETA			EDFVTWVDSSKIKRHVLEYNEERDDFDLEA
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SEO	Predicted	15	
ID	beginning	Predicted end	Amino acid segment containing signal peptide
NO:	nucleotide	nucleotide location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	Seserine, Teinreonine, Vevaline,
	amino acid	sequence	W=Tryptophan, Y=Tyrosins, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
1	sequence	poducinos	\=possible nucleotide insertion)
5511	276	1980	KLSRVLNLPPENLITSISAVPISQKEEVADFQLSVDSLLEKDND
1	1	1	HERBOTOVOVED PERI BEDTTERED SOREE VADROLS VDS LLEKDND
-		ŧ	HSRPDIQVQAKRLAEKLRCDTVVSBISTGQRTVNFKINRELLTK TVLQQVIEDGSKYGLKSELFSGLPQKKIVVEFSSPNVAKKFHVG
1	1	İ	HLRSTIIGNFIANLKEALGHQVIRINYLGDWGMQFGLLGTGFQL
	}		FGYEEKLQSNPLQHLFEVYVQVNKEAADDKSVAKAAQEFFQRLE
		[	LGDVQALSLWQKFRDLSIEEYIRVYKRLGVYFDEYSGESFYREK
1	· ]		SQEVLKLLESKGLLLKTIKGTAVVDLSGNGDPSSICTVMRSDGT
1		•	SLYATROLAAAIDRMDKYNFDTMIYVTDKGQKKHPQQVFQMLKI
1	1		MGYDWAERCQHVPFGVVQGMKTRRGDVTFLEDVLNEIQLRMLQN
1			MASIKTTKELKNPQETAERVGLAALIIQDFKGLLLSDYKFSWDR
			VFQSRGDTGVFLQYTHARLHSLEETFGCGYLNDFNTACLQEPQS
1.	]		VSILQHLLRFDEVLYKSSQDFQPRHIVSYLLTLSHLAAVAHKTL
			QIKDSPPEVAGARLHLFKAVRSVLANGMKLLGITPVCRM
5512	120	1015	DPSLLLTITVTGVTVLVLVLKSMNSRRREPITLQDPEAKYPLPL
1			IEKEKISHNTRRFRFGLPSPDHVLGLPVGNYVQLLAKIDNELVV
İ			RAYTPVSSDDDRGFVDLIIKIYFKNVHPQYPEGGKMTQYLENMK
ŀ		·	IGETIFFRGPRGRLFYHGPGNLGIRPDQTSEPKKTLADHLGMIA
<b>.</b> .			GGTGITPMLQLIRHITKDPSDRTRMSLIFANQTEEDILVRKELE
1	1.00	•	BIARTHPDQFDLWYTLDRPPIGWKYSSGFVTADMIKEHLPPPAK
			STLILVCGPPPLIQTAAHPNLEKLGYTQDMIFTY
5513	2	837	ARWRLPSDSPRIPPAGAETPGRGSCRNYLPSSSPPPPPEPSSFPS
			PPTSRGGPGSRDTMSDSEEESQDRQLKIVVLGDGASGKTSLTTC
1	1		FAQETFGKQYKQTIGLDFFLRRITLPGNLNVTLQIWDIGGQTIG
: <b> </b> *	'		GKMLDKYIYGAQGVLLVYDITNYQSFENLBDWYTVVKKVSEESE
1			TOPLVALVGNKIDLEHMRTIKPEKHLRFCQENGFSSHFVSAKTG
1			DSVFLCFQKVAAEILGIKLNKAEIEQSQRVVKADIVNYNQEPMS
		·	RTVNPPRSSMCAVQ
5514	1295	449	VNRPSWIMGNFRGHALPGTFFFIIGLWWCTKSILKYICKKQKRT
j i	j		CYLGSKTLFYRLEILEGITIVGMALTGMAGEOFIPGCPHLMLYD
	. 1		YKQGHWNQLLGWHHFTMYFFFGLLGVADILCFTISSLPVSI.TKT.
1		•	MLSNALFVEAFIFYNHTHGREMLDIFVHOLLVLVVFLTGLVAFT.
1	.		EFLVRNNVLLELLRSSLILLQGSWFFQIGFVLYPPSGGPAWDLM
[ .	,	•	DHENILFLTICFCWHYAVTIVIVGMNYAFITWLVKSRLKRLCSS
5515	1572		EVGLLKNAEREQESEEEM
. 3313	15/2	260	FVRLVGRGDCDPLLSVCLTTMPLYEGIGSGGEKTAVVIDLGEAF
			TKCGFAGETGPRCIIPSVIKRAGMPKPVRVVQYNINTEELYSYL
	٠		KEFIHILYFRHLLVNPRDRRVVIIESVLCPSHFRETLTRVLFKY
			FEVPSVLLAPSHLMALLTLGINSAMVLDCGYRESLVLPIYEGIP
			VLNCWGALPLGGKALHKELETQLLEQCTVDTSVAKEQSLPSVMG
			SVPEGVLEDIKARTCFVSDLKRGLKIQAAKFNIDGNNERPSPPP
		i	NVDYPLDGEKILHILGSIRDSVVEILFEQDNEEQSVATLILDSL
			IQCPIDTRKQLAENLVVIGGTSMLPGFLHRLLAEIRYLVEKPKY
	·		VYNOTCE I DENGCI NEED ENGRESS TO STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF TH
5516	3	735	YYNQTGRIPDWCSLNNPPLEMMFDVGKTQPPLMKRAFSTEK
	. 7	733	NSREPPQAGPGPSPRKSPTASSFLFPWRPLASSFWMGAQGAQES
. ]	•		IKAMWRVPGTTRRPVTGESPGMHRPEAMLLLLTLALLGGPTWAG
İ	1	[	KMYGPGGGKYFSTTEDYDHEITGLRVSVGLLLVKSVQVKLGDSW
ŀ	ł	· .	DVKLGALGGNTQEVTLQPGEYITKVFVAFQAFLRGMVMYTSKDR
		l	YFYFGKLDGQISSAYPSQEGQVLVGIYGQYQLLGIKSIGFEWNY PLEEPTTEPPVNLTYSANSPVGR
5517	246	499	SELYVAMRTDSSKMTDVESGVANFASSARAGRRNALPDIQSSAA
1			TDGTSDLPLKLEALSVKEDAKEKDEKTTQDQLEKPQNEEK
5518	3	1375	DAWADAWVRAWDLNMDFPCLWLGLLLPLVAALDFNYHRQEGMEA
1	ļ		FIXTUDONY SCUTUL DE TOUGHEGE DE L'UN DESCRIPCIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'ANDIONE DE L'AN
		1	FLKTVAQNYSSVTHLHSIGKSVKGRNLWVLVVGRFPKEHRIGIP
1		1	EPKYVANMHGDETVGRELLLHLIDYLVTSDGKDPEITNLINSTR
1		1	IHIMPSNNPDGFEAVKKPDCYYSIGRENYNQYDLNRNFPDAFBY
ĺ		1	MNVSRQPETVAVMKWLKTETFVLSANLHGGALVASYPFDNGVQA TGALYSRSLTPDDDVFQYLAHTYASRNPNMKKGDECKNKMNFPN
- 1	1	Ş	GVTNGYSWYPLQGGMQDYNYIWAQCFEITLELSCCKYPREEKLP
		·	SFWNNNKASLIEYIKQV:LGVKGQVFDQNGNPLPNVIVEVQDRK
		<u>-</u>	TOTAL TROUBLE OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
l l	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	Paproline, QaGlutamine, RaArginine,
1	amino acid	residue of	SaSerine, TaThreonine, VaValine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ļ	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	1	\=possible nucleotide insertion)
	<del> </del>	<del> </del>	HICPYRTNKYGEYYLLLLPGSYIINVTVPGHDPHITKVIIPEKS
			QNFSALKKDILLPFQGQLDSIPVSNPSCPMIPLYRNLPDHSAAT
i		į	KPSLFLFLVSLLHIFFK
5519	87	477	IKSKLNQQVEVQESEWRLTEAKGPTMGKESGWDSGRAAVAAVVG
Ì		1	GVVAVGTVLVALSAMGFTSVGIAASSIAAKMMSTAAIANGGGVA
,	1		AGSLVAILQSVGAAGLSVTSKVIGGFAGTALGAWLGSPPSS
5520	117	943	PTEGRQKVLKTFTVPRSALAMTKTSTCIYHFLVLSWYTFLNYYI
)		}	SQEGKDEVKPKILANGARWKYMTLLNLLLQTIFYGVTCLDDVLK
ļ			RTKGGKDIKFLTAFRDLLFTTLAFPVSTFVFLAFWILFLYNRDL
}			TYPENI TYPET TEMPERATURE TRANSPORT A THE REPORT OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERT
l.			IYPKVLDTVIPVWLNHAMHTFIPPITLAEVVLRPHSYPSKKTGL
l	1		TLLAAASIAYISRILWLYFETGTWVYPVFAKLSLLGLAAFFSLS
			YVFIASIYLLGEKLNHWKWVSVQILQRWRLESVGICFQWPDWKS PAKHQLVKNIR
5521	546	911	
1	310	311	KILNMQKSCEENEGKPQNMPKAEEDRPLEDVPQEAEGNPQPSEE
1			GVSQEAEGNPRGGPNQPGQGFKEDTPVRHLDPEEMIRGVDELER
5522	1224	637	LREEIRRVRNKFVMMHWKQRHSRSRPYPVCFRP
1 3322	1224	63 /	GSRPLGQRSREKMWVFGYGSLIWKVDFPYQDKLVGYITNYSRRF
1	1		WQGSTDHRGVPGKPGRVVTLVEDPAGCVWGVAYRLPVGKEEEVK
i '	1		AYLDFREKGGYRTTTVIFYPKDPTTKPFSVLLYIGTCDNPDYLG
			PAPLEDIAEQIFNAAGPSGRNTEYLFELANSIRNLVPEKADEHL
5523	3		FALEKLVKERLEGKQNLNCI
3323	3	1280	SKGKKRMGSSMSAATARRPVFDDKEDVNFDHFQILRAIGKGSFG
		,	KVCIVQKRDTEKMYAMKYMNKQQCIERDEVRNVFRELEILQEIE
1			HVFLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNVQFSEDTV
			RLYTCEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI
1			ATIIKDGERATALSGTKPYMAPEIFHSFVNGGTGYSFEVDWWSV
1			GVMAYELLRGWRPYDIHSSNAVESLVQLFSTVSVQYVPTWSKEM
1 1			VALLRKLLTVNPEHRLSSLQDVQAAPALAGVLWDHLSEKRVEPG
			FVPNKGRLHCDPTFELEEMILESRPLHKKKKRLAKNKSRDNSRD
			SSQSENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPES
5524	85		RDAAEPVEDEAERSALPMCGPICPSAGSG
3324	85	2318	RERERDHRPGESSQGQSGAGGCFPSPTMELRCGGLLFSSRFDSG
i i	1		NLAHVEKVESLSSDGEGVGGGASALTSGIASSPDYEFNVWTRPD
1 1	į		CABTEFENGNRSNFYFSVRGGMPGKLIKINIMNMNKQSKLYSQG
1 [	1		MAPFVRTLPTRPRWERIRDRPTFEMTETQFVLSFVHRFVEGRGA
1 1			TTFFAFCYPFSYSDCQELLNQLDQRFPENHPTHSSPLDTIYYHR
1 {	1		ELLCYSLDGLRVDLLTITSCHGLREDREPRLEQLFPDTSTPRPF
1 1	}		RFAGKRIFFLSSRVHPGETPSSFVFNGFLDFILRPDDPRAQTLR
]	•	1	RLFVFKLIPMLNPDGVVRGHYRTDSRGVNLNRQYLKPDAVLHPA
1	}	ļ	IYGAKAVLLYHHVHSRLNSQSSSEHQPSSCLPPDAPVSDLEKAN
1 1	{		NLQNEAQCGHSADRHNABAWKQTEPAEQKLNSVWINPQQSAGLE
i i	ł		ESAPDTIPPKESGVAYYVDLHGHASKRGCFMYGNSFSDESTQVE
1 1	ļ		NMLYPKLISLNSAHFDFQGCNFSEKNMYARDRRDGQSKEGSGRV
; l	]		AIYKASGITHSYTLECNYNTGRSVNSIPAACHDNGRASPPPPPPA
] ]			FPSRYTVELFEQVGRAMAIAALDMAECNPWPRIVLSEHSSLTNL
1 {	ſ		RAWMLKHVRNSRGLSSTLNVGVNKKRGLRTPPKSHNGLPVSCSE
; l		j	NTLSRARSFSTGTSAGGSSSSQQNSPQMKNSPSFPFHGSRPAGL
5525	105		PGLGSSTQKVTHRVLGPVRGKPVWEPLQHVFGCLGHCWGK
1 3323	103	834	SNTLDFERHLFIMGQQISDQTQLVINKLPEKVAKHVTLVRESGS
) 1		i	LTYEEFLGRVAELNDVTAKVASGQEKHLLFEVQPGSDSSAFWKV
	1	.]	VVRVVCTKINKSSGIVEASRIMNLYQFIQLYKDITSQAAGVLAQ
		ļ	SSTSEEPDENSSSVTSCQASLWMGRVKQLTDEEECCICMDGRAD
1	ì	i	LILPCAHSFCQKCIDKWSDRHRNCPICRLQMTGANESWVVSDAP
5526			TEDDMANYILNMADEAGQPHRP
3320	3	853	RRPCNPVRAAKRTGAAARAPRGLEVTMLRVAWRTLSLIRTRAVT
1	1		QVLVPGLPGGGSAKFPFNQWGLQPRSLLLQAARGYVVRKPAOSR
į	1		LDDDPPPSTLLKDYQNVPGIEKVDDVVKRLLSLEMANKKEMLKI
1	J		KQEQFMKKIVANPEDTRSLEARIIALSVKIRSYEBHLEKHRKDK
· [		1	AHKRYLLMSIDQRKKMLKNLRNTNYDVFEKICWGLGIEYTFPPL
			YYRRAHRRFVTKKALCIRVFQETQKLKKRRRALKAAAAAQKQAK

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	A-miscidine, i=isoteucine, k=Lysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
ł	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
Į.	residue of		S=Serine, T=Threonine, V=Valine,
1		amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			RRNPDSPAKAIPKTLKDSQ
5527	3225	565	LLRKYLLHQNPLLLRHQPNRTCISFSATMKLKDTKSRPKQSSCG
	1		KFQTKGIKVVGKWKEVKIDPNMFADGQMDDLVCFEELTDYQLVS
ĺ	i		PAKNPSSLFSKEAPKRKAQAVSEEEEEBEGKSSSPKKKIKLKKS
1	1		KNVATEGTSTQKEPEVKDPELEAQGDDMVCDDPEAGEMTSENLV
ı	l		QTAPKKKKNKGKKGLEPSQSTAAKVPKKAKTWIPEVHDQKADVS
	i		
1	i .		AWKDLFVPRPVLRALSFLGFSAPTPIQALTLAPAIRDKLDILGA
ŀ			AETGSGKTLAFAIPMIHAVLQWQKRNAAPPPSNTEAPPGETRTE
4	Į.		AGAETRSPGKAEAESDALPDDTVIESEALPSDIAAEARAKTGGT
1			VSDQALLFGDDDAGEGPSSLIREKPVPKQNENEEENLDKEQTGN
İ			LKQELDDKSATCKAYPKRPLLGLVLTPTRELAVQVKQHIDAVAR
1			PTGIKTAILVGGMSTQKQQRMLNRRPEIVVATPGRLWELIKEKH
i	j		YHLRNLRQLRCLVVDEADRMVEKGHFAELSQLLEMLNDSQYNPK
		,	ROTLVFSATLTLVHQAPARILHKKHTKKMDKTAKLDLLMQKIGM
1			RGKPKVIDLTRNEATVETLTETKIHCETDEKDFYLYYFLMQYPG
1	ļ		RSLVFANSISCIKRLSGLLKVLDIMPLTLHACMHOKORLRNLEO
1			FARLEDCVLLATDVAARGLDIPKVQHVIHYQVPRTSEIYVHRSG
ļ	J j		RTARATNEGLSLMLIGPEDVINFKKIYKTLKKDEDIPLFPVQTK
!			YMDVVKERIRLARQIEKSEYRNFQACLHNSWIEQAAAALEIELE
1			EDMYKGGKADQQEERRRQKQMKVLKKELRHLLSQPLFTESQKTK
1	Î ,		YPTQSGKPPLLVSAPSKSESALSCLSKQKKKKTKKPKEPQPEQP
			OPSTSAN
5528	3	895	GPFLSACRMWGACKVKVHDSLATISITLRRYLRLGATMAKSKFE
		0,5	
			YVRDFEADDTCLAHCWVVVRLDGRNFHRFAEKHNFAKPNDSRAL
<b>1</b>	i		QLMTKCAQTVMEELEDIVIAYGQSDEYSFVFKRKTNWFKRRASK
1			FMTHVASQFASSYVFYWRDYFEDQPLLYPPGFDGRVVVYPSNQT
		•	LKDYLSWRQADCHINNLYNTVFWALIQQSGLTPVQAQGRLQGTL
1 .			AADKNEILFSEFNINYNNEPPMYRKGTVLIWQKVDEVMTKEIKL
			PTEMEGKKMAVTRTRTKPCKPSHLPRAPCLRWL
5529	48	640	TPRLVSAHLKTRKLINPEAAERRWRDWDSRQGWLSVKMQRVSGL
<b>{</b>	• ]		LSWTLSRVLWLSGLSEPGAAROPRIMEEKALEVYDLIRTIRDPE
1			KPNTLEELEVVSESCVEVQEINEEEYLVIIRFTPTVPHCSLATL
[	1		IGLCLRVKLQRCLPFKHKLEIYISEGTHSTEEDINKQINDKERV
1 1			AAAMENPNLREIVEQCVLEPD
5530	4541	2606	AQIVHAISYCHKLHVOHRDLKPENVVFFEKQGLVKLTDFGFSNK
1 1	1		FQPGKKLTTSCGSLAYSAPEILLGDEYDAPAVDIWSLGVILFML
] ]	J		VCGQPPFQEANDSETLTMIMDCKYTVPSHVSKECKDLITRMLQR
1	ł.		DPKRRASLEEIENHPWLQGVDPSPATKYNIPLVSYKNLSEEEHN
ľ			SIIQRMVLGDIADRDAIVEALETNRYNHITATYFLLAERILREK
)	j		QEKEIQTRSASPSNIKAQFRQSWPTKIDVPQDLEDDLTATPLSH
1		1	PANDUCDYDD YDCAL NOAD GACH AND AND AND AND AND AND AND AND AND AND
1 1	l	į	ATVPQSPARAADSVLNGHRSKGLCDSAKKDDLPELAGPALSTVP
} l	· }		PASLKPTASGRKCLFRVEEDEEEDBEDKKPMSLSTQVVLRRKPS
j i	. [	ſ	VTNRLTSRKSAPVLNQIFEEGESDDEFDMDENLPPKLSRLKMNI
1 1	1	}	ASPGTVHKRYHRRKSQGRGSSCSSSETSDDDSESRRRLDKDSGF
j l			TYSWHRRDSSEGPPGSEGDGGGQSKPSNASGGVDKASPSENNAG
į į	ſ	ļ	GGSPSSGSGGNPTNTSGTTRRCAGPSNSMQLASRSAGELVESLK
l ł	ļ	1	LMSLCLGSQLHGSTKYIIDPQNGLSFSSVKVQEKSTWKMCISST
		1	GNAGQVPAVGGIKFFSDHMADTTTELERIKSKNLKNNVLQLPLC
<del> </del>			EKTISVNIQRNPKEGLLCASSPASCCHVI
5531	24	515	GSQPRAPRPRDSMERPEPELIRQSWRAVSRSPLEHGTVLFARLF
		Į	ALEPOLLPLPQYNCRQFSSPEDCLSSPEFLDHIRKVMLVIDAAV
[		Í	TNVEDLSSLEEYLASLGRKHRAVGVKLSSFSTVGESLLYMLEKC
1		J	LGPAFTPATRAAWSQLYGAVVQAMSRGWDGE
5532	3395	1402	SDWMVVGKRKMIIEDETEFCGEELLHSVLQCKSVFDVLDGEEMR
<b>]</b>	1	ļ	RARTRANPYEMIRGVFFLNRAAMKMANMDFVFDRMFTNPRDSYG
· [	Í	}	KPLVKDREAELLYFADVCAGPGGFSEYVLWRKKWHAKGFGMTLK
·	1	ļ	GPNDFKLEDFYSASSELFEPYYGEGGIDGDGDITRPENISAFRN
J	1		FVLDNTDRKGVHFLMADGGFSVEGQENLQEILSKQLLLCQFLMA
ļ	[	Í	LSIVRTGGHFICKTFDLFTPFSVGLVYLLYCCFRRVCLFKPITS
	·		RPANSERYVVCKGLKVGIDDVRDYLFAVNIKLNQLRNTDSDVNL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning .	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	Interest M. Mathiarine, K-Lysine,
Į.	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
- {	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
1	residue of		S=Serine, T=Threonine, V=Valine,
}	1	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
I	amino acid	sequence	Codon, /=possible nucleotide deletion,
<b> </b>	sequence		\=possible nucleotide insertion)
1	1	l	VVPLEVIKGDHEFTDYMIRSNESHCSLQIKALAKIHAFVQDTTL
	İ	Ĺ	SEPRQAEIRKECLRLWGIPDQARVAPSSSDPKSKFFELIOGTEI
			DIFSYKPTLLTSKTLEKIRPVFDYRCMVSGSEQKFLIGLGKSOI
1	}	ì	YTWDGRQSDRWIKLDLKTELPRDTLLSVEIVHELKGEGKAQRKI
			SAIHILDVLVLNGTDVREQHFNQRIQLAEKFVKAVSKPSRPDMN
1	1		PIRVKEVYRLEEMEKIFVRLEMKIIKGSSGTPKLSYTGRDDRHF
1			VPMGLYIVRTVNEPWTMGFSKSFKKKFFYNKKTKDSTFDLPADS
1	l ·	1	IAPFHICYYGRLPWEWGDGIRVHDSQKPQDQDKLSKEDVLSFIQ
ł	}		MHRA
5533	94	789	
)	, ,,,	103	MKERRAPQPVVARCKLVLVGDVQCGKTAMLQVLAKDCYPETYVP
1			TVFENYTACLETEEQRVELSLWDTSGSPYYDNVRPLCYSDSDAV
1	Į		LLCFDISRPETVDSALKKWRTEILDYCPSTRVLLIGCKTDLRTD
Ì	1		LSTLMELSHQKQAPISYEQGCAIAKQLGPEIYLEGSAFTSEKSI
1	1	}	HSIFRTASMLCLNKPSPLPQKSPVRSLSKRLLHLPSRSELISPT
			FKKEKAKXCSIM
5534	3	605	LVRGRARAANPGRVGAMDGLRQRVEHFLEQRNLVTEVLGALEAK
}			TGVEKRYLAAGAVTLLSLYLLFGYGASLLCNLIGFVYPAYASIK
1	·		AIESPSKDDDTVWLTYWVVYALFGLAEFFSDLLLSWFPFYYVGK
			CAFLLFCMAPRPWNGALMLYQRVVRPLFLRHHGAVDRIMNDLSG
L			RALDAAAGITRNVKPSQTPQPKDK
5535	1029	332	KSFMDSEARLCSLVELSDTQDETQKSDSENEDLKIDCLQESQEL
1			NLQKLKNSERILTEAKQKMRELTVNIKMKEDLIKELIKTGNDAK
1	i		SVSKQYTLKVTKLEHDABQAKVBLTETQKQLQELENKDLSDVAM
1			KVKLQKEFRKKVDAAKLRVQVLQKKQQDSKKLASLSIQNEKRAN
			ELEQSVDHMKYQKIQLQRKLQEENEKRKQLDAVIKRDQQKIKVI
1			LSYIPAKYNMKC
5536	942	282	AAATAASLSPRGCRLRTPSSDVSPSRAPPPSAAPLPTGRAQMSP
			SGRLCLLTIVGLILPTRGQTLKDTTSSSSADATIMDIQVPTRAP
			DAVVTELOPTEDTETTE APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPROPRIES APPR
1			DAVYTELQPTSPTPTWFADETPQPQTQTQQLBGTDGPLVTDPET
]			HKSTKAAHPTDDTTTLSERPSPSTDVQTDPQTLKPSGFHEDDPF
5537	3		FYDEHTLRKRGLLVAAVLFITGIIILTSGKCRQLSRLCRNHCR
1 223,	۱ ،	2391	RARVSSPQLRVFRSGRPRRLRVLRINRTSVALRLAGTGRFVAKT
1			PGHPGSWEMGLLTFRDVAVEFSLEEWEHLEPAQKNLYQDVMLEN
1 1			YRNLVSLGLVVSKPDLITFLEQRKEPWNVKSEETVAIQPDVFSH
}			YNKDLLTEHCTBASFOKVISRRHGSCDLENLHLRKRWKREECEG
[			HNGCYDEKTFKYDQFDESSVESLFHQQILSSCAKSYNFDQYRKV
] ]		•	FTHSSLLNQQEBIDIWGKHHIYDKTSVLFRQVSTLNSYRNVFIG
1 1	Í		EKNYHCNNSEKTLNQSSSPKNHQENYFLEKQYKCKEFEEVFLQS
1 1			MHGQEKQEQSYKCNKCVEVCTQSLKHIQHQTIHIRENSYSYNKY
			DKDLSQSSNLRKQIIHNEEKPYKCEKCGDSLNHSLHLTOHOIIP
1	1		TEEKPYKWKECGKVFNLNCSLYLTKQQQIDTGENLYKCKACSKS
1	1	i	FTRSSNLIVHQRIHTGEKPYKCKECGKAFRCSSYLTKHKRIHTG
]	[		EKPYKCKECGKAFNRSSCLTQHQTTHTGEKLYKCKVCSKSYARS
]	' }		SNLIMHQRVHTGEKPYKCKECGKVFSRSSCLTQHRKIHTGENLY
[ [	{		KCKVCAKPFTCFSNLIVHERIHTGEKPYKCKECGKAFPYSSHLI
1 1	ì		RHHRIHTGEKPYKCKACSKSFSDSSGLTVHRRTHTGEKPYTCKE
] ]			CGKAFSYSSDVIQHRRIHTGQRPYKCEECGKAFNYRSYLTTHQR
( 1	į		SHTGERPYKCEECGKAFNSRSYLTTHRRRHTGERPYKCDECGKA
j Ì			FSYRSYLTHRRSHSGERPYKCEECGKAFNSRSYLIAHQRSHTR
	!	ł	FSIRSIDITHRRSHSGERPIRCEECGRAFNSRSYLINHQRSHTR EXL
5538	926	161	
	720	707	HSMMMKIPNGSIPVLMLLLLGLIDISQAQLSCTGPPAIPGIPG
1 1	į	j	IPGTPGPDGQPGTPGIKGEKGLPGLAGDHGEFGEKGDPGIPGNP
			GKVGPKGPMGPKGGPGAPGAPGPKGESGDYKATQKIAFSATRTI
			NVPLRRDQTIRFDHVITNMNNNYEPRSGKFTCKVPGLYYFTYHA
j l			SSRGNLCVNLMRGRERAQKVVTFCDYAYNTFQVTTGGMVLKLEQ
- <del></del> -			GENVFLQATDKNSLLGMEGANS I FSGFLLFPDMEA
5539	38	1258	HRGPSGAAAPGCALPRGQALEGPRSCRRPQPMARRYDELPHYPG
		{	IVDGPAALASFPETVPAVPGPYGPHRPPQPLPPGLDSDGLKREK
1	1		DEIYGHPLFPLLALVFEKCELATCSPRDGAGAGLGTPPGGDVCS
	_		SDSFNEDIAAFAKQVRSERPLFSSNPELDNLVIQAIQVLRFHLL
			The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ł	location	corresponding	Hahistidine, Ialsoleucine, Kalysine,
1	corresponding	to first	L-Leucine, M-Methionine, N-Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	Watryptophan, Yatyrosine, Xaunknown, *astop
1	amino acid	sequence	Coder (mass(h))
ı	sequence	ocquence .	Codon, /=possible nucleotide deletion,
<del></del>	Dogueste	<del> </del>	\=possible nucleotide insertion)
1	1		ELEKVHDLCDNFCHRYITCLKGKMPIDLVIEDRDGGCREDFEDY
J	1		PASCPSLPDQNNMWIRDHEDSGSVHLGTPGPSSGGLASQSGDNS
	i		SDQGDGLDTSVASPSSGGEDEDLDQERRRNKKRGIFPKVATNIM
ł		}	RAWLFQHLSHPYPSEEQKKQLAQDTGLTILQVNNWFINARRRIV
			QPMIDQSNRTGQGAAFSPEGQPIGGYTETQPHVAVRPPGSVGMS
	<del> </del>		LNLEGEWHYL
5540	148	1440	PPLGAGAGVHARSPHPARRLPLTTAGVGGRAPDLLPTPWRQHRG
1	}		PSGAAAPGCALPRGQALEGPRSCRRPQPMARRYDELPHYPGIVD
		•	GPAALASFPETVPAVPGPYGPHRPPQPLPPGLDSDGLKRBKDEI
1		ļ	YGHPLFPLLALVFEKCELATCSPRDGAGAGLGTPPGGDVCSSDS
			FNEDNTAFAKQVRSERPLFSSNPELDNLMIQAIQVLRFHLLELE
1	1	}	KGKMPIDLVIEDRDGGCREDFEDYPASCPSLPDQNNIWIRDHED
			SGSVHLGTPGPSSGGLASQSGDNSSDQGVGLDTSVASPSSGGED
1	1	ļ	EDLEQEPRRNKKRGIFPKVATNIMRAWLFQHLSHPYPSEEQKKQ
	İ		LAQDTGLTILQVNNWFINARRIVQPMIDQSNRTGQGAAFSPEG
1	<b>!</b>		QPIGGYTETEPHVAFRAPASVGDEFGTRKEEWHYL
5541	148	1440	PPLGAGAGVHARS PHPARRLPLTTAGVGGRAPDLLPTPWRQHRG
1	1		PSGAAAPGCALPRGQALEGPRSCRRPQPMARRYDELPHYPGIVD
1			GPAALASFPETVPAVPGPYGPHRPPQPLPPGLDSDGLKREKDEI
1	1		YGHPLFPLLALVFEKCELATCSPRDGAGAGLGTPPGGDVCSSDS
ĺ			FARDUM PAYOUR CRIPT PROVENT DATE AND TO THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PR
	[	•	FNEDNTAFAKQVRSERPLFSSNPELDNLMIQAIQVLRFHLLELE
i			KGKMPIDLVIEDRDGGCREDFEDYPASCPSLPDQNNIWIRDHED
i	<b>!</b>		SGSVHLGTPGPSSGGLASQSGDNSSDQGVGLDTSVASPSSGGED
			EDLDQEPRRNKKRGIFPKVATNIMRAWLFQHLSHPYPSEEQKKQ
1		•	LAQDTGLTILQVNNWFINAKRRIVQPMIDQSNRTGQGAAFSPEG
5542	148		QPIGGYTETEPHVAFRAPASVGDEFGTRKEEWHYL
3312	140	1440	PPLGAGAGVHARSPHPARRLPLTTAGVGGRAPDLLPTPWRQHRG
	1	•	PSGAAAPGCALPRGQALEGPRSCRRPQPMARRYDELPHYPGIVD
1			GPAALASFPETVPAVPGPYGPHRPPQPLPPGLDSDGLKREKDBI
			YGHPLFPLLALVFEKCELATCSPRDGAGAGLGTPPGGDVCSSDS
1			FNEDNTAFAKQVRSERPLFSSNPELDNLMIQAIQVLRFHLLELE
1 1			KGKMPIDLVIEDRDGGCREDFEDYPASCPSLPDQNNIWIRDHED
ŀ			SGSVHLGTPGPSSGGLASQSGDNSSDQGVGLDTSVASPSSGGED
ł			EDLDQEPRRNKKRGIFPKVATNIMRAWLFQHLSHPYPSEEQKKQ
		•	LAQDTGLTILQVNNWFINARRRIVQPMIDQSNRTGQGAAF3PEG
1-per-			QPIGGYTETEPHVAFRAPASVGDEFGTRKEEWHYL
5543	2405	665	RWVREQPWPLRTSEAVKTPALRPFPGPRGVSPFPKPDWGKSPAP
1 1	· }		KRPFSDSGAFWSPERRPGVLEAPRRRPVPASFRAVPPKPTRVHG
1			SSASRDRVLARTMIVADSECRAELKDYLRFAPGGVGDSGPGEEO
1 1	1	ĺ	RESRARRGPRGPSAFIPVEEVLREGAESLEQHLGLEALMSSGRV
			DNLAVVMGLHPDYFTSFWRLHYLLLHTDGPLASSWRHYIAIMAA
[	•		ARHQCSYLVGSHMAEFLOTGGDPEWLLGLHRAPEKLRKI.GRINK
l	i		LLAHRPWLITKEHIQALLKTGEHTWSLAELIQALVLLTHCHSLS
1 1	(	Í	SPVFGCGILPEGDADGSPAPQAPTPPSEQSSPPSRDPLNNSGGF
]	j		ESARDVEALMERMOOLOESLLRDEGTSQEEMESRFELBKSESLL
1		ĺ	VTPSADILEPSPHPDMLCFVEDPTFGYEDFTRRGAQAPPTFRAQ
1	ŀ		DYTWEDHGYSLIQRLYPEGGQLLDEKFQAAYSLTYNTIAMHSGV
1		1	DTSVLRRAIWNYIHCVFGIRYDDYDYGEVNQLLERNLKVYIKTV
		]	ACYPEKTTRRMYNLFWRHFRHSEKVHVNLLLLEARMQAALLYAL
		i	RAITRYMT
5544	1895	514	
1			LGGLLGRQRLLLRMGAGRLGAPMERHGRASATSVSSAGEQAAGD PEGRRQEPLRRRASSASVPAVGASAEGTRRDRLGSYSGPTSVSR
ļ		ļ	ODURE DEVEDI FOUNCE DE COME LOS COMES DE COME DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE COMES DE
l		ļ	QRVESLRKKRPLFPWFGLDIGGTLVKLVYFEPKDITAEEBEEEV
i	Ì		ESLKSIRKYLTSNVAYGSTGIRDVHLELKDLTLCGRKGNLHFIR
	1		FPTHDMPAFIQMGRDKNFSSLHTVFCATGGGAYKFEQDFLTIGD
- 1	1	l	LQLCKLDELDCLIKGILYIDSVGFNGRSQCYYFENPADSEKCQK
ļ	}		LPFDLKNPYPLLLVNIGSGVSILAVYSKDNYKRVTGTSLGGGTF
- 1	1	}	FGLCCLLTGCTTFEEALEMASRGDSTKVDKLVRDIYGGDYBRFG
			LPGWAVASSFGNMMSKEKREAVSKEDLARATLITITNNIGSIAR
f	1		MCALNENINQVVFVGNFLRINTIAMRLLAYALDYWSKGQLKALF
	<u>-</u> _L		SEHEGYFGAVGALLELLKIP

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
DI	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H-Histidine, I-Isoleucine, K-Lysine,
1	corresponding	to first	L-Leucine, M-Methionine, N-Asparagine,
ì	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	residue of	residue of	S-Serine, T-Threonine, V-Valine,
	amino acid	amino acid sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
	sequence	sequence	\=possible nucleotide insertion)
5545	802	131	GAMWSAGRGGAAWPVLLGLLLALLVPGGGAAKTGAELVTCGSVL
1	]		KLINTHHRVRLHSHDIKYGSGSGQQSVTGVEASDDANSYWRIRG
1	[		GSEGGCPRGSPVRCGQAVRLTHVLTGKNLHTHHFPSPLSNNQEV
j			SAFGEDGEGDDLDLWTVRCSGQHWEREAAVRFQHVGTSVFLSVT
İ	1		GEQYGSPIRGQHEVHGMPSANTHNTWKAMEGIFIKPSVEPSAGH
L			DEL
5546	1592	146	FVPRGGHSSMGQSGRSRHQKRARAQAQLRNLEAYAANPHSFVFT
<b>F</b>	(		RGCTGRNIRQLSLDVRRVMEPLTASRLQVRKKNSLKDCVAVAGP
ļ	ļ		LGVTHFLILSKTETNVYFKLMRLPGGPTLTFQVKKYSLVRDVVS
ľ			SLRRHRMHEQQFAHPPLLVLNSFGPHGMHVKLMATMFQNLFPSI
[			NVHKVNLNTIKRCLLIDYNPDSQELDFRHYSIKVVPVGASRGMK
			KLLQEKFPNMSRLQDISELLATGAGLSESEAEPDGDHNITELPQ
			AVAGRGNMRAQQSAVRLTEIGPRMTLQLIKVQEGVGEGKVMFHS FVSKTEEELQAILEAKEKKLRLKAQRQAQQAQNVQRKQEQREAH
1			RKKSLEGMKKARVGGSDEEASGIPSRTASLELGEDDDEQEDDDI
			EYFCQAVGEAPSEDLFPEAKQKRLAKSPGRKRKRWEMDRGRGRL
			CDQKFPKTKDKSQGAQARRGPRGASRDGGRGRGRGRGRFGKRVA
5547	1592	146	FVPRGGHSSMGQSGRSRHQKRARAQAQLRNLEAYAANPHSFVFT
1 1			RGCTGRNIRQLSLDVRRVMEPLTASRLQVRKKNSLKDCVAVAGP
J j			LGVTHFLILSKTETNVYFKLMRLPGGPTLTFQVKKYSLVRDVVS
)			SLRRHRMHEQQFAHPPLLVLNSFGPHGMHVKLMATMFQNLFPSI
1			NVHKVNLNTIKRCLLIDYNPDSQELDFRHYSIKVVPVGASRGMK
1			KLLQEKFPNMSRLQDISELLATGAGLSESEAEPDGDHNITELPQ
1	ļ		AVAGRGNMRAQQSAVRLTEIGPRMTLQLIKVQEGVGEGKVMFHS
			FVSKTEEBLQAILEAKEKKLRLKAQRQAQQAQNVQRKQEQREAH RKKSLEGMKKARVGGSDEEASGIPSRTASLELGEDDDEQEDDDI
			EYFCQAVGEAPSEDLFPEAKQKRLAKSPGRKRKRWEMDRGRGRL
1 1	,		CDQKFPKTKDKSQGAQARRGPRGASRDGGRGRGRGRGRPGKRVA
5548	1	2153	DOTGPPETIAPTFPRSTMEPLCPLLLVGFSLPLARALRGNETTA
1 [			DSNETTTTSGPPDPGASQPLLAWLLLPLLLLLLLLLLLAAYFFRF
}. ·			RKQRKAVVSTSDKKMPNGILEEQEQQRVMLLSRSPSGPKKYFPI
1		•	PVEHLEEEIRIRSADDCKOFREEFNSLPSGHIQGTFELANKEEN
1 1		·	REKNRYPNILPNDHSRVILSQLDGIPCSDYINASYIDGYKEKNK
	·		FIAAQGPKQETVNDFWRMVWEQKSATIVMLTNLKERKEEKCHQY
1 1			WPDQGCWTYGNIRVCVEDCVVLVDYTIRKFCIQPQLPDGCKAPR
1 }	}		LVSQLHFTSWPDFGVPFTPIGMLKFLKKVKTLNPVHAGPIVVHC SAGVGRTGTFIVIDAMMAMMHAEQKVDVFEFVSRIRNQRPQMVQ
1 1			TDMQYTFIYQALLEYYLYGDTELDVSSLEKHLQTMHGTTTHFDK
i			IGLEEEFRKLTNVRIMKENMRTGNLPANMKKARVIQIIPYDFNR
} [			VILSMKRGQEYTDYINASFIDGYRQKDYFIATQGPLAHTVEDFW
[			RMIWEWKSHTIVMLTEVQBREQDKCYQYWPTEGSVTHGEITIEI
1 1			KNDTLSEAISIRDFLVTLNQPQARQEEQVRVVRQFHFHGWPEIG
1 1	1	.	IPAEGKGMIDLIAAVQKQQQQTGNHPITVHCSAGAGRTGTFIAL
	Ī	i	SNILERVKAEGLLDVFQAVKSLRLQRPHMVQTLEQYEFCYKVVQ
5549	915	256	DFIDIFSDYANFK
		450	FEATGGKRLAFKMAGTARHDREMAIQAKKKLTTATDPIERLRLQ
	İ		CLARGSAGIKGLGRVFRIMDDDNNRTLDFKEFMKGLNDYAVVME KEEVBELFQRFDKDGNGTIDFNEFLLTLRPPMSRARKEVIMOAF
		ļ	RKLDKTGDGVITIEDLREVYNAKHHPKYQNGEWSEEQVFRKFLD
			NFDSPYDKDGLVTPEEFMNYYAGVSASIDTDVYFIIMMRTAWKL
5550	2364	1210	RKRKVFLKMRRLNRKKTLSLVKELDAFPKVPESYVETSASGGTV
			SLIAFTTMALLTIMEFSVYQDTWMKYEYEVDKDFSSKLRINIDI
ĺ	l		TVAMKCQYVGADVLDLAETMVASADGLVYEPTVFDLSPQQKENQ
	į		RMLQLIQSRLQEEHSLQDVIFKSAFKSTSTALPPREDDSSQSPN
	1	ľ	ACRIHGHLYVNKVAGNFHITVGKAIPHPRGHAHLAALVNHESYN
	ļ	j	FSHRIDHLSFGBLVPAIINPLDGTEKIAIDHNQMFQYFITVVPT
	ļ	İ	KLHTYKISADTHQFSVTERERIINHAAGSHGVSGIFMKYDLSSL
}	ł	1	MVTVTEEHMPFWQFFVRLCGIVGGIFSTTGMLHGIGKFIVEIIC
5551	211	1700	CRFRLGSYKPVNSVPFEDGHTDNHLPLLENNTH MORDHTMDYKESCPSVSIPSSDEHREKKKRFTVYKVLVSVGRSE
			WAYDOWN TWESCES ASTERSONEWKEYKYKELA I KATARAKE

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine.
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding to first	to first	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	Joquence	Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			WFVFRRYAEFDKLYNTLKKQFPAMALKIPAKRIFGDNFDPDFIK
}	}		QRRAGLNEFIQNLVRYPELYNHPDVRAFLQMDSPKHQSDPSEDE
ĺ			DERSSQKLHSTSQNINLGPSGNPHAKPTDFDFLKVIGKGSFGKV
i		j	LLAKRKLDGKFYAVKVLQKKIVLNRKEQKHIMAERNVLLKNVKH
		İ	PFLVGLHYSFQTTEKLYFVLDFVNGGELFFHLORERSFPEHRAR
1		}	FYAAEIASALGYLHSIKIVYRDLKPENILLDSVGHVVLTDFGLC
			KEGIAISDTTTTFCGTPEYLAPEVIRKQPYDNTVDWWCLGAVLY
1	1		EMLYGLPPFYCRDVAEMYDNILHKPLSLRPGVSLTAWSILEELL
			EKDRQNRLGAKEDFLEIQNHPFFESLSWADLVQKKIPPPFNPNV
1	1		AGPDDIRNFDTAFTEETVPYSVCVSSDYSIVNASVLEADDAFVG FSYAPPSEDLFL
5552	2748	930	LGPAAGAAMGKKHKKHKAEWRSSYEDYADKPLEKPLKLVLKVGG
			SEVTELSGSGHDSSYYDDRSDHERERHKEKKKKKKKKSEKEKHL
			DDEERRKRKEEKKRKREREHCDTEGEADDFDPGKKVEVEPPPDR
			PVRACRTQPAENESTPIQQLLEHFLRQLQRKOPHGFFAFPVTDA
ł			IAPGYSMIIKHPMDFGTMKDKIVANEYKSVTEFKADFKLMCDNA
į			MTYNRPDTVYYKLAKKILHAGFKMMSKQAALLGNEDTAVEEPVP
1			EVVPVQVETAKKSKKPSREVISCMFEPEGNACSLTDSTABEHVL
			ALVEHAADEARDRINRFLPGGKMGYLKRNGDGSLLYSVVNTAEP DADEEETHPVDLSSLSSKLLPGFTTLGFKDERRNKVTFLSSATT
ł			ALSMONNSVFGDLKSDEMELLYSAYGDBTGVQCALSLQEFVKDA
1			GSYSKKVVDDLLDQITGGDHSRTLFQLKQRRNVPMKPPDEAKVG
	1		DTLGDSSSSVLEFMSMKSYPDVSVDISMLSSLGKVKKELDPDDS
1	1 1		HLNLDETTKLLQDLHEAQAERGGSRPSSNLSSLSNASERDOHHL
5553	74	1095	GSPSRLSVGEQPDVTHDPYEFLQSPEPAASAKT
]	'	1095	LGREAVYLVSRMDGPVAEHAKQEPFHVVTPLLESWALSQVAGMP
Ì	1		VFLKCENVQPSGSFKIRGIGHFCQEMAKKGCRHLVCSSGGNAGI AAAYAARKLGIPATIVLPESTSLQVVQRLQGEGAEVQLTGKVWD
1			EANLRAQELAKRDGWENVPPFDHPLIWKGHASLVQELKAVLRTP
1	}		PGALVLAVGGGGLLAGVVAGLLEVGWQHVPIIAMETHGAHCFNA
Į.	ļ·		AITAGKLVTLPDITSVAKSLGAKTVAARALECMOVCKIHSEVVE
1			DTEAVSAVQQLLDDERMLVEPACGAALAAIYSGLLRRLOAEGCI.
5554	166	2318	PPSLTSVVVIVCGGNNINSRELQALKTHLGQV
	1	2318	CSGRTGGRGSLRPAENVCLTCKLSGAETRGLLCPALRTWIMKVL
}			GRSFFWVLFPVLPWAVQAVEHEEVAQRVIKLHRGRGVAAMQSRQ WVRDSCRKLSGLLRQKNAVLNKLKTAIGAVEKDVGLSDEEKLFQ
			VHTFEIFQKFLNESENSVFQAVYGLQRALQGDYKDVVNMKESSR
]			QRLEALREAAIKEETEYMELLAABKHQVEALKNMQHQNQSLSML
		·	DEILEDVRKAADRLEEBIEEHAFDDNKSVKGVNFEAVLRVEEER
l. 1			ANSKONITKREVEDDLGLSMLIDSONNOYILTKPRDSTIPRADH
			HFIKDIVTIGMLSLPCGWLCTAIGLPTMFGYIICGVLLGPSGLN
1 1			SIKSİVQVETLGEFGVFFTLFLVGLEFSPEKLRKVWKISLQGPC
j l		1	YMTLLMIAFGLLWGHLLRIKPTQSVFISTCLSLSSTPLVSRFLM GSARGDKEGDIDYSTVLLGMLVTQDVQLGLFMAVMPTLIQAGAS
i 1		ĺ	ASSSIVVEVLRILVLIGQILFSLAAVFLLCLVIKKYLIGPYYRK
1 1			LHMESKGNKEILILGISAFIFLMLTVTELLDVSMELGCFLAGAL
<b>[</b> [	·		VSSCGPVVTEEIATSIEPIRDFLAIVFFASIGLHVFPTFVAYET.
!!!	1	ŀ	TVLVFLTLSVVVMKFLLAALVLSLILPRSSQYIKWIVSAGLAGV
·	}		SEPSFVLGSRARRAGVISREVYLLILSVTTLSLLLAPVLWRAAI
5555	212	1425	TRCVPRPERRSSL
		1425	LSLRTRETPAPPRCEAASQGRVGWRADAAAEEAVRSVWNRTRDR
{	[	. [	GTMAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRSASIKDIK KAYPKLALOLUPDRNADDEROAGRYFODY GRAVENI ODGENERAL
			KAYRKLALQLHPDRNPDDFQAQEKFQDLGAAYEVLSDSEKRKQY DTYGEEGLKDGHQSSHGDIFSHFFGDFGFMFGSTPRQQDRNIPR
		1	GSDIIVDLEVTLEEVYAGNPVEVVRNKPVARQAPGKRKCNCRQE
	1		MRTTQLGPGRFQMTQEVGCDECPNVKLVNEERTLEVEIEPGVRD
		1	GMEYPFIGEGEPHVDGEPGDLRFRIKVVKHPIFERRGDDLYTNV
		- 1	TISLVESLVGFEMDITHLDGHKVHISRDKITRPGAKLWKKGEGL
		1	PNFDNNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQK
5556	5835		VYNGLQGY
		5570	RTRGMSKNCVPMEFEEYLLRMFQGTFYLLQKITKDNNAHTVKSR

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ł	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
}	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
ļ	sequence	ļ	\=possible nucleotide insertion)
1			LEELDESYIEKFTDFLRLFVSVHLRRIESYSQFPVVEFLTLLFK
ł		ì	YTFHQPTHEGYFSCLDIWTLFLDYLTSKIKSRLGDKEAVLNRYE
j j			DALVLLITEVLNRIQFRYNQAQLEELDDETLDDDQQTEWQRYLR
1		Î	QSLEVVAKVMELLPTHAFSTLPPVLQDNLEVYLGLQQFIVTSGS
İ		(	GHRLNITAENDCRRLHCSLRDLSSLLQAVGRLAEYFIGDVFAAR
Ì			FNDALTVVERLVKVTLYGSQIKLYNIETAVPSVLKPDLIDVHAQ
			SLAALQAYSHWLAQYCSEVHRQNTQQFVTLISTTMDAITPLIST KVQDKLLLSACHLLVSLATTVRPVFLISIPAVQKVFNRITDASA
		ĺ	LRLVDKAQVLVCRALSNILLLPWPNLPENEQQWPVRSINHASLI
	}	}	SALSRDYRNLKPSAVAPQRKMPLDDTKLIIHQTLSVLEDIVENI
	J		SGESTKSRQICYQSLQESVQVSLALFPAFIHQSDVTDEMLSFFL
1		}	TLFRGLRVQMGVPFTEQIIQTFLNMFTREQLAESILHEGSTGCR
1	1	ľ	VVEKFLKILQVVVQEPGQVFKPFLPSIIALCMEQVYPIIAERPS
1	j .		PDVKAELFELLFRTLHHNWRYFFKSTVLASVQRGIAEEQMENEP
1	<u>†</u>		QFSAIMQAFGQSFLQPDIHLFKQNLFYLETLNTKQKLYHKKIFR
Ī		i	TAMLFQFVNVLLQVLVHKSHDLLQEEIGIAIYNMASVDFDGFFA
j			AFLPEFLTSCDGVDANQKSVLGRNFKMDRVRRERGRAKRRAEWA
L		<u></u>	RKPGTCAARRGHIEASGRGLCPPCSLAAAHEMPADLVL
5557	1712	491	VILGAGLRDKDMWIPVVGLPRRLRLSALAGAGRFCILGSEAATR
1	1		KHLPARNHCGLSDSSPQLWPEPDFRNPPRKASKASLDFKRYVTD
1			RRLAETLAQIYLGKPSRPPHLLLECNPGPGILTQALLEAGAKVV
			ALESDKTFIPHLESLGKNLDGKLRVIHCDFFKLDPRSGGVIKPP
1	[		AMSSRGLFKNLGIEAVPWTADIPLKVVGMFPSRGEKRALWKLAY
i			DLYSCTSIYKFGRIEVNMFIGEKEFQKLMADPGNPDLYHVLSVI
	]		WQLACEIKVLHMEPWSSFDIYTRKGPLENPKRRELLDQLQQKLY LIQMIPRQNLFTKNLTPMNYNIFFHLLKHCFGRRSATVIDHLRS
ı			LTPLDARDILMQIGKQEDEKVVNMHPQDFKTLFETIERSKDCAY
1			KWLYDETLEDR
5558	1509	96	RAGCTHPQVPADLGAPAEPRRPQKTCVCLLQPQPGGQRGPTTMI
1			TGVFSMRLWTPVGVLTSLAYCLHQRRVALAELQEADGQCPVDRS
			LLKLKMVQVVFRHGARSPLKPLPLEEQVEWNPQLLEVPPQTQFD
ì			YTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQLTKVGMQQMFA
1	i j		LGERLRKNYVEDIPFLSPTFNPQEVFIRSTNIFRNLESTRCLLA
1		•	GLFQCQKEGPIIIHTDEADSEVLYPNYQSCWSLRQRTRGRRQTA
1 .			SLQPGISEDLKKVKDRMGIDSSDKVDFFILLDNVAAEQAHNLPS
1	'		CPMLKRFARMIEQRAVDTSLYILPKEDRESLQMAVGPFLHILES
1			NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLLMTLGIFDHKWPP
[			FAVDLTMELYQHLESKEWFVQLYYHGKEQVPRGCPDGLCPLDMF
5559	150	1983	LNAMSVYTLSPEKYHALCSQTQVMBVGNEE PLAATAHFAKMSRVAKYRRQVSEDPDIDSLLETLSPEEMEELEK
			ELDVVDPDGSVPVGLRQRNQTEKQSTGVYNREAMLNFCEKETKK
]			LMQREMSMDESKQVETKTDAKNGEERGRDASKKALGPRRDSDLG
			KEPKRGGLKKSFSRDRDEAGGKSGEKPKEEKIIRGIDKGRVRAA
			VDKKEAGKDGRGEERAVATKKEEEKKGSDRNTGLSRDKDKKREE
Į			MKEVAKKEDDEKVKGERRNTDTRKEGEKMKRAGGNTDMKKEDEK
			VKRGTGNTDTKKDDEKVKKNEPLHEKEAKDDSKTKTPEKQTPSG
f 1	1		PTKPSEGPAKVEEEAAPSIFDEPLERVKNNDPEMTEVNVNNSDC
} }			ITNEILVRFTEALEFNTVVKLFALANTRADDHVAFAIAIMLKAN
j	1.		KTITSLNLDSNHITGKGILAIFRALLQNNTLTELRFHNQRHICG
	İ		GKTEMEIAKLLKENTTLLKLGYHFELAGPRMTVTNLLSRNMDKQ
	1		ROKRLOEOROAQEAKGEKKOLLEVPKAGAVAKGSPXPSPQPSPK
ļ /	j		PSPKNSPKKGGAPAAPPPPPPPPLAPPLIMENLKNSLSPATQRKM
5560	<del>- 9</del> -	621	GDKVLPAQEKNSRDQLLAAIRSSNLKQLKKVEVPKLLQ
3300	7	921	SSVVEFSALSVSMACLSPSQLQKFQQDGFLVLEGFLSAEECVAM
}	ļ		QQRIGEIVAEMDVPLHCRTEFSTQEEEQLRAQGSTDYFLSSGDK
<b> </b>			IRFPFEKGVFDEKGNFLVPPEKSINKIGHALHAHDPVFKSITHS   FKVQTLARSIGLQMPVVVQSMYIFKQPHFGGEVSPHQDASFLYT
[ ]	ľ		EPLGRVLGVWIAVEDATLENGCLWFIPGSHTSGVSRRMVRAPVG
1 1	1		SAPGTSFLGSEPARDNSLFVPTPVQRGALVLIHGEVVHKSKQNL
<u>[</u> ]	İ		SDRSRQAYTFHLMEASGTTWSPENWLQPTAELPFPQLYT
5561	2175	1775	CYFIFQFFSSPYPGLHPHQTPAPLPNPGLYPPPVSMSPGQPPPQ

SEQ	Predicted	Predicted end	Imino nold
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
į	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	-	\=possible nucleotide insertion)
	<del></del>		QLLAPTYFSAPGVMNFGNPSYPYAPGALPPPPPPHLYPNTQAPS
}	]		QVYGGVTYYNPAQQQVQPKPSPPRRTPQPVTIKPPPPEVVSRGS
L			S
5562	342	1385	SSGKNDMAAAGAAGLVRGLKAGVLSQADYLNLVQCETLEDLKLH
İ			LQSTDYGNFLANEASPLTVSVIDDRLKEKMVVEFRHMRNHAYEP
1	Ī		LASFLDFITYSYMIDNVILLITGTLHQRSIAELVPKCHPLGSFE
1			QMEAVNIAQTPAELYNAILVDTPLAAFFQDCISEQDLDEMNIEI
	1		IRNTLYKAYLESFYKFCTLLGGTTADAMCPILEFEADRRAFIIT
1			INSFGTELSKEDRAKLPPHCGRLYPEGLAQLARADDYEQVKNVA
J	1		DYYPEYKLLFEGAGSNPGDKTLEDRFFEHEVKLNKLAFLNOFHF
L			GVFYAFVKLKEQECRNIVWIAECIAQRHRAKIDNYIPIF
5563	342	1385	SSGKNDMAAAGAAGLVRGLKAGVLSQADYLNLVQCETLEDLKLH
1			LOSTDYGNFLANEASPLTVSVIDDRLKEKMVVEFRHMRNHAYEP
j	1		LASFLDFITYSYMIDNVILLITGTLHQRSIABLVPKCHPLGSFE
1	]		QMEAVNIAQTPAELYNAILVDTPLAAFFQDCISEQDLDEMNIEI
i			IRNTLYKAYLESFYKFCTLLGGTTADAMCPILEFEADRRAFIIT
Ī	ĺ		INSFGTELSKEDRAKLFPHCGRLYPEGLAOLARADDYEOVKNVA
-			DYYPEYKLLFEGAGSNPGDKTLEDRFFEHEVKLNKLAFLNOFHF
FFCA			GVFYAFVKLKEQECRNIVWIAECIAQRHRAKIDNYIPIF
5564	3	914	RVRRDKRAVWTARGRRRCGDSMSGGWMAQVGAWRTGALGLALLL
			LLGLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFOCRTSGLC
[			VPLTWRCDRDLDCSDGSDEBECRIEPCTOKGOCPPPPGLPCPCT
1			GVSDCSGGTDKKLRNCSRLACLAGELRCTLSDDCIPLTWRCDGH
<b>1</b>			PDCPDSSDELGCGTNEILPEGDATTMGPPVTLESVTSLRNATTM
1 1			GPPVTLESVPSVGNATSSSAGDQSGSPTAYGVIAAAAVLSASLV
5565	993		TATLLLLSWLRAGERLRPLGLLVAMKESLLLSEQKTSLP
3303	293	138	RWNSPNPARAGSISRPQRAPGSVSAVAMTAAVFFGCAFIAFGPA
1 1			LALYVFTIATEPLRIIPLIAGAFFWLVSLLISSLVWFMARVIID
)			NKDGPTQKYLLIFGAFVSVYIQEMPRFAYYKLLKKASEGLKSIN
			PGETAPSMRLLAYVSGLGFGIMSGVFSFVNTLSDSLGPGTVGIH
1 1	ł		GDSPQFFLYSAFMTLVIILLHVFWGIVFFDGCEKKKWGILLIVL LTHLLVSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRS
1 1	J		LKLCLLCQDKNFLLYNQRSR
5566	2043	1232	SHIQHHGRGAQAPVKMVSWMISRAVVLVFGMLYPAYYSYKAVKT
1 1	i	•	KNVKEYVRWMYWIVPALYTVIETVADQTVAWPPLYYELKIAFV
1 1			IWLLSPYTKGASLIYRKFLHPLLSSKEREIDDYIVQAKERGYET
{ 1	ļ		MVNFGRQGLNLAATAAVTAAVKSQGAITERLRSFSMHDLTTIQG
1 1			DEPVGQRPYQPLPEAKKKSKPAPSESAGYGIPLKDGDEKTDEEA
1.			EGPYSDNEMLTHKG?RRSQSMKSVKTTKGRKEVRYGSLKYKVKK
			RPQVYF
5567	1554	233	EFLGSGVSPDLANEDGLTALHQCCIDDFREMVQQLLEAGANINA
1		[	CDSECWTPLHAAATCGHLHLVELLIASGANLLAVNTDGNMPYDL
1	1	i	CDDEQTLDCLETAMADRGITQDSIEAARAVPELRMLDDIRSRLO
1	]		AGADLHAPLDHGATLLHVAAANGFSEAAALLLEHRASLSAKDOD
	1	[	GNEPLHAAAYWGQVPLVELLVAHGADLNAKSLMDETPLDVCGDE
1	1	ļ	EVRAKLLELKHKHDALLRAGSRORSLLRRRTSSAGSRGKVVRRV
]			SLTQRTDLYRKQHAQEAIVWQQPPPTSPEPPEDNDDROTGAELR
j	[		PPPPEEDNPEVVRPHNGRVGGSPVRHLYSKRLDRSVSYOLSPLD
1 1	J	J	STTPHTLVHDKAHHTLADLKRORAAAKLORPPPEGPESPETAEP
5568			GLPGDTVTPQPDCGFRAGGDPPLLKLTAPAVEAPVERRPCCLLM
2200	1731	587	AEDROPASRRGAGTTAAMAASGPGCRSWCLCPEVPSATFFTALL
( . l			SLLVSGPRLFLLQQPLAPSGLTLKSEALRNWOVYRLVTYIFVVF
[ [		Í	NPISLLCGAIIIWRFAGNFERTVGTVRHCFFTVIFAIFSAIIFL
(		,	SFEAVSSLSKLGEVEDARGFTPVAFAMLGVTTVRSRMRRALVPG
		ł	MVVPSVLVPWLLLGASWLIPOTSFLSNVCGLSIGLAYGLTYCYS
	ľ	Ī	IDLSERVALKLDQTFPFSLMRRISVFKYVSGSSAERRAAOSRKI.
-		ļ	NPVPGSYPTQSCHPHLSPSHPVSQTQHASGQKLASWPSCTPGHM
		Í	PTLPPYQPASGLCYVQNHFGPNPTSSSVYPASAGTSLGIQPPTP
5569	2	835	VNSPGTVYSGALGTPGAAGSKESSRVPMP
		033	QTPCPLAWERGSRSEDISVPGQKPPTCSSFSGMDVGPSSLPHLG

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
i	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ſ	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	1	\=possible nucleotide insertion)
	1		LKLLLLLLPLRGQANTGCYGIPGMPGLPGAPGKDGYDGLPGP
1	i	1	KGEPGIPAIPGIRGPKGQKGEPGLPGHPGKNGPMGPPGMPGVPG
	}		PMGIPGEPGEEGRYKQKFQSVFTVTRQTHQPPAPNSLIRFNAVL
		1	TNPQGDYDTSTGKFTCKVPGLYYFVYHASHTANLCVLLYRSGVK
1	ł	1	VVTFCGHTSKTNQVNSGGVLLRLQVGEEVWLAVNDYYDMVGIQG
	<b>!</b>	]	SDSVFSGFLLFPD
5570	264	946	RDRRDRGGVATSTEEPARPRAPQSRGPGPVSQTGRGRERGGGDT
ł	1	}	MSSPSPGKRRMDTDVVKLIESKHEVTILGGLNEFVVKPYGPQGT
	ļ	Į.	PYEGGVWKVRVDLPDKYPFKSPSIGFMNKIFHPNIDEASGTVCL
1		ł	DVINGTNTALYDLTNIFESFLPQLLAYPNPIDPLNGDAAAMYLH
1			RPEBYKQKIKBYIQKYATEEALKEQEEGTGDSSSESSMSDFSED
İ	i I		EAODMEL
5571	264	946	RDRRDRGGVATSTEEPARPRAPQSRGPGPVSQTGRGRERGGGDT
1			MSSPSPGKRRMDTDVVKLIESKHEVTILGGLNEFVVKFYGPQGT
ĺ			PYEGGVWKVRVDLPDKYPFKSPSIGFMNKIFHPNIDEASGTVCL
I			DVINQTWTALYDLTNIFESFLPQLLAYPNPIDPLNGDAAAMYLH
			RPEBYKOKIKBYIOKYATEEALKEQEEGTGDSSSESSMSDFSED
1			EAQDMEL
5572	2802	2085	RTDYRTGIPGRRFRVMAAGDGDVKLGTLGSGSESSNDGGSESPG
			DAGAAAEGGGWAAAALALLTGGGEMLLNVALVALVLLGAYRLWV
1			RWGRRGLGAGAGAGEESPATSLPRMKKRDFSLEQLRQYDGSRNP
i			RILLAVNGKVFDVTKGSKFYGPAGPYGIFAGRDASRGLATFCLD
1			KDALRDEYDDLSDLNAVQMESVREWEMQFKEKYDYVGRLLKPGE
1			EPSEYTDEEDTKDHNKOD
5573	2562	219	VPARTPNAEDQGPEARAATATPCQSGGRERAGEAAEDGVKMAAF
		•	SEMGVMPEIAQAVEEMDWLLPTDIQAESIPLILGGGDVLMAAET
	į į		GSGKTGAFSIPVIQIVYETLKDQQEGKXGKTTIKTGASVLNKWQ
1			MNPYDRGSAFAIGSDGLCCQSREVKEWHGCRATKGLMKGKHYYE
1	ŀ		VSCHDQGLCRVGWSTMQASLDLGTDKFGFGFGGTGKKSHNKQFD
			NYGEEFTMHDTIGCYLDIDKGHVKFSKNGKDLGLAFEIPPHMKN
1 '	ĺ		QALFPACVLKNAELKFNFGEEEFKFPPKDGFVALSKAPDGYIVK
1 1	}		SCHSGNAQVTQTKFLPNAPKALIVEPSRELAEQTLNNIKQFKKY
1 1			IDNPKLRELLIIGGVAARDQLSVLENGVDIVVGTPGRLDDLVST
i i			GKLNLSQVRFLVLDEADGLLSQGYSDFINRMHNQIPQVTSDGKR
) )	j		LQVIVCSATLHSFDVKKLSEKIMHFPTWVDLKGEDSVPDTVHHV
1			VVPVNPKTDRLWERLGKSHIRTDDVHAKDNTRPGANSPEMWSEA
1 1	j		IKILKGEYAVRAIKEHKMDQAIIFCRTKIDCDNLEQYFIQQGGG
] ]			PDKKGHQFSCVCLHGDRKPHERKQNLERFKKGDVRFLICTDVAA
1 1	. 1		RGIDIHGVPYVINVTLPDEKQNYVHRIGRVGRAERMGLAISLVA
1 1	}		TEKEKVWYHVCSSRGKGCYNTRLKEDGGCTIWYNEMQLLSEIEE
] [	}		HLNCTISQVEPDIKVPVDEFDGKVTYGQKRAAGGGSYKGHVDIL
			APTVQELAALEKEAQTSFLHLGYLPNQLFRTF
5574	1731	952	NEGLEVFKEQELQPEDKGAVPEDASTERSAMASLGLOLVGYILG
1			LLGLLGTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHS
1 1	1	i	TGITQCDIYSTLLGLPADIQAAQAMMVTSSAISSLACIISVVGM
j l			RCTVFCQESRAKDRVAVAGGVFFILGGLLGFIPVAWNLHGILRD
] [	Į		FYSPLVPDSMKFEIGEALYLGIISSLFSLIAGIILCFSCSCQRN
L			RSNYYDAYQAQPLATRSSPRPGQPPKVKSEFNSYSLTGYV
5575	456	766	LLWALPCPPPTAAAVLLSSTGLMELLEKMLALTLAKADSPRTAL
]			LCSAWLLTASFSAQQHKGSLQKDPLLSQACVGCLEALLDYLDAR
	i		SPDIGRNSPHYLMFP
5576	249	2146	RSWGAPWFWRMRLLRRRHMPLRLAMVGCAFVLFLFLLHRDVSSR
1			EEATEKPWLKSLVSRKDHVLDLMLEAMNNLRDSMPKLQIRAPEA
		1	QQTLPSINQSCLPGFYTPAELKPFWERPPQDPNAPGADGKAFQK
		1	SKWTPLETQEKBEGYKKHCFNAFASDRISLQRSLGPDTRPPECV
		}	DQKFRCPPLATTSVIIVFHNEAWSTLLRTVYSVLHTTPAILLK
•	İ	Į	EIILVDDASTEEHLKEKLEQYVKQLQVVRVRQBERKGLITARL
	l	ľ	LGASVAQAEVLTFLDAHCECFHGWLEPLLARIAEDKTVVVSPDI
1	j		VTIDLNTFEFAKPVQRGRVHSRGNFDWSLTFGWETLPPHEKQRR
			KDETYPIKSPTFAGGLFSISKSYFEHIGTYDNQMBIWGGENVEM
			The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
}	corresponding	to first	hantscluthe, laisoleucine, kalysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
ł	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
1			S=Serine, T=Threonine, V=Valine,
Í	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence	<u> </u>	\=possible nucleotide insertion)
			SFRVWQCGGQLE1IPCSVVGHVFRTKSPHTFPKGTSVIARNQVR
1		·	LAEVWMDSYKKIFYRRNLQAAKMAQEKSFGDISERLQLREQLHC
ļ	1		HNFSWYLHNVYPEMFVPDLTPTFYGAIKNLGTNQCLDVGENNRG
1		ļ	GKPLIMYSCHGLGGNQYFEYTTQRDLRHNIAKQLCLHVSKGALG
1	l		LGSCHFTGKNSQVPKDEEWELAQDQLIRNSGSGTCLTSQDKKPA
			MAPCNPSDPHQLWLFV
5577	3	1275	RNSDCSCGBISVHCLPWVLFILDLKVBSSMFCPLKLILLPVLLD
	1	"""	YSLGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCIFKIDWTL
1	ĺ		
1	}		SPGEHAKDEYVLYYYSNLSVPIGRFQNRVHLMGDILCNDGSLLL
1	İ		QDVQEADQGTYICEIRLKGESQVFKKAVVLHVLPEEPKELMVHV
j	l .		GGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEEIVFRYYHKLRM
1			SVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESDGGNYTCS
1	ł		IHLGNLVFKKTIVLHVSPEEPRTLVTPAALRPLVLGGNQLVIIV
1			GIVCATILLLPVLILIVKKTCGNKSSVNSTVLVKNTKKTNPEIK
ľ	1		EKPCHFERCEGEKHIYSPIIVREVIEEEEPSEKSEATYMTMHPV
			WPSLRSDRNNSLEKKSGGGMPKTQQAF
5578	3	783	AVESMASPGACRAPPELPERNCGYREVEYWDQRYQGAADSAPYD
t '			WFGDFSSFRALLEPELRPEDRILVLGCGNSALSYELFLGGFPNV
			TSVDYSSVVVAAMQARYAHVPQLRWETMDVRKLDFPSASFDVVL
j			EKGTLDALLAGERDPWTVSSEGVHTVDQVLSEVSRVLVPGGRFI
ì			SMTSAAPHFRTRHYAQAYYGWSLRHATYGSGFHFHLYLMHKGGK
!	}		LSVAQLALGAQILSPPRPPTSPCFLQDSDHEDFLSAIQL
5579	. 3	1540	RNSGLARGASALARHGGGLAGGVGWDCGACASRCQGVMEGLLTR
í			CRALPALATCSRQLSGYVPCRFHHCAPRRGRRLLLSRVFQPQNL
	į .		REDRVLSLQDKSDDLTCKSQRLMLQVGLIYPASPGCYHLLPYTV
i i		•	RAMEKLVRVIDQEMQAIGGQKVNMPSLSPAELWQATNRWDLMGK
J			
ł			BLLRLRDRHGKEYCLGPTHEEAITALIASQKKLSYKQLPFLLYQ
) )			VTRKFRDEPRPRFGLLRGREFYMKDMYTFDSSPEAAQQTYSLVC
			DAYCSLFNKLGLPFVKVQADVGTIGGTVSHEFQLPVDIGEDRLA
			ICPRCSFSANMETLDLSQMNCPACQGPLTKTKGIEVGHTFYLGT
			KYSSIFNAQFTNVCGKPTLAEMGCYGLGVTRILAAAIEVLSTED
1 1			CVRWPSLLAPYQACLIPPKKGSKEQAASELIGQLYDHITEAVPQ
<b>i</b>			LHGEVLLDDRTHLTIGNRLKDANKFGYPFVIIAGKRALEDPAHF
<u></u>			EVWCQNTGEVAFLTKDGVMDLLTPVQTV
5580	1681	450	ADAGTRCIPGFVVPSGAGYSAPAQRGRRSSGRMRAAAAPGLTAP
[			WRLLQCCELEAGELGMAVPAAAMGPSALGQSGPGSMAPWCSVSS
			GPSRYVLGMQELFRGHSKTREFLAHSAKVHSVAWSCDGRRLASG
			SFDKTASVFLLEKDRLVKENNYRGHGDSVDQLCWHPSNPDLFVT
1 1			ASGDKTIRIWDVRTTKCIATVNTKGENINICWSPDGQTIAVGNK
j i			DDVVTFIDAKTHRSKAEEQFKFEVNEISWNNDNNMFFLTNGNGC
[ [	ļ .		INILSYPELKPYQSINAHPSNCICIKFDPMGKYFATGSADALVS
j ]			LWDVDELVCVRCFSRLDWPVRTLSFSHDGKMLASASEDHFIDIA
	ĺ		EVETGDKLWEVQCESPTFTVAWHPKRPLLAFACDDKDGKYDSSR
			EAGTVKLFGLPNDS
5581	54	947	GGGSGPRAPSATLLDTGESVAAVASGEDKGIAASAAAAAVFACS
1			CSPDPQSSTMNPVYSPVQPGAPYGNPKNMAYTGYPTAYPAAAPA
			YNPSLYPTNSPSYAPEFQFLHSAYATLLMKQAWPQNSSSCGTEG
1			
	j		TFHLPVDTGTENRTYQASSAAFRYTAGTPYKVPPTQSNTAPPPY
[		ĺ	SPSPNPYQTAMYPIRSAYPQQNLYAQGAYYTQPVYAAQPHVIHH
ŀ	j		TTVVQPNSIPSAIYPAPVAAPRTNGVAMGMVAGTTMAMSAGTLL
5582	<del></del>	2=2	TTPQHTAIGAHPVSMPTYRAQGTPAYSYVPPHW
2202	5775	2739	IITNNNNVIIPLVIAYHLSGSAQARGERSPAERLMERQKRKADI
	}		EKGLQF1QSTLPLKQEEYBAFLLKLVQNLFAEGNDLFREKDYKQ
	ł		ALVQYMEGLNVADYAASDQVALPRELLCKLHVNRAACYFTMGLY
)			EKALEDSEKALGLDSESIRALFRKARALNELGRHKEAYECSSRC
	l		SLALPHDESVTQLGQELAQXLGLRVRKAYKRPQELETFSLLSNG
	1		TAAGVADQGTSNGLGSIDDIETDCYVDPRGSPALLPSTPTMPLF
	1		PHVLDLLAPLDSSRTLPSTDSLDDFSDGDVFGPELDTLLDSLSL
	Ì	J	VQCGLSGSGVPSELPQLIPVPPGGTPLLPPVVCGSIPVSSPLPP
. 1	[		ASFGLVMDPSKKLAASVLDALDPPGPTLDPLDLLPYSETRLDAL

SEQ	Predicted	I nacazara	
ID	beginning	Predicted end	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine.
	location	corresponding	K=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ļ	amino acid	sequence	Codon, /=possible nucleotide deletion.
1	sequence		\=possible nucleotide insertion)
	<del> </del>		DSFGSTRGSLDKPDSFMEETNSQDHRPPSGAQKPAPSPEPCMPN
1			TALLIKNPLAATHEFKQACQLCYPKTGPRAGDYTYREGLEHKCK
ſ		1	RDILLGRLRSSEDQTWKRIRPRPTKTSFVGSYYLCKDMINKODC
	,		KYGDNCTFAYHQEEIDVWTEERKGTLNRDLLFDPLGGVKRGSLT
1			IAKLLKBHQGIFTFLCEICFDSKPRIISKGTKDSPSVCSNLAAK
J	J		HSFYNNKCLVHIVRSTSLKYSKIRQFQEHFQFDVCRHEVRYGCL
1			REDSCHFAHSFIELKVWLLQQYSGMTHEDIVQESKKYWQQMEAH
1			AGKASSSMGAPRTHGPSTFDLQMKFVCGQCWRNGQVVEPDKDLK
1			YCSAKARHCWTKERRVLLVMSKAKRKWVSVRPLPSIRNFPQQYD
1			LCIHAQNGRKCQYVGNCSFAHSPEERDMWTFMKENKILDMQQTY
1			DMWLKKHNPGKPGEGTPISSREGEKQIQMPTDYADIMMGYHCWL
i	1	Ì	CGKNSNSKKQWQQHIQSEKHKEKVFTSDSDASGWAFRFPMGEFR
j	}		LCDRLQKGKAC?DGDKCRCAHGQEELNEWLDRREVLKQKLAKAR
	<del> </del>	<u> </u>	KDMLLCPRDDDFGKYNFLLQEDGDLAGATPEAPAAAATATTGE
5583	3	1265	SSGCROGRPGRSDRPRPPPRRHKMVKETRYYDILGVKPSASPEE
1	i	•	IKKAYRKLALKYHPDKNPDEGEKFKLISQAYEVLSDPKKRDVYD
ł			QGGEQAIKEGGSGSPSFSSPMDIFDMFFGGGGRMARERRGKNVV
			HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGGKKGSVEKCPL
{	1		CKGRGMHIHIQQIGPGMVQQIQTVCIECKGQGERINPKDRCESC
ļ			SGAKVIREKKI1EVHVEKGMKDGQKILFHGEGDQEPELEPGDVI
[	1		IVLDQKDHSVFQRRGHDLIMKMKIQLSEALCGFKKTIKTLDNRI
1			LVITSKAGEVIKHGDLRCVRDEGMPIYKAPLEKGILIIQFLVIF
1			PEKHWLSLEKLPQLEALLP?RQKVRITDDMDQVELKEFCPNEQN WRQHREAYEEDEDGPQAGVQCQTA
5584	3	1265	SSGCRQGRPGRSDRPRPPPPRRHKMVKETRYYDILGVKPSASPEE
	]	1205	IKKAYRKLALKYHPDKNPDEGEKFKLISQAYEVLSDPKKRDVYD
Í			QGGEQAIKEGGSGSPSFSSPMDIFDMFFGGGGRMARERRGKNVV
j	]		HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGGKKGSVEKCPL
[			CKGRGMHIHIQQIGPGMVQQIQTVCIECKGQGERINPKDRCESC
1	}		SGAKVIREKKIIEVHVEKGMKDGQKILFHGEGDQEPELEPGDVI
			IVLDQKDHSVFQRRGHDLIMKMKIQLSEALCGFKKTIKTLDNRI
ĺ	1 1		LVITSKAGEVIKHGDLRCVRDEGMPIYKAPLEKGILIIQFLVIF
			PEKHWLSLEKLPQLEALLPPRQKVRITDDMDQVELKEFCPNEQN
			WRQHREAYEEDEDGPQAGVQCQTA
5585	2619	915	LPAGTPESSLHEALDQCMTALDLFLTNQFSEALSYLKPRTKESM
			YHSLTYATILEMQAMMTFDPQDILLAGNMMKEAQMLCQRHRRKS
1 .		•	SVTDSFSSLVNRPTLGQFTEEEIHAEVCYAKCLLQRAALTFLQD
			ENMVSFIKGGIKVRNSYQTYKELDSLVQSSQYCKGENHPHFEGG
1			VKLGVGAFNLTLSMLPTRILRLLEFVGFSGNKDYGLLQLEEGAS
			GHSFRSVLCVMLLLCYHTFLTFVLGTGNVNIEBAEKLLKPYLNR
			YPKGAIFLFLAGRIEVIKGNIDAAIRRFEECCBAQQHWKQFHHM
)			CYWELMWCFTYKGQWKMSYFYADLLSKENCWSKATYIYMKAAYL
			SMFGKEDHKPFGDDEVELFRAVPGLKLKIAGKSLPTEKFAIRKS
			RRYFSSNPISLPVPALEMMYIWNGYAVIGKQPKLTDGILEIITK
	·		AEEMLEKGPENEYSVDDECLVKLLKGLCLKYLGRVQEAEENFRS
			ISANEKKIKYDHYLIPNALLELALLLMEQDRNEEAIKLLESAKQ
5586	2619	915	NYKNYSMESRTHFRIQAATLQAKSSLBNSSRSMVSSVSL LPAGTPESSLHEALDQCMTALDLFLTNQFSEALSYLKPRTKESM
		743	YHSLTYATILEMQAMMTFDPQDILLAGNMMKEAQMLCQRHRRKS
	j		SVTDSFSSLVNRPTLGQFTEEEIHAEVCYAKCLLQRAALTFLQD
			ENMVSFIKGGIKVRNSYOTYKELDSLVQSSOYCKGENHPHFEGG
	ŀ		VKLGVGAFNLTLSMLPTRILRLLEFVGFSGNKDYGLLOLEEGAS
	Ì		GHSFRSVLCVMLLLCYHTFLTFVLGTGNVNIEEAEKLLKPYLNR
	1		YPKGAIFLFLAGRIEVIKGNIDAAIRRFEECCEAQQHWKQFHHM
	j		CYWELMWCFTYKGQWKMSYFYADLLSKENCWSKATYIYMKAAYL
	1		SMFGKEDHKPFGDDEVELFRAVPGLKLKIAGKSLPTEKFAIRKS
	}		RRYFSSNPISLPVPALEMMYIWNGYAVIGKQPKLTDGILEIITK
	ŀ		AEEMLEKGPENEYSVDDECLVKLLKGLCLKYLGRVQEAEENFRS
'	İ		ISANEKKIKYDHYLIPNALLELALLLMEQDRNEEAIKLLESAKQ
1			nyknysmesrthfriqaatlqaksslenssrsmvssvsl
5587	1768	148	SSAVPDGAVGRPVAVAVGGPPHSCRCRPCCLMAAIGVHLGCTSA

SEQ Pz	cdicted	Predicted end	Amino acid segment containing signal peptide
	ginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	cleotide	location	Glutamic Acid, P=Phenylalanine, G=Glycine,
	cation	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
co	rresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
am	ino acid	residue of	S=Serine, T=Threonine, V=Valine,
re	sidue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
am	ino acid	sequence	Codon, /=possible nucleotide deletion,
se	quence	1 -	\=possible nucleotide insertion)
			CVAVYKDGRAGVVANDAGDRVTPAVVAYSENEEIVGLAAKQSRI
	•		RNISNTVMKVKQILGRSSSDPQAQKYIAESKCLVIBKNGKLRYE
1 1			IDTGEETKFVNPEDVARLIFSKMKETAHSVLGSDANDVVITVPF
			DFGEKQKNALGEAARAAGFNVLRLIHEPSAALLAYGIGODSPTG
1 1			KSNILVFKLGGTSLSLSVMEVNSGIYRVLSTNTDDNIGGAHFTE
1 1			TLAQYLASEFQRSFKHDVRGNARAMMKLTNSAEVAKHSLSTLGS
]			ANCFLDSLYEGODFDCNVSRARFELLCSPLFNKCIEAIRGLLDO
			NGFTADDINKVVLCGGSSRIPKLQQLIKDLFPAVELLNSIPPDE
			VIPIGAAIEAGILIGKENLLVEDSLMIECSARDILVKGVDESGA
			SRFTVLFPSGTPLPARRQHTLQAPGSISSVCLELYESDGKNSAK
1			EETKFAQVVLQDLDKKENGLRDILAVLTMKRDGSLHVTCTDOET
			GKCEAISIEIAS
5588	3	589	TPPPPEQAMVAATVAAAWLLLWAAACAQQEQDFYDFKAVNIRGK
1 1			LVSLEKYRGSVSLVVNVASECGFTDQHYRALQQLQRDLGPHHFN
			VLAFPCNQFGQQEPDSNKBIESFARRTYSVSFPMFSKIAVTGTG
( 1			AHPAFKYLAQISGKEPTWNFWKYLVAPDGKVVGAWDPTVSVEEV
1			RPQITALVRKLILLKREDL
5589	1884	553	LRQAWHEGGIGQTDKERGAAALPGEEGDPTRGRSLGRASWESGS
1		-	PRRPRSPFSSFLPRPICLSLEARPCSIEDRRNWSLIGRPGAPAS
			GLNRSSGLWLGPDRCRPRSRCSCRVMENPSPAAALGKALCALLL
1			ATLGAAGQPLGGESICSARAPAKYSITFTGKWSQTAFPKQYPLF
	ì		RPPAQWSSLLGAAHSSDYSMWRKNQYVSNGLRDFAERGEAWALM
1			KEIEAAGEALQSVHAVFSAPAVPSGTGQTSAELEVQRRHSLVSF
1			VVRIVPSPDWFVGVDSLDLCDGDRWREQAALDLYPYDAGTDSG?
1			TFSSPNFATIPODTVTEITSSSPSHPANSFYYPRLKALPPIARV
			TLLRLRQSPRAFIPPAPVLPSRDNEIVDSASVPETPLDCEVSLW
	ļ		SSWGLCGGHCGRLGTKSRTRYVRVQPANNGSPCPELEEEAECVP
	İ		DNCV
5590	72	896	LCSSGALRLLPAMVAWRSAFLVCLAFSLATLVQRGSGDFDDFNL
1 1			EDAVKETSSVKQPWDHTTTTTTNRPGTTRAPAKPPGSGLDLADA
<b>!</b>		*	LDDQDDGRRKPGIGGRERWNHVTTTTKRPVTTRAPANTLGNDFD
1 1			LADALDDRNDRDDGRRKPIAGGGGFSDKDLEDIVGGGEYKPDKG
j j	j		KGDGRYGSNDDPGSGMVAEPGTIAGVASALAMALIGAVSSYISY
			QQKKFCFSIQQGLNADYVKGENLEAVVCEEPQVKYSTLHTQSAE
			PPPPPEPARI
5591	68	1494	AGSSRRAAAERLLVSAGCRSLAGRASGVLLLPAELLPGEEEAMA
	ĺ		LRVTRNSKINAENKAKINMAGAKRVPTAPAATSKPGLRPRTALG
	1		DIGNKVSEQLQAKMPMKKEAKPSATGKVIDKKLPKPLEKVPMLV
1	i		PVPVSEPVPEPEPEPEPEPVKEEKLSPEPILVDTASPSPMETSG
1 1	1	į	CAPAEEDLCQAFSDVILAVNDVDAEDGADPNLCSBYVKDIYAYL
	j		RQLEEEQAVRPKYLLGREVTGNMRAILIDWLVQVQMKFRLLQET
	į		MYMTVSIIDRFMQNNCVPKKMLQLVGVTAMFIASKYEEMYPPRI
1 1	ł		GDFAFVTDNTYTKHQIRQMEMKILRALNFGLGRPLPLHFLRRAS
	l	ļ	KIGEVDVEQHTLAKYLMELTMLDYDMVHPPPSQIAAGAFCLALK
1 1	ľ	İ	ILDNGEWTPTLQHYLSYTEESLLPVMQHLAKNAAMVNQGLTKHM
5592			TVKNKYATSKHAKISTLPQLNSALVQDLAKAVAKV
3392	242	924	YGESKDWNQKDLLSALVLTTVNCLPTPIMAKSAEVKLAIFGRAG
1 1	ŀ	ł	VGKSALVVRFLIKRFIWEYDPTLESTYRHQATIDDEVVSMEILD
] ]	ļ	· ]	TAGQEDTIQREGHMRWGEGFVLVYDITDRGSFEEVLPLKNILDE
	ſ		IKKPKNVTLILVGNKADLDHSRQVSTEEGEKLATELACAFYECS
	J		ACTGEGNITEIFYELCREVRRRRMVQGKTRRRSSTTHVKQAINK
			MLTKISS
		1113	HASGGRAANMAAERGAGQQQSQEMMEVDRRVESEESGDEEGKKH
5593	3	Į.	
5593	3		SSGIVADLSEQSLKDGEERGEEDPEEEHELPVDMETINLDRDAE
5593	3		DVDLNHYRIGKIEGFEVLKKVKTLCLRQNLIKCIENLEBLQSLR
5593	3		DVDLNHYRIGKIEGFEVLKKVKTLCLRQNLIKCIENLEBLQSLR BLDLYDNQIKKIENLEALTELEILDISPNLLRNIEGVDKLTRLK
5593	3		DVDLNHYRIGKIEGFEVLKKVKTLCLRQNLIKCIENLEELQSLR BLDLYDNQIKKIENLEALTELEILDISPNLLRNIEGVDKLTRLK KLFLVNNKISKIENLSNLHQLQMLELGSNRIRAIENIDTLTNLE
5593	3		DVDLNHYRIGKIEGFEVLKKVKTLCLRONLIKCIENLEBLOSLR BLDLYDNQIKKIENLEALTELEILDISPNLLRNIEGVDKLTRLK KLFLVNNKISKIENLSNLHOLOMLELGSNRIRAIENIDTLTNLB SLFLGKNKITKLONLDALTNLTVLSMQSNRLTKIEGLONLVNLR
5593	3		DVDLNHYRIGKIEGFEVLKKVKTLCLRQNLIKCIENLEELQSLR BLDLYDNQIKKIENLEALTELEILDISPNLLRNIEGVDKLTRLK KLFLVNNKISKIENLSNLHQLQMLELGSNRIRAIENIDTLTNLE

SEO	Predicted	Predicted end	Their and an arrant containing of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
1.0.	location		
1	1	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S-Scrine, T-Threonine, V=Valine,
Ì	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ļ	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
			MLALPSVRQIDATFVRF
5594	3	1113	HASGGRAANMAAERGAGQQQSQEMMEVDRRVESEESGDEEGKKH
1	1	[	
	1	<b>[</b>	SSGIVADLSEQSLKDGEERGEEDPEEHBLPVDMETINLDRDAE
1	Į	ļ	DVDLNHYRIGKIEGFEVLKKVKTLCLRQNLIKCIENLBELQSLR
	1		ELDLYDNQIKKIENLEALTELEILDISFNLLRNIEGVDKLTRLK
	[ -		KLFLVNNKISKIENLSNLHQLQMLELGSNRIRAIENIDTLTNLE
1	1		SLFLGKNKITKLQNLDALTNLTVLSMQSNRLTKIEGLQNLVNLR
1			ELYLSHNGIEVIEGLENNNKLTMLDIASNRIKKIENISHLTELQ
[	1		EFWMNDNLLESWSDLDELKGARSLETVYLERNPLQKDPQYRRKV
1	1		MLALPSVROIDATFVRP
5595	3	1476	ARWNGRWVQVPAWPGPGCGTNASGERQRQLPRAWRPVGRTLGSE
	1		PIALAWSPPLYLFPIPLPSWAVSQPTPTLGTMFADLDYDIEEDK
}	)		
1			LGIPTVPGKVTLQKDAQNLIGISIGGGAQYCPCLYIVQVFDNTP
1			AALDGTVAAGDEITGVNGRSIKGKTKVEVAKMIQEVKGEVTIHY
			NKLQADPKQGMSLDIVLKKVKHRLVENMSSGTADALGLSRAILC
1	} '		NDGLVKRLEBLERTAELYKGMTEHTKNLLRAFYELSQTHRAFGD
ł			VPSVIGVREPQPAASEAFVKFADAHRSIEKFGIRLLKTIKPMLT
1			DLNTYLNKAIPDTRLTIKKYLDVKFEYLSYCLKVKEMDDBEYSC
1			IALGEPLYRVSTGNYEYRLILRCRQEARARFSQMRKDVLEKMEL
1	<u>J</u>		LDQKHVQDIVFQLQRLVSTMSKYYNDCYAVLRDADVFPIBVDLA
			HTTLAYGLNQEEFTDGEEEEEEEDTAAGEPSRDTRGAAGPLDKG
f .			GSWCDS
5595	698	219	GAVLAPSSLPAAELAAQGESQSLEDLSNTSRPTSEVYKISFIFP
1		4-2	NGDKYDGDCTRTSSGIYERNGIGIHTTPNGIVYTGSWKDDKMNG
	ľ	i.	FOR FURGOANDECOEVENISMOND COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMMENCE COMM
			FGRLEHFSGAVYEGQFKDNMFHGLGTYTFPNGAKYTGNFNENRV
5597			KGEGEYTHIQGTRMDVVTFHFTSCSQT
3391	3	731	ISCKMAADGQSSLPASWRSVTLTHVEYPAGDLSGHLLAYLSLSP
1	i .		VFVIVGFVTLIIFKRELHTISFLGGLALNEGVNWLIKNVIQEPR
			PCGGPHTAVGTKYGMPSSHSQFMWFFSVYSFLPLYLRMHQTNNA
1			RFLDLLWRHVLSLGLLAVAFLVSYSRVYLLYHTWSQVLYGGIAG
			GLMAIAWFIFTQEVLTPLFPRIAAWPVSEFFLIRDTSLIPNVLW
, ,			FEYTVTRAEARNRQRKLGTKLQ
5598	326	2440	GIGPIAASFIPCKVASLYIFLSPPPPSVSGVPYSPANSSWSCAL
1			VPLLGSGVPPHPPAPSPCCSGQTMLKMLSFKLLLLAVALGFFEG
1	' I		DAKFGERNEGSGARRRCLNGNPPKRLKRRDRRMMSQLELLSGG
)		•	
1 1	1		EMLCGGFYPRLSCCLRSDSPGLGRLENKIFSVTNNTECGKLLEE
1 1			IKCALCSPHSQSLFHSPEREVLERDLVLPLLCKDYCKEFFYTCR
1			GHIPGFLQTTADEFCFYYARKDGGLCFPDFPRKQVRGPASNYLD
[ · [	· •		QMEEYDKVEEISRKHKHNCFCIQEVVSGLRQPVGALHSGDGSQR
1 1			LFILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGGDERGLL
1	ļ		SLAFHPNYKKNGKLYVSYTTNQERWAIGPHDHILRVVEYTVSRK
1 - 1	1		NPHQVDLRTARVFLEVAELHRKHLGGQLLFGPDGFLYIILGDGM
] [	ļ		ITLDDMEEMDGLSDFTGSVLRLDVDTDMCNVPYSIPRSNPHFNS
] .	Ì		TNOPPEVFAHGLHDPGRCAVDRHPTDININLTILCSDSNGKNRS
[ ]			SARILQIIKGKDYESEPSLLEFKPFSNGPLVGGFVYRGCQSERL
[ ]		•	YGSYVFGDRNGNFLTLQQSPVTKQWQBKPLCLGTSGSCRGYFSG
[ ]	j		
[	ļ	j	HILOFGEDELGEVYILSSSKSMTQTHNGKLYKIVDPKRPLMPEE
5599	- 22		CRATVQPAQTLTSECSRLCRNGYCTPTGKCCCSPGWEGDFCRTG
ا وورد ا	326	2440	GIGPIAASFIFCKVASLYIFLSPPPPSVSGVPYSPANSSWSCAL
1			VPLLGSGVPPHPPAPSPCCSGQTMLKMLSFKLLLLAVALGFFEG
			DAKFGERNEGSGARRRRCLNGNPPKRLKRRDRRMMSQLELLSGG
[			EMLCGGFYPRLSCCLRSDSPGLGRLENKIFSVTNNTECGKLLEE
}	1	,	IKCALCSPHSQSLFHSPEREVLERDLVLPLLCKDYCKEFFYTCR
		į	GHIPGFLQTTADEFCFYYARKDGGLCFPDFPRKQVRGPASNYLD
			QMEEYDKVEEISRKHKHNCFCIQEVVSGLRQPVGALHSGDGSQR
			LFILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGGDERGLL
1	1		SLAFHPNYKKNGKLYVSYTTNQERWAIGPHDHILRVVEYTVSRK
		ļ	NPHQVDLRTARVFLEVAELHRKHLGGQLLFGPDGFLYIILGDGM
1			ITLDDMEEMDGLSDFTGSVLRLDVDTDMCNVPYSIPRSNPHFNS
L			TNOPPEVFAHGLHDPGRCAVDRHPTDININLTILCSDSNGKNRS

000			
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F-Phenylalanina, G-Glycine,
i	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P-Proline, Q-Glutamine, R-Arginine,
ļ	amino acid	residue of	S-Serine, T-Threonine, V-Valine,
I	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			SARILQIIKGKDYESEPSLLEFKPFSNGPLVGGFVYRGCQSERL
			YGSYVFGDRNGNFLTLQQSPVTKQWQEKPLCLGTSGSCRGYFSG
1	í	<u> </u>	HILGFGEDBLGEVYILSSSKSMTQTHNGKLYKIVDPKRPLMPEE
		1	CRATVQPAQTLTSECSRLCRNGYCTPTGKCCCSPGWEGDFCRTG
5600	1977	1244	SLRVLSGHLMQTRDLVQPDKPASPKFIVTLDGVPSPPGYMSDOE
5000	1	1233	
ŀ	l.	ļ	EDMCFEGMKPVNQTAASNKGLRGLLHPQQLHLLSRQLEDPNGSF
1			SNAEMSELSVAQKPEKLLERCKYWPACKNGDECAYHHPISPCKA
1			FPNCKFAEKCLFVHPNCKYDAKCTKPDCPFTHVSRRIPVLSPKP
1	ł		AVAPPAPPSSSQLCRYFPACKKMECPFYHPKHCRFNTQCTRPDC
	ļ		TFYHPTINVPPRHALKWIRPQTSE
5601	1977	1244	SLRVLSGHLMQTRDLVQPDKPASPKFIVTLDGVPSPPGYMSDQE
İ			EDMCFEGMKPVNQTAASNKGLRGLLHPQQLHLLSRQLEDPNGSF
	1.	1	SNAEMSELSVAQKPEKLLERCKYWPACKNGDECAYHHPISPCKA
1			FPNCKFAEKCLFVHPNCKYDAKCTKPDCPFTHVSRRIPVLSPKP
1	ļ.		AVAPPAPPSSSQLCRYFPACKKMECPFYHPKHCRFNTQCTRPDC
L			TFYHPTINVPPRHALKWIRPQTSE
5602	246	766	YHTSCTVWRTAKEALENTEVPVGCLMVYNNEVVGKGRNEVNQTK
		-	NATRHAEMVAIDQVLDWCRQSGKSPSEVFEHTVLYVTVEPCIMC
1	1	i	AAALRLMKIPLVVYGCQNERFGGCGSVLNIASADLPNTGRPFQC
j.		J	IPGYRAEEAVEMLKTFYKQENPNAPKSKVRKKECQQILNMF
5603	1	565	FRGRTPISGGERGCAQYPIPATPARSGENRTMPGAGDGGKAPAR
			WLGTGLLGLFLLPVTLSLEVSVGKATDIYAVNGTEILLPCTFSS
	1	ĺ	CFGFEDLHFRWTYNSSDAFKILIEGTVKNEKSDPKVTLKDDDRI
	1		TLVGSTKEKRNNISIVLRDLEFSDTGKYTCHVKNPKENNLQHHA TIFLQVVDRRMQ
5604	1	1506	EDIFPAQLLKLQRHERVWQQEPPVRDHRSWGGSGAGGVAGREWT
5551	1 -	1300	
i	l .		DOGOVALGGHYMAEGEGYFAMSEDELACSPYIPLGGDFGGGDFG
1			GGDFGGGDFGGGGSFGGHCLDYCESPTAHCNVLNWEQVQ
1	1		RLDGILSETIPIHGRGNFPTLELQPSLIVKVVRRRLAEKRIGVR
			DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGEFQTVKDV
1	ŀ		VLDCLLDFLPEGVNKEKITPLTLKEAYVQKMVKVCNDSDRWSLI
			SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE
			NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG
ł			LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL
			ESYLONHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL
1			ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV
L			QPVFTCQQQTYSTWLPCN
5605	35	1821	SQRSCPRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL
			MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHRTRFVFQ
J.	Į i		KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDERLQRHRTSG
1			GDHAPDSPSGENSPAPQGRLAEVQDSSMPVPAQPKAGGSGSYWP
	]		ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKSPRVAP
į į		· ·	GSARPWPALRSLLHRNLVLRTHQPARYSLTPEGLELAQKLAESE
	]		GLSLLNVGIGPKEPPGEETAVPGAASAELASEAGVQQQPLELRP
1			GBYRVLLCVDIGETRGGGHRPELLRELQRLHVTHTVRKLHVGDF
1 !			VWVAQETNPRDPANPGELVLDHIVERKRLDDLCSSIIDGRFREQ
1	]		KFRLKRCGLERRVYLVEEHGSVHNLSLPESTLLQAVTNTQVIDG
			FFVKRTADIKESAAYLALLTRGLQRLYQGHTLRSRPWGTPGNPE
]			
) 1			SGAMTSPNPLCSLLTFSDFNAGAIKNKAQSVREVFARQLMQVRG
į .			VSGEKAAALVDRYSTPASLLAAYDACATPKEQETLLSTIKCGRL
5606	3	1000	QRNLGPALSRTLSQLYCSYGPLT
1 2000	ا	1099	GRSRCPGPGARGGTMSPRSCLRSLRLLVFAVFSAAASNWLYLAK
1 .	1		LSSVGSISEEETCEKLKGLIQRQVQMCKRNLEVMDSVRRGAQLA
			IBECQYQFRNRRWNCSTLDSLPVFGKVVTQGTREAAFVYAISSA
			GVAFAVTRACSSGELEKCGCDRTVHGVSPQGFQWSGCSDNIAYG
			GVAFAVTRACSSGELEKCGCDRTVHGVSPQGFQWSGCSDNIAYG
			GVAFAVTRACSSGELEKCGCDRTVHGVSPQGFQWSGCSDNIAYG VAFSQSFVDVRERSKGASSSRALMNLHNNEAGRKAILTHMRVEC
			GVAFAVTRACSSGELEKCGCDRTVHGVSPQGFQWSGCSDNIAYG VAFSQSFVDVRERSKGASSSRALMNLHNNEAGRKAILTHMRVEC KCHGVSGSCEVKTCWRAVPPFRQVGHALKEKFDGATEVEPRRVG SSRALVPRNAQFKPHTDEDLVYLEPSPDFCEQDMRSGVLGTRGR
			GVAFAVTRACSSGELEKCGCDRTVHGVSPQGFQWSGCSDNIAYG VAFSQSFVDVRERSKGASSSRALMNLHNNEAGRKAILTHMRVEC KCHGVSGSCEVKTCWRAVPPFRQVGHALKEKFDGATEVEPRRVG

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
į	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
į.	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	WaTruntophan Valuesias V VII
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
5607	521	141	PPVCNPAEAMPSPGTVCSLLLLGMI,WLDLAMAGSSFLSPEHQRV
ſ			QQRKESKKPPAKLQPRALAGWLRPEDGGQAEGAEDELEVRFN\(\lambda\)P
j			FDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADK
5608	2	983	WFQSPLRQADPGPPRHTLFMDFVAGAIGGVCGDAVGYPLDTVKV
	_		RIQTEPKYTGIWHCVRDTYHRERVWGFYRGLLLPVCTVSLVSSE
ł			VFGTYRHCLAHICRLRFGNPDAKPTKADITLSGCASGLVRVFLT
1			SPITEWAYURI OTOTOA OYOODDA GA GGDY AND TUSTOS OF THE SPITEWAYURI OTOTOA OYOODDA GA GGDY AND TUSTOS OF THE SPITEWAYURI OTOTOA OYOODDA GA GGDY AND TUSTOS OF THE SPITEWAYURI OTOTOA OYOODDA GA GGDY AND TUSTOS OF THE SPITEWAYURI OTOTOA OYOODDA GA GGDY AND TUSTOS OF THE SPITEWAYURI OTOTOA OYOODDA GA GGDY AND TUSTOS OF THE SPITEWAYURI OTOTOA OYOODDA GA GGDY AND TUSTOS OF THE SPITEWAYURI OTOTOA OYOODDA GA GGDY AND TUSTOS OF THE SPITEWAYURI OTOTOA OYOODDA GA GGDY AND TUSTOS OF THE SPITEWAYURI OTOTOA OYOODDA GA GGDY AND TUSTOS OF THE SPITEWAYURI OTOTOA OYOODDA GA GGDY AND TUSTOS OF THE SPITEWAYURI OTOTOA OYOODDA GA GGDY AND TUSTOS OF THE SPITEWAYURI OTOTOA OYOODDA GA GGDY AND TUSTOS OF THE SPITEWAYURI OTOTOA OYOODDA GA GGDY AND TUSTOS OF THE SPITEWAYURI OTOTOA OYOODDA GA GGDY AND TUSTOS OF THE SPITEWAYURI OTOTOA OYOODDA GA GGDY AND TUSTOS OF THE SPITEWAYURI OTOTOA OYOODDA GA GGDY AND TUSTOS OF THE SPITEWAYURI OTOTOA OYOODDA GA GGDY AND TUSTOS OF THE SPITEWAYURI OTOTOA OYOODDA GA GGDY AND TUSTOS OTOTOA OYOODDA GA GGDY AND TUSTOS OTOTOA OYOODDA GA GGDY AND TUSTOS OTOTOA OYOODDA GA GGDY AND TUSTOS OTOTOA OYOODDA GA GA GA GA GA GA GA GA GA GA GA GA GA
-{	i i		SPTEVAKVRLQTQTQAQKQQRRLSASGPLAVPPMCPVPPACPBP
1	·		KYRGPLHCLATVARBEGLCGLYKGSSALVLRDGHSFATYFLSYA
			VLCEWLSPAGHSRPDVPGVLVAGGCAGVLAWAVATPMDVIKSRL
			QADGQGQRRYRGLLHCMVTIVREEG?RVLFKGLVLNCCRAFPVN MVVFVAYBAVLRLARGLLT
5609	1628	304	
			AKGVWVLPSPPPRPGRGALVSGSGLRRGRSGTSWRPRRMNHKSK
			KRIREAKRSARPELKDSLDWTRHNYYESFSLSPAAVADNVERAD
1			ALQLSVEEFVERYERPYKPVVLLNAQEGWSAQEKWTLERLKRKY
[			RNQKFKCGEDNDGYSVKMKMKYYIEYMESTRDDSPLYIFDSSYG
1	l		EHPKRRKLLEDYKVPKFFTDDLFQYAGEKRRPPYRWFVMGPPRS GTGIHIDPLGTSAWNALVQGHKRWCLFPTSTPRELIKVTRDEGG
1			NQQDEAITWFNVIYPRTQLPTWPPEFKPLEILQKPGETVFVPGG
	i l		WWHYVLNLDTTIAITQNFASSTNFPVVWHKTVRGRPKLSRKWYR
]			ILKQEHPELAVLADSVDLQESTGIASDSSSDSSSSSSSSSSSDSD
1 1		•	SECESGEGDGTVHRRKKRRTCSMVGNGDTTSQDDCVSKERSSS
			R CHESSESSET VARARARRICS MVGNGDITS QDDCVSKERSSS
5610	54	1196	LERTPASADMAWTKYQLFLAGLMLVTGSINTLSAKWADNFMAEG
			CGGSKEHSFQHPFLQAVGMFLGEFSCLAAFYLLRCRAAGQSDSS
1 1			VDPQQPFNPLLFLPPALCDMTGTSLMYVALNMTSASSFQMLRGA
			VIIFTGLFSVAFLGRRLVLSQWLGILATIAGLVVVGLADLLSKH
1			DSQHKLSEVITGDLLIIMAQIIVAIQMVLEEKFVYKHNVHPLRA
!			VGTEGLFGFVILSLLLVPMYYIPAGSFSGNPRGTLEDALDAFCQ
i l			VGQQPLIAVALLGNISSIAFFNFAGISVTKELSATTRMVLDSLR
1	1		TVVIWALSLALGWEAFHALQILGFLILLIGTALYNGLHRPLLGR
1 1	,		LSRGRPLAEESEQERLLGGTRTPINDAS
5611	2	577	FVLPNRLGIPGSTFRGPGACASSSSLAASAKPGAGGSPALAMSG
			ELSNRFQGGKAFGLLKARQERRLABINREFLCDQKYSDEENLPE
ł I		·	KLTAFKEKYMEPDLNNEGEIDLMSLKRMMEKLGVPKTHLEMKKM
1 1			ISEVTGGVSDTISYRDFVNMMLGKRSAVLKLVMMFEGKANESSP
L			KPVGPPPERDIASLP
5612	1	721	ASRDGYMDATIAPHRIPPEMPQYGBENHIFELMQAMWLCKHLNS
j			SLLTLENLILNEFSYTATEARRLYLQRKTVPSALLVQLIQERLA
1			EEDCIKQGWILDGIPETREQALRIQTLGITPRHVIVLSAPDTVL
]	•	1	IERNLGKRIDPQTGEIYHTTFDWPPBSEIQNRLMVPEDISELET
]	}	ļ	AQKLLEYHRNIVRVIPSYPKILKVISADQPCVDVFYQALTYVQS
<u> </u>		<b>I</b>	NHRTNAPFTPRVLLLGPVGS
5613	115	1279	RGVDPALRRAEKMLPLSIKDDEYKPPKFNLFGKTSGWFRSTLSD
. [	İ		KTSRNLFFFLCLNLSFAFVBLLYGIWSNCLGLISDSFHMFFDST
	. ]		AILAGLAASVISKWRDNDAFSYGYVRAEVLAGFVNGIFITPTAF
1			FIFSEGVERALAPPDVHHERLLLVSILGFVVNLIGIFVFKHGGH
i i			GHSHGSGHGHSHSLFNGALDQAHGHVDHCHSHEVKHGAAHSHDH
	Ì	1	AHGHGHFHSHDGPSLKETTGPSROILOGVFLHTLADTLGSTGVT
1	ļ	1	ASAIMMONFGLMIADPICSILIAILIVVSVIPLLRESVGILMOR
1	• [	ľ	TPPLLENSLPQCYQRVQQLQGVYSLOEOHFWTLCSDVYVGTI.KI.
			IVAPDADARWILSQTHNIFTQAGVRQLYVQIDFAAM
5614	3	1268	LLSRNEHACPLQAGLGLTQRKPKAIRGREGRATNOGOGETONER
! !		ł	APWGARQRLGVMAELQQLQEFEIPTGREALRGNHSALLRVADVC
1			EDNYVQATDKRKALEETMAFTTOALASVAYOVGNLAGHTLRMLD
1		i i	LQGAALRQVEARVSTLGQMVNMHMEKVARREIGTLATVORLDDG
J			QKVIAPENLPPLTPYCRRPLNFGCLDDIGHGIKDISTOLSPTCT
1	İ	ſ	LSRKSIKAPATPASATLGRPPRIPEPVHLPVVPDGRLSAASSAS
1	1		SLASAGSAEGVGGAPTPKGQAAPPAPPLPSSLDPPPPPPAAVEVF
ļ		1	QRPPTLEELSPPPPDEELPLPLDLPPPPPPLDGDELGLPPPPPGF
			GPDEPSWVPASYLEKVVTLYPYTSQKDNELSFSEGTVICVTRRY

SEO	Predicted	Predicted end	I have paid comment and delivery
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H-Histidine, I=Isoleucine, K=Lysine,
ļ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ļ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	204251100	\=possible nucleotide insertion)
		<del></del>	SDGWCEGVSSEGTGFFPGNYVEPSC
5615	9	1558	ALGRRRPGDPREMEAAATPAAAGAARREELDMDVMRPLINEQNF
ł			DGTSDEEHEQELLPVQKHYQLDDQEGISFVQTLMHLLKGNIGTG
	}		LLGLPLAIKNAGIVLGPISLVFIGIISVHCMHILVRCSHFLCLR
	ł		FKKSTLGYSDTVSFAMEVSPWSCLQKQAAWGRSVVDFFLVITQL
i			GFCSVYIVFLAENVKQVHEGFLESKVFISNSTNSSNPCERRSVD
i			LRIYMLCFLPFIILLVFIRELKNLFVLSFLANVSMAVSLVIIYQ
	ŀ		YVVRNMPDPHNLPIVAGWKKYPLFFGTAVFAFEGIGVVLPLENQ
1			MKESKRFPQALNIGMGIVTTLYVTLATLGYMCFHDEIKGSITLM
1			LPQDVWLYQSVKILYSFGIFVTYSIQFYVPAEIIIPGITSKFHT
}			KWKQICEFGIRSFLVSITCAGAILIPRLDIVISFVGAVSSSTLA
			LILPPLVEILTFSKEHYNIWMVLKNISIAFTGVVGPLLGTYITV
			BEIIYPTPKVVAGTPQSPFLNLNSTCLTSGLK
5616	1	719	DDFVRCGPQSAAMGASARLLRAVIMGAPGSGKGTVSSRITTHFE
1		•	LKHLSSGDLLRDNMLRGTEIGVLAKAFIDQGKLIPDDVMTRLAL
			HELKNLTQYSWLLDGFPRTLPQAEALDRAYQIDTVINLNVPFEV
			IKQRLTARWIHPASGRVYNIEFNPPKTVGIDDLTGEPLIQREDD
			KPETVIKRLKAYEDQTKPVLEYYQKKGVLETFSGTETNKIWPYV
1			YAFLQTKVPQRSOKASVTP
5617	176	765	PWRGRGSRPRGAGAMAEEQVNRSAGLAPDCEASATAETTVSSVG
	}		TCEAAGKSPEPKDYDSTCVFCRIAGRQDPGTELLHCENEDLICF
1			KDIKPAATHHYLVVPKKHIGNCRTLRKDQVELVENMVTVGKTIL
			ERNNFTDFTNVRMGFHMPPFCSISHLHLHVLAPVDQLGFLSKLV
L			YRVNSYWFITADHLIBKLRT
5618	3	1692	YLNYINLKSENKLSGKEDLWEKLQYLWKSTLNLPEDLLRVPDES
1 1			LFLNSGGDSLKSIRLLSEIEKLVGTSVPGLLEIILSSSILEIYN
1 1			HILQTVVPDEDVTFRKSCATKRKLSNINGERASGTSLHQKAIMT
	Į.		FTCHNEINAFVVLSRGSQILSLNSTRFLTKLGHCSSACPSDSVS
1.			QTNIQNLKGLNSPVLIGKSKDPSCVAKVSEEGKPAIGTOKMELH
1	Í	•	VRWRSDTGKCVDASPLVVIPTFDKSSTTVYIGSHSHRMKAVDFY
1 1			SGKVKWEQILGDRIESSACVSKCGNFIVVGCYNGLVYVLKSNSG
1 !	1		EKYWMFTTEDAVKSSATMDPTTGLIYIGSHDOHAYALDIYRKKC
1 1			VWKSKCGGTVFSSPCLNLIPHHLYFATLGGLLLAVNPATGNVIW
1			KHSCGKPLFSSPQCCSQYICIGCVDGNLLCFTHFGEQVWQFSTS
1 1			GPIFSSPCTSPSEQKIFFGSHDCFIYCCNMKGHLQWKFETTSRV
j	ľ		YATPFAFHNYNGSNEMLLAAASTDGKVWILESQSGQLQSVYELP
5619	2160		GEVFSSPVVLESMLIIGCRDNYVYCLDLLGGNQK .
3019	2100	1477	DSPVLPTSGNVISTAQPAQPWSAVEAALRSLGSPPGAGRGCPCP
{			AQSLHSHQLAAWDPLKPSLRSYPPHLLQHPQLRSLTASSGHLGR
]	1		RSCPQPRPLEELLRAGSSTRPQPLTSSCCGMSCMYSFLGHCSVL
1			LWGTKGRGSGSPSSPGCCLHPPAQHSQDLPLVHVDVGWQPPLGP
1 1	1		TVGLRPGLLGERQRGALRAGDPQCQCPLPATVREDLGVPSPWAA ECSPPATP
5620	930	182	
1	1	102	PLPPPTLAMFLTRSEYDRGVNTFSPEGRLFQVEYAIEAIKLGST
i l			AIGIOTSEGVCLAVEKRITSPLMEPSSIEKIVEIDAHIGCAMSG
1	ĺ	ļ	LIADAKTLIDKARVETQNHWFTYNETMTVESVTQAVSNLALQFG
1		ì	EEDADPGAMSRPFGVALLFGGVDEKGPQLFHMDPSGTFVQCDAR
1	i	l	AIGSASEGAQSSLQEVYHKSMTLKEAIKSSLIILKQVMEEKLNA
5621	<del></del>	819	TNIELATVQPGQNFHMFTKEELEEVIKDI
[ ]	-	023	VVEFVEYTATDANVKNESLSSVQQLGIKMTVRYGKFLSLLKDGA
	ļ	İ	ENDLTWVLKHCERFLKQQQTSIKSSLLCLQGNYAGHDWFVSSLF
[ ]	1	ļ	MIMLGDKEKTFQFLHQFSRLLTSAFLWLPRLHISSYLPNDTVES
i i			GIHPVYFCSTHYIEMLLKAELPLVFSAFHMSGFAPSQICLQWIT
l i		I	QCFWNYLDWIEICHYIATCVFLGPDYQVYICIAVFKHLQQDILQ
	j	İ	HTQTQDLQVFLKEEALHGFRVSDYFEYMEILEQNYRTVLLRDMR NIRLOST
5622	1122		
i		1	AASTKDAVSRKRSHSASEKSGTGTSISKRINMNPQIRNPMKAMY
			PGTFYFQFKNLWBANDRNETWLCFTVEGIKRRSVVSWKTGVFRN
			QVDSETHCHAERCFLSWFCDDILSPNTKYQVTWYTSWSPCPDCA
			GEVAEFLARHSNVNLTIFTARLYYFQYPCYQEGLRSLSQEGVAV

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	Intercine Memorbiosis ReLysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
İ	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
1	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ł	sequence	sequence	Codon, /=possible nucleotide deletion,
	-		\=possible nucleotide insertion)
1			BIMDYEDFKYCWENFVYNDNEPFKPWKGLKTNFRLLKRRLRESL
5623	3	0.5.4	Q
3023	1	954	PLPFFIRAPKISRNGQWLFTFTTPFPFANKALPGWEGIVPACFW
ı	İ		RKKILTPSTGTMELLQVTILFLLPSICSSNSTGVLEAANNSLVV
ł		[	TTTKPSITTPNTESLQKNVVTPTTGTTPKGTITNELLKMSLMST
l		ļ	ATFLTSKDEGLKATTTDVRKNDSIISNVTVTSVTLPNAVSTLQS
ļ			SKPKTETQSSIKTTEIPGSVLQPDASPSKTGTLTSIPVTIPEN'T
1			SQSQVIGTEGGKNASTSATSRSYSSIILPVVIALIVITLSVFVL
1			VGLYRMCWKADPGTPENGNDQPQSDKESVKLLTVKTISHESGEH
5504			SAQGKTKN
5624	159	898	PGVAAAAGALPQYHGPAPALVSCRRELSLSAGSLQLERKRRDFT
1			SSGSRKLYFDTHALVCLLEDNGFATQQAEIIVSALVKILEANMD
1			IVYKDMVTKMQQEITFQQVMSQIANVKKDMIILEKSEFSALRAE
			NEKIKLELHQLKQQVMDEVIKVRTDTKLDFNLEKSRVKELYSLN
			EKKLLELRTEIVALHAQQDRALTQTDRKIETEVAGLKTMLESHK
			LDNIKYLAGSIFTCLTVALGFYRLWI
5625	1	1180	TIPSSAAAQRAGPPAGALEALSPGGARAHAERRGEMRATPLAAP
			AGSLSRKKRLELDDNLDTERPVQKRARSGPOPRLPPCLLPLSPP
		1	TAPDRATAVATASRLGPYVLLEPEEGGRAYOALHCPTGTRYTCR
]	ļ		VYPVQEALAVLEPYARLPPHKHVARPTEVLAGTOLLYAFFTRTH
1			GDMHSLVRSRHRIPEPEAAVLFROMATALAHCHOHGLVIRDIKI.
			CRFVFADRERKKLVLENLEDSCVLTGPDDSLWDKHACPAYVGPE
			ILSSRASYSGKAADVWSLGVALFTMLAGHYPFODSEPVLLFGKI
			RRGAYALPAGLSAPARCLVRCLLRREPAERLTATGILLHPWIRO
			DPMPLAPTRSHLWEAAQVVPDGLGLDEAREEEGDREVVLYG
5626	3123	2011	PPRALGSVAMENQVLTPHVYWAQRHRELYLRVELSDVONPAISI
			TENVLHFKAQGHGAKGDNVYEFHLEFLDLVKPEPVYKLTQRQVN
1	1		ITVQKKVSQWWBRLTKQEKRPLFLAPDFDRWLDESDAEMELRAK
	1		EEERLNKLRLESEGSPETLTNLRKGYLFMYNLVOFLGFSWIFVN
1 1			LTVRFCILGKESFYDTFHTVADMMYFCQMLAVVETINAAIGVTT
1			SPVLPSLIQLLGRNFILFIIFGTMEEMQNKAVVFFVFYLWSAIR
1			IFRYSFYMLTCIDMDWKVLTWLRYTLWIPLYPLGCLAEAVSVIO
1 1			SIPIFNETGRFSFTLPYPVKIKVRFSFFLQIYLIMIFLGLYINF
		<u> </u>	RHLYKQRRRRYGQKKKKIH
5627	3123	2011	PPRALGSVAMENQVLTPHVYWAQRHRELYLRVELSDVQNPAISI
ļ			TENVLHFKAQGHGAKGDNVYEFHLEFLDLVKPEPVYKLTQRQVN
1 1			ITVQKKVSQWWERLTKQEKRPLFLAPDFDRWLDESDAEMELRAK
1			EEERLNKLRLESEGSPETLTNLRKGYLFMYNLVQFLGFSWIFVN
			LTVRFCILGKESFYDTFHTVADMMYFCQMLAVVETINAAIGVTT
1 1			SPVLPSLIQLLGRNFILFIIFGTMEEMQNKAVVFFVFYLWSAIE
1	İ		IFRYSFYMLTCIDMDWKVLTWLRYTLWIPLYPLGCLAEAVSVIO
1	1		SIPIFNETGRESETLPYPVKIKVRESEFLOIYLIMIFLGLYINE
<b></b>			RHLYKQRRRRYGQKKKKIH
5628	75	1455	VAGAMASKCLKAGFSSGSLKSPGGASGGSTRVSAMYSSSPCKLP
j l	İ		SLSPVARSFSACSVGLGRSSYRATSCLPALCLPAGGFATSYSGG
1 1	1		GGWFGEGILTGNEKETMQSLNDRLAGYLEKVRQLEQENASLESR
	j	i	IREWCEQQVPYMCPDYQSYFRTIEELQKKTLCSKAENARLVVEI
<b>!</b>	İ	ľ	DNAKLAADDFRTKYETEVSLRQLVESDINGLRRILDDLTLCKSD
1			LEAQVESLKEELLCLKKNHEEEVNSLRCQLGDRLNVEVDAAPPV
	!	· [	DLNRVLEEMRCQYETLVENNRRDAEDWLDTQSEELNQQVVSSSE
		ĺ	QLQSCQAEIIELRRTVNALEIELQAQHSMRDALESTLAETEARY
1		ŀ	SSQLAQMQCMITNVEAQLABIRADLERQNQEYQVLLDVRARLEC.
]		ł	BINTYRGLLESEDSKLPCNPCAPDYSPSKSCLPCLPAASCGPSA
J		į	ARTNCSARPICVPCPGGRF
5629	2287	938	GRPRSSSDNRNFLRERAGLSSAAVQTRIGNSAASRRSPAARPPV
ļ	!		PAPPALPRGRPGTEGSTSLSAPAVLVVAVAVVVVVVSAVAMAMA
1			NYIHVPPGSPEVPKLNVTVQDQEEHRCREGALSLLQHLRPHWDP
i	1	ļ	QBVTLQLFTDGITNKLIGCYVGNTMEDVVLVRIYGNKTELLVDR
!		ļ	DBEVKSFRVLQAHGCAPQLYCTFNNGLCYEFIQGEALDPKHVCN
	ļ		PAIFRLIARQLAKIHAIHAHNGWIPKSNLWLKMGKYFSLIPTGF
			THE TENED THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE

SEQ	Predicted	Predicted end	Amino agid something
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
•	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first		L=Leucine, M=Methionine, N=Asparagine,
ŀ	amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine,
		residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion.
	sequence		\=possible nucleotide insertion)
1			ADEDINKRFLSDIPSSQILQEEMTWMKEILSNLGSPVVLCHNDL
1			LCKNIIYNEKQGDVQFIDYEYSGYNYLAYDIGNHFNEFAGVSDV
1			DYSLYPDRELQSQWLRAYLEAYKEFKGFGTEVTEKEVEILFIQV
1			NQFALASHPFWGLWALIQAKYSTIEFDFLGYAIVRFNQYFKMKP
i		Ì	BYTALKUPE
5630	1194	278	
ł			GFWAIAQTCAHHLPPGSPWLVPASPWRLPEMSSFGYRTLTVALF
1	ļ		TLICCPGSDEKVFEVHVRPKKLAVEPKGSLEVNCSTTCNQPEVG
ŀ	Į.	}	GLETSLDKILLDEQAQWKHYLVSNISHDTVLQCHFTCSGKQESM
		}	KSNVSVYQPPRQVILTLQPTLVAVGKSFTIECRVPTVEPLDSLT
1	i		LFLFRGNETLHYETFGKAAPAPQEATATFNSTADREDGHRNFSC
j	1		LAVLDLMSRGGNIFHKHSAPKMLEIYEPVSDSQMVIIVTVVSVL
5631			LSLFVTSVLLCFIFGQHLRQQRMGTYGVRAAWRRLPQAFRP
3037	1053	290	SRVDDFVRPEPSRAEPSRSGRRRPARRAATMSVFGKLFGAGGGK
1			AGKGGPTPQEAIQRLRDTEEMLSKKQEFLEKKIEGELTAAKKHG
i			TKNKRAALQALKRKKRYEKQLAQIDGTLSTIBFOREALENANTN
1			TEVLKNMGYAAKAMKAAHDNMDIDKVDELMODIADOOELAEETS
	]		TAISKPVGFGEEFDEDELMAELEELEQEELDKNLLEISGPETVP
			LPNVPSIALPSKPAKKKEEEDDDMKELENWAGSM
5632	3	952	VVLGWSPPRRLWWGSLGAAQRPAVPVSGLARSLHVETRRPHRRA
1			SVRVARGRLGVWAQPQPLLPRPVGSRREMQPPGPPPAYAPTNGD
			FTFVSSADAEDLSGSIASPDVKLNLGGDFIKESTATTFLRQRGY
]	!		GWLLEVEDDDPEDNKPLLEELDIDLKDIYYKIRCVLMPMPSLGF
1 1			MPOWED DEPONDED AND EDGES OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF T
i l			NRQVVRDNPDFWGPLAVVLFFSMISLYGQFRVVSWIITIWIFGS
] ]			LTIFLLARVLGGEVAYGQVLGVIGYSLLPLIVIAPVLLVVGSFE
ļ. I			VVSTLIKLFGVFWAAYSAASLLVGEEFKTKKPLLIYPIFLLYIY
5633	771	460	FLSLYTGV
		460	QGCSKTMSVGRPFYRSSEFMEQLLSSHLHQVPFFCCFTVVCLCN
}			CLPENSVSKLYMLCFNFFMSIFFYSLSITKLNLIYLWGLSYQSL
5634	1446		LLLLLSGHRPWGSSMV
3034	1446	855	PRATGRIRSRAAASRPRAGAGASGAEPRSGRERERLSGRRAPAM
1	1		ARNTLSSRFRRVDIDEFDENKFVDEQEEAAAAAAEPGPDPSEVD
	1		GLLRQGDMLRAFHAALRNSPVNTKNQAVKERAOGVVLKVLTNFK
1 1			SSEIEQAVQSLDRNGVDLLMKYIYKGFEKPTENSSAVLLQWHEK
			ALAVGGLGSIIRVLTARKTV
5635	3	943	DRGPRS'TA''DTGRARVSFWRFPLDPGVKNSNVQISGEKRRFRTL
1			RSLFHPFPVTRSGAPRAVLVGSSWPAKMVAPAVKVARGWSGLAL
}	}		GVRRAVLQLPGLTQVRWSRYSPEFKDPLIDKEYYRKPVEELTEE
	Ì	İ	EKYVRELKKTQLIKAAPAGKTSSVFEDPVISKFTNMMMIGGNKV
ļ		l	LARSLMIQTLEAVKRKQFEKYHAASAEEQATIERNPYTIFHQAL
l f	ĺ	f	KNCEPMIGLVPILKGGRFYQVPVPLPDRRRRFLAMKWMITECRD
	l,		KKHQRTLMPEKLSHKLLEAFHNQGPVIKRKHDLHKMAEANRALA
I	[		HYRWW
5636	2253	1143	LEDTICQHPPAEKKLYLYHRKLREVERNGIPRLPKDVFMDTHQG
I	-		TADADA KALCEGERANDO MAGARIA SEKRAGI PREPKDA LADADA LADADA MAGARIA SEKRAGI PREPKDA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADADA LADA
- 1		J	LTDVRAKVTGFSEGVVDSVKGGFSSFSQATHSAAGAVVSKPREI
ł	1	i	ASLIRNKFGSADNIPNLKDSLEEGQVDDAGKALGVISNFQSSPK
İ	1		YGSEEDCSSATSGSVGANSTTGGIAVGASSSKTNTLDMQSSGFD
-	Í		ALLHEIQEIRETQARLEESFETLKEHYQRDYSLIMQTLQEERYR
]	ļ	ļ	CERLEEQLNDLTELHQNEILNLKQELASMEEKIAYQSYERARDI
ŀ		į	QEALEACQTRISKMELQQQQQQVVQLEGLENATARNLLGKLINI
1		j	LLAVMAVLLVFVSTVANCVVPLMKTRNRTFSTLFLVVFIAFLWK
5637	- 046		HWDALFSYVERFFSSPR
2021	948	2532	MSFCGARANAKMMAAYNGGTSAAAAGHHHHHHHHLPHLPPPHLH
1		1	HHHHPQHHLHPGSAAAVHPVQOHTSSAAAAAAAAAAAAAAAMLNPG
- 1	j		QQQPYFPSPAPGQAPGPAAAAPAQVQAAAAATVKAHHHQHSHHP
1		ì	QQQLDIEPDRPIGYGAFGVVWSVTDPRDGKRVALKKMPNVFQNL
1		1	VSCKRVFRELKMLCFFKHDNVLSALDILQPPHIDYFEBIYVVTE
j	1	1	LMQSDLHKIIVSPQPLSSDHVKVFLYQILRGLKYLHSAGILHRD
- 1	ĺ		IKPGNLLVNSNCVLKICDFGLARVEELDESRHMTQEVVTQYYRA
	ļ	i i	PEILMGSRHYSNAIDIWSVGCIFAELLGRRILFQAQSPIQQLDL
j	ļ		TTDLLGTDSLEAMDERGESSESSESSESSESSESSESSESSESSESSESSESSESS
	<u>-</u>		ITDLLGTPSLEAMRTACEGAKAHILRGPHKQPSLPVLYTLSSQA

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L-Leucine, M-Methionine, N-Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
- [	amino acid	sequence	Codon, /=possible nucleotide deletion,
ŀ	sequence	_	\=possible nucleotide insertion)
		<del> </del>	THEAVHLLCRMLVFDPYKRISAKDALAHPYLDEGRLRYHTCMCK
	ļ		CCFSTSTGRVYTSDFEPVTNPKFDDTFEKNLSSVRQVKEIIHQF
İ	,		ILEQQKGNRVPLCINPQSAAFKSFISSTVAQPSEMPPSPLVWE
563B	125	1155	DRKMSELDQLRQEAEQLKNQIRDARKACADATLSQITNNIDPVG
		•	RIQMRTRRTLRGHLAKIYAMHWGTDSRLLVSASQDGKLIIWDSY
į			TTNKVHAIPLRSSWVMTCAYAPSGNYVACGGLDNICSIYNLKTR
İ		}	EGNVRVSRELAGHTGYLSCCRFLDDNQIVTSSGDTTCALWDIET
	·		GQQTTTFTGHTGDVMSLSLAPDTRLFVSGACDASAKLWDVREGM
		ļ	CROTFTGHESDINAICFFPNGNAFATGSDDATCRLFDLRADQEL
			MTYSHDNIICGITSVSFSKSGRLLLAGYDDFNCNVWDALKADRA
			GVLAGHDNRVSCLGVTDDGMAVATGSWDSFLKIWN
5639	125	1155	DRKMSELDQLRQEAEQLKNQIRDARKACADATLSQITNNIDPVG
1			RIQMRTRRTLRGHLAKIYAMHWGTDSRLLVSASQDGKLIIWDSY
1	1		TTNKVHAIPLRSSWVMTCAYAPSGNYVACGGLDNICSIYNLKTR
	}		EGNVRVSRELAGHTGYLSCCRFLDDNQIVTSSGDTTCALWDIET
			GQQTTTFTGHTGDVMSLSLAPDTRLFVSGACDASAKLWDVREGM
	<b>[</b>		CROTFTGHESDINAICFFPNGNAFATGSDDATCRLFDLRADQEL
İ			MTYSHDNIICGITSVSFSKSGRLLLAGYDDFNCNVWDALKADRA
			GVLAGHDNRVSCLGVTDDGMAVATGSWDSFLKIWN
5640	280	1092	QQGNKKTMLSHNTMMKQRKQQATAIMKZVHGNDVDGMDLGKKVS
Í			IPRDIMLEELSHLSNRGARLFKMRQRRSDKYTFENFQYQSRAQI
			NHSIAMQNGKVDGSNLEGGSQQAPLTPPNTPDPRSPPNPDNIAP
			GYSGPLKEIPPEKFNTTAVPKYYQSPWEQAISNDPELLBALYPK
			LFKPEGKAELPDYRSFNRVATPFGGFEKASRMVKFKVPDFELLL
			LTDPRFMSFVNPLSGRRSFNRTPKGWISENIPIVITTEPTDDTT
j			VPESEDL
5641	27	332	CRHNCNGDVKLLSNQMDKLFAFHLPTFHGLLHFLDGSIQKLIQA
ì			EIILSDNSSILVLENNFLFKVKSKQFIHLIAKKFYISITIVSAS
1			NGESFVLSMIVTG
5642	199	1247	ITPCRMDFLVLFLFYLASVLMGLVLICVCSKTHSLKGLARGGAQ
			IFSCI_PECLQRAMHGLLHYLFHTRNHTFIVLHLVLQGMVYTEY
1			TWEVFGYCOELELSLHYLLLPYLLLGVNLFFFTLTCGTNPGIIT
1			KANELLFLHVYEFDEVMFPKNVRCSTCDLRKPARSKHCSVCNWC
1			VHRFDHHCVWVNNCIGAWNIRYFLIYVLTLTASAATVAIVSTTF
1 1			LVHLVVMSDLYQETYIDDLGHLHVMDTVFLIQYLFLTFPRIVFM
			LGFVVVLSFLLGGYLLFVLYLAATNQTTNEWYRGDWAWCQRCPL
			VAWPPSAEPQVHRNIHSHGLRSNLQEIFLPAFPCHERKKQB
5643	1	847	PSGGVRDVETRGPGSRAARGPRVVMFRRGVGAGAIAKKKLAEAK
		ĺ	YKERGTVLAEDQLAQMSKQLDMFKTNLEEFASKHKQEIRKNPEF
]		ļ	RVQFQDMCATIGVDPLASGKGFWSEMLGVGDFYYELGVQIIEVC
1 1			LALKHRNGGLITLEELHQQVLKGRGKFAQDVSQDDLIRAIKKLK
1			ALGTGFGIIPVGGTYLIQSVPAELNMDHTVVLQLAEKNGYVTVS
1 1	j		EIKASLKWETERARQVLEHLLKEGLAWLDLQAPGEAHYWLPALF
			TDLYSQEITAEEAREALP
5644	83	1138	PRRMGSWVQLITSVGVQQNHPGWTVAGQFQEKKRFTEEVIEYFQ
1 1	1		KKVSPVHLKILLTSDEAWKRFVRVAELPREEADALYEALKNLTP
1 1	l		YVAIEDKDMQQKEQQFREWFLKEFPQIRWKIQESIERLRVIANE
Į !	i	}	IEKVHRGCVIANVVSGSTGILSVIGVMLAPFTAGLSLSITAAGV
<b>[</b> [			GLGIASATAGIASSIVENTYTRSAELTASRLTATSTDQLEALRD
1		1	ILHDITPNVLSFALDFDEATKMIANDVHTLRRSKATVGRPLIAW
i l		f	RYVPINVVETLRTRGAPTRIVRKVARNLGKATSGVLVVLDVVNL
			VQDSLDLHKGEKSESAELLRQWAQELEENLNELTHIHQSLKAG
5645	537	799	VQSVRDLKRLSPTDPPGDSGNRDVTREDPVTGPLNSASSQVPTL
			YLCLONSLIGHSSVEDARATMELYQISQRIRARRGLPRLAVSD
5646	3745	3328	AEQYGTSPHLLPTMLLSSCLPPANVTTKAATPPPLVLSLTTADP
1 1			AGKPAPCRVTLTLLRASIPATKRASFLSSFIKMFPBELEYILGF
	ł		LSLLKPHVHVSVYSAICHFQKEGTGNSRSFTCTPELFPRLQTHL
			RAEGGAQ
5647	288	800	GVIMATSELSCEVSEENCERREAFWAEWKDLTLSTRPBEGCSLH
			EEDTQRHETYHQQGQCQVLVQRSPWLMMRMGILGRGLQEYQLPY
	-		

SEQ	Predicted	Predicted end	Amino acid compost
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ŀ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S-Serine, T-Threonine, V-Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	_	\=possible nucleotide insertion)
		1	QRVLPLPIFTPAKMGATKEEREDTPIQLQELLALETALGGQCVD
L			RQEVAEITKQLPPVVPVSKPGALRRSLSRSMSQEAQRG
5648	7	1518	VLSELCGRHEALREVGAEWPPPTCSPNICSGLQQAGNTDWSLTM
1			APQSLPSSRMAPLGMLLGLLMAACFTFCLSHQNLKEFALTNPEK
1			SSTKETERKETKAEEBLDAEVLEVFHPTHEWQALQPGQAVPAGS
ĺ	1		HVRLNLOTGEREAKLQYEDKFRNNLKGKRLDINTNTYTSQDLKS
			ALAKEKEGAEMEGGKEDKADOA EUKOA DER TOTA TOTA TOTA TOTA TOTA TOTA TOTA TOT
ļ			ALAKFKEGAEMESSKEDKARQAEVKRLFRPIEELKKDFDELNVV
ŀ		j	IETDMQIMVRLINKFNSSSSSLEEKIAALFDLEYYVHQMDNAQD
1	1		LLSFGGLQVVINGLNSTEPLVKEYAAFVLGAAFSSNPKVQVEAI
1			EGGALQKLLVILATEQPLTAKKKVLFALCSLLRHFPYAQRQFLK
			LGGLQVLRTLVQEKGTEVLAVRVVTLLYDLVTEKMFAEEEAELT
	}		QEMSPEKLQQYRQVHLLPGLWEQGWCEITVHLLALPEHDAREKV
1 '			LQTLGVLLTTCRDRYRQDPQLGRTLASLQAEYQVLASLELQDGE DEGYFQELLGSVNSLLKELR
5649	1172	3006	MI OBOY DA YNEGADIANO BENEFICIAL
		3000	MLQEQLDAINEEIRMIQEEKESTELRAEEIETRVTSGSMEALNL
1			KQLRKRGSIPTSLTDLSLASASPPLSGRSTPKLTSRSAAQDLDR
1			MGVMTLPSDLRKHRRKLLSPVSREENREDKATIKCETSPPSSPR
1			TLRLEKLGHPALSQEEGKSALEDQGSNPSSSNSSQDSLHKGAKR
			KGIKSSIGRLFGKKEKGRLIQLSRDGATGHVLLTDSEFSMQEPM
			VPAKLGTQAEKDRRLKKKHQLLEDARRKGMPFAQWDGPTVVSWL
			ELWVGMPAWYVAACRANVKSGAIMSALSDTEIQREIGISNALHR
1			LKLRLAIQEMVSLTSPSAPPTSRTSSGNVWVTHEEMETLETSTK
1			TDSEEGSWAQTLAYGDMNHEWIGNEWLPSLGLPQYRSYFMECLV
			DARMLDHLTKKDLRVHLKMVDSFHRTSLQYGIMCLKRLNYDRKE
			LEKRREESQHEIKDVLVWTNDQVVHWVQSIGLRDYAGNLHESGV
1			HGALLALDENFOHNTLALILQIFTONTQARQVMEREFNNLLALG
1			TDRKLDDGDDKVFRRAPSWRKRFRPREHHGRGGMLSASABTLPA GFRVSTLGTLQPPPAPPKKIMPEAHSHYLYGHMLSAFRD
5650	1172	3006	MIOFOLDATING TEMPORAL PARTY DATES
1 1			MLQEQLDAINEEIRMIQEEKESTELRAEEIETRVTSGSMEALNL KQLRKRGSIPTSLTDLSLASASPPLSGRSTPKLTSRSAAQDLDR
i l	i		MGVMTI DEDI DYUDDYL I ODVODDOVINO OD OD OD OD OD OD OD OD OD OD OD OD OD
	j		MGVMTLPSDLRKHRRKLLSPVSREENREDKATIKCETSPPSSPR TLRLEKLGHPALSQEEGKSALEDQGSNPSSSNSSQDSLHKGAKR
ĺĺĺ	ĺ		KGIKSSIGRLFGKKEKGRLIQLSRDGATGHVLLTDSEFSMQEPM
1 1			V?AKLGTQAEKDRRLKKKHQLLEDARRKGMPFAQWDGPTVVSWL
	· I		ELWVGMPAWYVAACRANVKSGAIMSALSDTEIQREIGISNALHR
1 1			LKLRLAIQEMVSLTSPSAPPTSRTSSGNVWVTHEEMETLETSTK
1 1			TDSEEGSWAQTLAYGDMNHEWIGNEWLPSLGLPQYRSYFMECLV
{			DARMLDHLTKKDLRVHLKMVDSFHRTSLQYGIMCLKRLNYDRKE
ĺĺ			LEKRREESQHEIKDVLVWTNDQVVHWVQSIGLRDYAGNLHESGV
			HGALLALDENFOHNTLALILQIPTQNTQARQVMEREFNNLLALG
í			TDRKLDDGDDKVFRRAPSWRKRFRPREHHGRGGMLSASAETLPA
Ĺ [			GFRVSTLGTLQPPPAPPKKIMPEAHSHYLYGHMLSAFRD
5651	646	1869	ARQGQRQPWG*EARAKGPASESPRV*EGSGWEGPASP*TPGSTL
	i		AWGEGAGIR+ASGLTAAGAASAAAA/PPPTRGGPAPAGCGRAPP
1	1		WPAPLRVPTHGRAPAPRSRAAPRAPALSHGTAAAALSPASPAGP
1	1		ADP*LPGHSSQSPPRG*RWGRSRSAPAPAHPEHPAPAGSASASQ
1			QTPGWPGSCCLAQGWQAEPLGAPGAEDG\PVPPQRGFPLGTLGS
	. 1		PAGSWAGLAGYG*AGAPGTQATAPRAAGQTPVAAAPNCRV*GSA
			PALHRAPAAADPGSPLQAPPRAWASPAAAGPGLSSSDYCGGLGA
J			GWRAGISPELLGAAGLSDNWARCPGPGPAB*GGQPGCRTIPASA
f		ĺ	CMPSPPVEGSLGLSRKGHGDLPSQAR+GWHECRRARHLVPLPRL
_			LGPRGRTGRPSSPS
5652	735	343	
		* * * *	HHKKYQHIHQKSFSCPEPACGKSFNFKKHLKEHMKLHSDTRDYI
1		1	CEFCARSFRTSSNLVIHRRIHTGEKPLQCEICGFTCRQKASLNW
5653	66	1401	HORKHAETVAALRFPCEFCGKRFEKPDSVAAHRSKSHPALLLA
			RGRLQSRGRLTLGLVLLLLDILGARQHGQRVSHGWKGGFLTAPL
1	1	i	CFPQPCQPGTRRGRRSLKEATEPQLAMAEEFVTLKDVGMDFTL
ł			GDWEQLGLEQGDTFWDTALDNCQDLFLLDPPRPNLTSHPDGSED
	ĺ		LEPLAGGSPEATSPDVTETKNSPLMEDFFEEGFSQEI/SRDVIQ
		L	GWLLELQFRRSLYRGHLVR*FARRSRKSSEV*YCHQRGKSHGMQ
			· · · · · · · · · · · · · · · · · · ·

SEQ	Predicted	Predicted end	l heries and described to the second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
ı	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
i	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	sequence	Codon, /=possible nucleotide deletion,
	sequence	ļ	\=possible nucleotide insertion)
			ES*IKERTQSCVHRPHGRRFHG\DNVSEKTLTPAKSKEYRGEFP
			SYSDHSQQDSVQEGEKPYQCSECGKSFSGSYRLTQHWITHTREK
ľ			PTVHQECEQGFDRKASHSGYPKTHTGYKPYVCNEYGTPFSQSTY
1			LWHQKTHAGEKPCKSQDSDHPPSHDTQSGEHQKTHTDSKSYNCN
l l			ECGKAFTRIFHLTRHQKIHTRKRYECSKCQATFNLRKHLIQHQK
			THAANV .
5654	3	598	TLPLF?GRRFRGWRRCGAVAARKNSTGGNVSINQRRDSVRMSAL
1	1	1	NWKPFVYGGLASITAECGTFPIDLTKTRFQIOGOTNDAKFKEII
1	ł	}	YRGMLHALVRIGREEGLKALYSG*VGLHAFLCHCSLFHMGIDFR
			PRLHRSQVKSLRCV*KEQIA**/MFSLLISTLISKYIYYAADVL
L			EKLFYYIQVQTDNNKKICLFKNI
5655	2	867	RPPGIRAPRQLHPAAGRRPDASARPRFRPTVLLHDPFQLSFPPP
			PLSYPSVFPAVARVLPQRSGDYRAAGMPQLSGGGGGGGGDPELC
1		i	ATDEMIPFKDEGDPQ\REKIFAEIVNPEEEGDLADIKSSLVNES
		!	EIIPASNGHEVARQAQTSQEPYHDKAREHPDDGKHPDGGLYNKG
1		-	PSYSSYSGYIMMPNMNNDPYMSNGSLSPPIPRTSNKVPVVQPSH
1			AVHPLTPLITYSDEHFSPGSHPSHIPSDVNSKQGMSRHPPAPDI
i			PTFYPLSPGGGGQITPPLGWQGQP
5656	228	1066	PRRVPPLPEFASGPGAAFFHSGRLQRSLTKDSAGCFSQCRSRAM
j j		1	LVLRSGLTKALASRTLAPQVCSSFATGPRQYDGTFYEFRTYYLK
			PSNMNAFMENLKKNIHLRTSYSELVGFWSVEFGGRTNKVPHIWK
			VINEBURA MEMBARATANG PROPERTY AND
1 1			YDNPPHRAEVRKALANCKEWQEQSIIPNLARIDKQETEITYLIP WSKLQKPPKEGVYELAVFQMKPGGPALWGDAPERAINAHVNLGY
			TKVVGVFHTEYGELNRVHVLWWNESADSRAAVRHKSHEDPISWG
1			GVRESVNYL\VSQQNM
5657	105	1052	
	203	1034	GORLOSPRVOMPVOPPSKOTEEMEAEGDSAABMNGEEEESEEER
1 1			SGSQTESEESSEMDDEDYERRRSECVSEMLDLEKQFSELKEKL
1			FRERLSQLRLRLEEVGAERAPEYTEPLGGLQRSLKIRIQVAGIY
1 1			KGFCLDVIRNKYECELQGAKQHLESEKLLLYDTLQGELQBRIQR
1 1			LEEDROSLDLSSEWWDDKLHARGSSRSWDSLPPSKRKKAPLVSG
			PYIVYMLQEIDILEDWTAIKKARAAVSPQKRKSD\DLDPAVHSQ
1			GDPQSSWHCTQDSRLPPADRRTHRPLRVCPARLLWCCWALPLHL
5658	2346		ALVWTPPL
3636	. 2346	3541	TERRVYNPWPEPDPD\CIQEDPWNLPNSIKTLVDNIQRYVEDGK
1			NQLLLALLKCTDTELQLRRDAIFCOALVAAVCTFSEQLLAALGY
i i			RYNNNGEYEESSRDASRKWLEQVAATGVLLHCQSLLSPATVKEE
1 1			RTMLEDIWVTLSELDNVTFSFKQLDENYVANTNVFYHIEGSRQA
l i			LKVIFYLDSYHFSKLPSRLEGGASLRLHTALFTKVLENVEGLPS
ļ .		•	PGSQAAEDLQQDINAQSLEKVQQYYRKLRAFYLERSNLPTDAST
1 1			TAVKIDQLIRPINALDELCRLMKSFVHPKPGAAGSVGAGLIPIS
<u> </u>	,		SELCYRLGACQMVMCGTGMQRSTLSVSLEQAAILARSHGLLPKC
[ ]			IMQATDIMRKQGPRVEILAKNLRVKDQMPQGAPRLYRLCQPKMN
<b> </b>			GDL
5659	2	696	WKRSGEVS PKGELGAWRGNSGRPKIIGRAAEAENEDRTLGRLLP
1			GNERSQPRSPLRLLAPQLKAEAAADKGLAPVPPPFSSGHSGPC\
		ļ	EREGEGORGRGRSRRGAHLBLKPSPGLRAGAPTDRGRGGPAEVA
<u> </u>	!	1	AAGGRRMVQKESQATLEERESELSSNPAASAGASLEPPAAPAPG
1			EDNPAGAGG\AAVAGAAGGARRFLCGVVEGFYGRPWVMEQRKEL
		_	FRRLQKWELNTYL
5660	229	853	PVTMWAFSELPMPLLINLIVSLLGFVATVTLIPAFRGHFIAARL
1		* ]	CGQDLNKTSRQQIPESQGVISGAVFLIILFCFIPFPFLNCFVKE
		. 1	QRKAFPHHEFVALIGALLAICCMIFLGFADDVLNLRWRHKLLLP
t t		1	TAASLPLLMVYFINFGNTTIVVPKPFRPILGLHLDLGR*SYHCC
,		İ	PYGTYFREPFLVLHILLQVFLFCLCVFPDPFW
5661	2	473	LNLYPSPCGGIPKLPGLPREAAAALGASFLAEAPLPVTVRGSGL
	İ		AGMAVTCDPKAFLSICFVTLVFLQLPLASICQN*GTDSCASRGK
		ł	ADEDUTCHER DILLAMACCURE OCCUPATED TO THE STREET
[		ļ	ADFDVTGPHAPILAMAGGHVELQCQLFPNISAEDMELRWYRCQP SLAVHMHERGMDMDGEQKWQYRGRT
5662	2	1318	
_ [	-		LRKEGRCRRGSNRGVWAAPAEGLGGRGMLGVRCLLRSVRFCSSA
			PFPKHKPSAKLSVRDALGAQNASGERIKIQGWIRSVRSQKEVLF

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenvlalanine, G=Glucine
	location	corresponding	H=Histidine, I=Isoleucine, K=Lvsine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine.
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	<del></del>	\=possible nucleotide insertion)
1			LHVNDGSSLESLQVVADSGLDSRELTFGSSVEVQGQLIKSPSKR
			QNVELKAEKIKVIGNCDAKDFPIKYKERHPLEYLRQYPHFRCRT NVLGSILRIRSEATAAIHSFFKDSGFVHIHTPIITSNDSEGAGE
1			LFQLEPSGKLKVPEENFFNVPAFLTVSGQLHLEVMSGAFTQVFT
1		<u> </u>	FGPTFRAENSQSRRHLAEFYMIEAEISFVDSLQDLMQVIEELFK
	· .		ATTMMVLSKCPEDVELCHKFIAPGQKDRL*HMLKNNFLIISYTE
			AVEILKQASQNFTFTPEWGADLRTEHEKYLVKHCGNIPVFVINY
Ĺ	<u>L</u> .		PLTLKPFYMRDNEDGPQELEGSVA+HSLGLMILLSIVVIGOP
5663	119	698	PADIGRSTAKTPGPPRSLEMDDPRYGMCPLKGASGCPGAERSLL
			VQSYFEKGPLTFRDVAIEFSLEEWQCLDSAQQGLYRKVMLENYR
ł			NLVFLGIALTKPDLITCLEQGKEPWNIKRHEMVAKPPVICSHFP
	i		QDLWAEQDIKDSFQEAILKKYGKYGHANFQLQKGCKSVDECKVH
5664			KEHDNKLNQCLIPKKKK
3664	118	572	SLSMESNHKSGDGLSGTQKEAALRALVQRTGYSLVQENGQRKYG
			GPPPGWDAAPPERGCEIFIGKLPRDLFEDELIPLCEKIGKIYEM
1			RMMMDFNGNNRGYAFVTFSNKVEAKNAIKQLNNYEIRNGRLLGV
5665	347	702	CASVDNCRLFVGGIPKTKK
1		702	VVQHLIILLHCERTSPAMITSELPVLQDSTNETTAHSDAGSELE ETEVKGKRKRGRPGRPPSTNKKPRKSPGEKSRIEAGIRGAGRGR
			ANGHPQQNGEGEPVTLPEVVKLGKSAMQRC
5666	213	540	VSCLPTSCKMITLNNQDQPVPFNSSHPDEYKIAALVFYSCIFII
			GLFVNITALWVFSCTTKKRTTVTIYMMVVALVDLIFIMTLPFRM
			FYYAKDEWPFGEYFCQILGA
5667	1	695	HPLPSASLGLPSVSLGVSLCVRSALLEAVVPMLPKRRRARVGSP
i .			SGDAASSTPPSTRFPGVAIYLVEPRMGRSRRAFLTGLARSKGFR
1			VLDACSSEATHVVMEETSAEEAVSWQERRMAAAPPGCTPPALLD
			ISWLTESLGAGQPVPVECRHRLEVAGPSKGPLSPAWMPAYACQR
			PTPLTHHNTGLSEALEILAEAAGFEGSEGRLLTFCRAASVLKAL
5668	691	894	PSPVTTLSQLQ CSFLFCIPDLFLQFLLGRKEEEAVLVGGEWSPSLDGLDPQADPQ
		954	VLVRTAIRCAQAQTGIDLSGCTKW
5669	407	<u> </u>	DSGAPEGLSPLMSTQEGLSMHAHPQAYTPFIYLHARKRRGEIGD
1		_	ADSRFNDRYAHKSAQLYFLYFVCWIFQDVYYPTIKEKNHFFFPK
1			ARGAPTKYSGSPIGSPTTTPPTRPPSFNLHPAPHLLASMQLQKL
			NSQ
5670	3	373	SSECLTMAWIPLLLPLLILCTVSVASYELAQPSSVSVSPGQTAK
1			ITCSGDVLAKKYARWFQQKPGQAPVLVIYKDTERPSGIPERFSG
5671		· · · · · · · · · · · · · · · · · · ·	STSGTTVTLTISGAQVEDRADYFCYSATDNFLWVF
36,1	280	524	KFPPKKTPPHLGMESAITLWQFLLQLLLDQKHEHLICWTSNDGE
5672	2	EET	FKLLKAKKVAKLWGLRKNKTNMNYDKLSRALRLLFMT
	• •	557	FVPATPDPGVWLPPSRDPAMAKRSSLYIRIVEGKNLPAKDITGS
	· [		SDPYCIVKVDNEPIIRTATVWKTLCPFWGEEYQVHLPPTFHAVA
	ļ		FYVMDEDALSRDDVIGKVCLTRDTIASHPKGKFSLPSHTGLPSP WPPSHSETSPLGSVWSPAQGKPFLLSPEAGAIFCTPGLCSAACS
1			QAWLLLPLP
5673	327	696	ITVADQISHWSAGRIKNRTRIPECIHSSAATTLAGPHTMEGESV
			KLSSQTLIQAGDDEKNQRTITVNPAHMGKAFKVMNELRSKQLLC
			DVMIVAEDVEIEAHRVVLAACSPYFCAMFTGDMS
5674	17	984	GGGSMEGESTSAVLSGFVLGALAFQHLNTDSDTEGFLLGEVKGE
[ ]	,		AKNSITDSQMDDVEVVYTIDIQKYIPCYQLFSFYNSSGEVNEOA
	,		LKKILSNVKKNVVGWYKFRRHSDQIMTFRERLLHKNLOEHFSNO
	1		DLVFLLLTPSIITESCSTHRLEHSLYKPQKGLFHRVPLVVANLG
	ŀ		MSEQLGYKTVSGSCMSTGFSRAVQTHSSKFFEEDGSLKEVHKIN
	1		EMYASLQEELKSICKKVEDSEQAVDKLVKDVNRLKREIEKRRGA
1		1	QIQAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMSLKID
5675	80	753	MFLKVAVTTTTISM
		, , ,	EGSRRGPTRLARLSARAGRLHFPPGFSSRLIHFRGVSECRRPPG KSGVPVSAPGSDGKWWEERPGMF9LMASCCGWFKRWREPVRKVT
		1	LLMVGLDNAGKTATAKGIQGEYPEDVAPTVGFSKINLRQGKFEV
	İ	į	TIFDLGGGIRIRGIWKNYYAESYGVIFVVDSSDEERMEETKEAM
	<del></del>	<del></del>	THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE TENED TO THE T

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
-	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S-Serine, T-Threonine, V-Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
	<del>                                     </del>		SEMLRHPRISGKPILVLANKQDKEGALGEADVIECLSLEKLVNE
1	i		HKCL
5676	2	930	FVSSPPPRPVQPARPGGFGLSGRRSLLCQVASTPAHVGVMRSPV
ł	_		RDLARNDGEESTDRTPLLPGAPRAEAAPVCCSARYNLAILAFFG
ŧ	ļ		FFIVYALRVNLSVALVDMVDSNTTLEDNRTSKACPEHSAPIKVH
}			HNQTGKKYQWDAETQGWILGSFFYGYIITQIPGGYVASKIGGKM
i			LLGFGILGTAVLTLFTPIAADLGVGPLIVLRALEGLGEGVTFPA
			MHAMWSSWAPPLERSKLLSISYAGAQLGTVISLPLSGIICYYMN
1	l'		WTYVFYFFGTIGIPWFLLWIWLVSDTPQKHKRISHYEKEYILSS
1			L
5677	1	1028	PPRDGFLELRRLSVPLCSGPCPLTSLSRQGERSGGHLVAAARAA
	1 -		VTAETHPLPLLAPLAVCQSVKSPAACQVRPRPRAVALPAALGGP
1			GRSLPGLTAATMSSFSESALEKKLSELSNSQQSVQTLSLWLIHH
			RKHAGPIVSVWHRELRKAKSNRKLTFLYLANDVIQNSKRKGPEF
		·	TREFESVLVDAFSHVAREADEGCKKPLERLLNIWQERSVYGGEF
:			IQQLKLSMEDSKSFPPKATEEKKSLKRTFQQIQEEEDDDYPGSY.
1	,		SPQDPSAGPLLTEELIKALQDLENAASGDATVRQKIASLPQEVQ
ı		•	DVSLLEKITDKEAAERLSKTVDEACLRNRGPGTS
5678	3	593	SSSPPSSTPSLPLPFYLLLGQLRLQLLWGTAHLSGAGEAAPCPG
1	,	-	GSGRTAAPRTRADPAAQSLMIMNKMKNFKRRFSLSVPRTETIER
		,	SLAEFTEQFNQLHNRRNENLQLGPLGRDPPQECSTFSPTDSGEE
			PGQLSPGVQFQRRQNQRRFSMEVRASGALPRQVAGCTHKGVHRR
		·	AAALQPDFDVSKRLSLPMDI
5679	2	623	LNSRVDDFVAVPGAIMDEDYYGSAAEWGDEADGGQQEDDSGEGE
			DDAEVQQECLHKFSTRDYIMEPSIFNTLKRYFQAGGSPENVIQL
[		,	LSENYTAVAQTVNLLAEWLIQTGVEPVQVQETVENHLKSLLIKH
}			FDPRKADSIFTEEGETPAWLEQMIAHTTWRDLFYKLAEAHPDCL
	·		MLNFTVKVGRVLELRRKVFMNVYFWLLVCFL
5680	258	592	RRLTSTSEKLQNRNSHTPLESLIHPQPSYKGFGIMFGKKKKKIE
			ISGPSNFEHRVHTGFDPQEQKFTGLPQQWHSLLADTANRPKPMV
	i		DPSCITPIQLAPMKTIVRGNKPC
5681	45	869	LLCAKTLGVRTKESQAEGYNRSGINNHQAEDPRFCPSFCWMRSA
1			ROTRPORLRKEAARPPTPGSCPGGTGMDGKKCSVWMFLPLVFTL
i			FTSAGLWIVYFIAVEDDKILPLNSAERKPGVKHAPYISIAGDDP
1	•		PASCVFSQVMNMAAFLALVVAVLKFIQLKPKVLNPWLNISGLVA
i i		*	LCLASFGMTLLGNFQLTNDEEIHNVGTSLTFGFGTLTCWIOAAL
1			TLKVNIKNEGRRVGIPRVILSASITLCVGPLLHPHGPKHPHVCS
			QGPVGPGHVL
5682	3.9	622	PSRSCLGTMRKWRHREVNLPEVTQQDAVCPAPIPSPGLSAQTGL
1 1			QKIWGTIHCQVCPGAPAWPGSPWHEEMGLLLLVPLLLLPGSYGL
			PFYNGFYYSNSANDONLGNGHGKDLLNGVKLVVETPEETLFTYO
	]		GASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPEKDVLVAIG
			LRHRSFGDYQGRVHLRQD
5683	89	778	GSCGATALITRCLAWSVLISRLAMATYTCITCRVAFRDADMQRA
	İ		HYKTDWHRYNLRRKVASMAPVTAEGFQERVRAQRAVAEEESKGS
			ATYCTVCSKKFASFNAYENHLKSRRHVELEKKAVQAVNRKVEMM
	į		NEKNLEKGLGVDSVDKDAMNAAIQQAIKAQPSMSPKKAPPAPAK
			EARNVVAVGTGGRGTHDRDPSEKPPRLQWFEQQAKKLAKHSEDD
5684			SEDEBHDLC
3684	195	677	TWCFRGYLGPRVIMKALDEPPYLTVGTDVSAKYRGAFCEAKIKT
	1		AKRLVKVKVTFRHDSSTVEVQDDHIKGPLKVGAIVEVKNLDGAY
			QEAVINKLTDASWYTVVFDDGDEKTLRRSSLCLKGERHFAESET
5685			LDQLPLTNPEHFGTPVIGKKTNRGRRYE
3003	779	1262	LLLQQPVVHCFLLFPPFRFSHHMIPGPPGPHTTGIPHPAIVTPQ
			VKQEHPHTDSDLMHVKPQHEQRKEQEPKRPHIKKPLNAFMLYMK
	1		EMRANVVAECTLKESAAINQILGRRWHALSREEQAKYYELARKE
5686			RQLHMQLYPGWSARDNYVSPSSIPVALHS
2000	128	1181	CTWWQVNITLLDINDNHPTWKDAPYYINLVEMTPPDSDVTTVVA
			VDPDLGENGTLVYSIQPPNKFYSLNSTTGKIRTTHAMLDRENPD
			PHEAELMRKIVVSVTDCGRPPLKATSSATVFVNLLDLNDNDPTF

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, FaPhenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ı	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
j	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
i	amino acid	residue of	S=Serine, T=Threonine, V=Valine.
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown *-Ston
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
ì			QNLPFVAEVLEGIPAGVSIYQVVAIDLDEGLNGLVSYRMDVGMP
1			RMDFLINSSSGVVVTTTELDRERIAEYOLRVVASDAGTPTKSST
1			STLTIHVLDVNDETPTFFPAVYNVSVSEDVPR\GSGWSG*AARN
į.	1		NDVGLNAELSYFITGGNVDGKFSVGYRDAVVRTVVGLDRETTAA
F.600			YMLILEAIDNGPVGKRHTGTATVFVTVLDVNDKRPIIIOSSYV
5687	17	917	AAPPAPPDG/PPP/PPPAPPT/PGPAA/APASSCOPRISACPAA
1			QGDGGAAAVGHVLVVPAVGPVRVNPGLOTPVPRPELLPGP\SSS
İ			LHSDSSYPPDAGLSDDEEPPDASLPPDPPPLTVP/ADA/PMPVT
			SGCRMPSTSASE/AAGGQGACTHAKGSETPPPASPQTSEPAPSP
}			LPPHLTGGPGMYSSEAKLPNSFSCLGLAGTGAGI+GTASAHGTG
			PPVLPHVCTPSLANPQP\AVGPEASSLPLGVSGIGMSA/SAPIS
			SSPFVAIGSCWLRGIPPPGSGFLCPGRAPGPVPITTHGQEGQGP
5688	1	470	VLDI
-555	*	420	LTKWDLFGNCYRLLKTGIEHGAMPEQVGVYWYS/CLYDSRKLFF
			*SHMIIRSLL*KVIDDSLGQLPLLRELLL**LNVIDRCIILAYV
			LRVEKTFAITYLKNFTVKVDFSLLGEIPLISMAAILKLWIMKID DGYIPAVF
5689	1504	3	
1		•	HBLSGKHISMVSGNTCNWHPGGHSPGGGGGGGEITSKDRGEIPAL
			IWA/RKPIGTWTATKPTHRAG*GGAEEYQPPFQPCEGPRSTSRG GEG*GHAVGPGREIGKEGSLPFLGPKALGF*SASCQRAFEGGAH
			GSTARKPAPATPGTRHPRTMETREVAQGWPAGPRSQFWDQHPHS
1 1			PGEHRPSG\SPLPACPPRAWPKAGAVASATGTG\PQLPGSRGKQ
1 [			KLPRTREPPLLQAGWAVRKPPWSEAKEGLGQAGRPSGMDSSAS\
1 1			POTPGGRGSLEWGLPLYLGPHHDVK*RSDRLG*PP*GGQGGGH
ŀ			GAPSTPGPGGEAW+LPQQTSRPKPGPQAY+GE\GSPGLQCPCSK
1			EL*RVPPGSLGPSTQCMYEPTDKHS\GGADAQLEVSTAGSRSTF
1 1			GQELKGPLDAGRLWPGAPSASSHR*GG*ERARAGAGHRGST*A
1 1			SSKIEQGRPRPGPTSDALADVEGGAES/GPHPWPLPGTLPNR/P
			GSPPPA*ASAGRKGTVSTLGGGLL
5690	1424	58	PSPPAGVCAAPAPLPLLALARRDRRPCSPGAEAAPWQTGGPAID
1 1			GAWRTSVSALRRGATG/APCSPGAEAAPWQTGGPAIDG\DGELP
1 1	1		*VRSEEAPRGCGAEGGGPGSGPVRRPGAGRGAHAGQGRQQDPEP
			DGLRHRQHGAASHARHRLQRLRPGHHQNRHVRRDPQAPPGGPAP
1 1			GHAAALPERTRGVAEPPAWAHAGSDAWRAGR*SQRT*ERARPRH
1	· ]		PTFQGRAGS\GQPGYQPPNPHPGPSSPPAAP\GPRGA*GNPQLE
i I			KAPRSDRNPSQGLRTRIRRPETPDCGPPSPAGSSASASTFRCTS
1 1	•	ĺ	SLSLLGP/PGAHNLDTAPQDR*HGP*GDKRGAPGVAGEDPRPP*
			GNFVR*LLLMP/GVA*RHGTSPFLGPSLGENGGQWDSGNLFGTP KG*SHPAFTKST*SMEAEKSYWNHPHR\DRGRQGVRINCLRVGE
1 1	j		SEMWGPYSAPRPGTVFLSSFLSPASEEH\PEGSSSFNTPFPPAG
] [	ľ		PEGDPGLNSPGLLP
5691	107	550	ISNDPSPGYNIEQMAKRGKKLVELPYTVKGMDVSFSGILSFIED
	1		VAHRMLATGECTPEDLCFSLQVMQ*KTGTESWG*RFYIVEQN*S
1	1		GDAPLIFSPYLSLTGNCGFAMLVEITERAMAH\CGSPGGPSLWG
		J	GVGVYVLLESVPLSYS
5692	1193	548	TQAWTRAEKDRKGSVRALRLHLERGPPT*RGSHPL\OSVPCTOK
1 1			PSIFSSYPI/GLPQSGGEPGPVGEQQPVRRPEQPSCGPASRMPL
[	İ		TSRSVPPGRGALPPDSLSTRKGLPRPSTAGHRVRESGHKVPVSO
j		Į.	RLNLPVMGATRSNLQPPRKVAVPGPTR*RDODSKODFSSKPLOS
الجييا			VPGLASTQQTLTPADSGPGTGGRDATRAGLPGVETMGNGVD
5693	1258	1330	ALTVVPVRKGTTWWAQPHGCSNLVSRARLDLSSRPSONTEPOAD
			*QAGPPSSLRPP\SRRR*APEWPKRATGSRCRGLSAPPWPWPAA
] [	j		RGE/PGSAPSHAP/PNSPRPSGTRHP/PGPSSRVLYSPSI.PRNS
		1	PEAIVWRSSRFPLWFPLRCCFWVSGFKDPNPVLRFF
5694	3	1338	GSKEPARSLHRRGSGHKSSAGKWGSVTLSTAGALG*KOLHO*WT
		1	QRCL\NNLSSEEFNASSSLNSLPSTPTASRRNSTIVLRTDSEKR
		i	SLAESGLSWFSESEBKAPKKLEYDSGSLKMEPGTSKWRRERPES
ĺ		l.	CDDSSKGGELKKPISLGHPGSLKKGKTPPVAVTSPITHTAOSAL
	1	ı	KVAGKPEGKATDKGKLAVKNTGLORSSSDAGRDRLSDAKKPPSG
Ll_	<u></u>		IARPSTSGSFGYKKPPPATGTATVMQTGGSATLSKIQKSSGIPV

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
J	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ł	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /-possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
	<del></del>		KPVNGRKTSLDVSNSAEPGFLAPGARSNIQYRSLPRPAKSSSMS
1			VTGGRGGPRPVSSSIDPSLLSTKQGGLTPSRLKEPTKVASGRTT
1	1		PAPVNQTDREKEKAKAKAVALDSDNISLKSIGSPESTPKNQASH
			PTATKLAFI DOTTOLDATAK GERKADOS TATA DETERMINASH
1	j		PTATKLAELPPTPLRATAKSFVKPPSLAŅLDKVNSNSLDLPSSS DTTOCI
5695	3	1338	· · · · • • · · ·
		1330	GSKEPARSLHRRGSGHKSSAGKWGSVTLSTAGALG*KQLHQ*WT
1			QRCL\NNLSSEEFNASSSLNSLPSTPTASRRNSTIVLRTDSEKR
1			SLAESGLSWFSESEKAPKKLEYDSGSLKMEPGTSKWRRERPES
1			CDDSSKGGELKKPISLGHPGSLKKGKTPPVAVTSPITHTAQSAL
<b>i</b> :	ł i		KVAGKPEGKATDKGKLAVKNTGLQRSSSDAGRDRLSDAKKPPSG
			IARPSTSGSFGYKKPPPATGTATVMQTGGSATLSKIQKSSGIPV
1			KPVNGRKTSLDVSNSAEPGFLAPGARSNIQYRSLPRPAKSSSMS
1	}		VTGGRGGPRPVSSSIDPSLLSTKQGGLTPSRLKEPTKVASGRTT
1			PAPVNQTDREKEKAKAKAVALDSDNISLKSIGSPESTPKNQASH
	:		PTATKLABLPPTPLRATAKSFVKPPSLANLDKVNSNSLDLPSSS
5696	3	1338	
1 1	_	1000	GSKEPARSLHRRGSGHKSSAGKWGSVTLSTAGALG*KQLHQ*WT
1 1			QRCL\NNLSSEEFNASSSLNSLPSTPTASRRNSTIVLRTDSEKR
1 }			SLAESGLSWFSESEEKAPKKLEYDSGSLKMEPGTSKWRRERPES
			CDDSSKGGELKKPISLGHPGSLKKGKTPPVAVTSPITHTAQSAL
			KVAGKPEGKATDKGKLAVKNTGLQRSSSDAGRDRLSDAKKPPSG
)			IARPSTSGSFGYKKPPPATGTATVMQTGGSATLSKIQKSSGIPV
	}		KPVNGRKTSLDVSNSAEPGFLAPGARSNIQYRSLPRPAKSSMS
1 1			VTGGRGGPRPVSSSIDPSLLSTKQGGLTPSRLKEPTKVASGRTT
1 1			PAPVNQTDREKEKAKAKAVALDSDNISLKSIGSPESTPKNQASH
1 1	]		PTATKLAELPPTPLRATAKSFVKPPSLANLDKVNSNSLDLPSSS DTTOCI
5697	1147	47	PSEALSPPACPSAPAPRRSIISRLFGTSPATEAAPPPPEPVPAA
1 1	i		QGPATVQSVEDFVPDDRLDRSFLEDTTPARDEKKVGAKAAQQDS
			DSDGEALGGNPMVAGFQDDVDLEDQPRGSPPLPAGPVPSQDITL
1		•	SSEEEAEVAAPTKGPAPAPQQCSEPETKWSSIPASKPRRGTAPT
]		•	RTAAPPWPGGVSVRTGPEKRSSTRPPAEMEPGKGEQASSSESDP
] ]			EGPIAAQMLSFVMDDPDFESEGSDTQRRADDFPVRDDPSDVTDE
1 1			DEGPAEPPPPPKLPLPAFRLKNDSDLFGLGLEEAGPKESSEEGK
1			EGKTPSKENKKKKKGKBEEEKAAKKKSKHKKSKDKEEGKEERR
i i			RRQQRPPRSRERTAA
5698	2	666	GARAAEPQEDLPPLSQSSRFFQEQQKMNKSLGPVSFKDVAVDFT
1 1	İ		QEEMQQLDPEQKITYRDVMLENYSNLVSVGYHIIKPDVISKLEQ
1			GEEPWIVEGEFLLQSYPDEVWQTDDLIERIQEEENKPSRQTVFI
	1		ETLI*R/ERGNVPGNTFDVETNPVPSRKIAYTHSLCNSCER\GF
	i		NASSBYISSDGRYARMKADECSGCGKSLLHIKLEKTHPGDQAYE
			FNO
5699	2	1448	RVRQPPGLWVRRTVPAMQCPAGLSRVPGVAG/DPSLPSFRGPRD
	1		EAAHRGTIQTARHTRKLYVQGPASGPPLPRVSTQVAI*DEKPLA
!!!			RPS/GRTNAPFPQGQKPAGKAAPGPAAAGRVAMR\PGHPGLLAS
		•	DSQRSSSKGSGWETPVPWS*AQPGWVSGLLLLGDPSGPGSL*RS
1		J	TWLVGGARGPEGSGVRGSGWPSGCSDIGWALAGWNHS*HLDPNT
1			WTQKWTGE/SPAPGEEG/VAPAPRGPTAEHGHCELTTESQYSNN
1		I	VPILFONPSGALRSRRTEPAGWVPPTRHE+DDG+TAAPASGGAP
l l			VSTPTWAGTP/LNASLGPTDPQGKPGCRPPCALPKPAGPERSA+
į	1	ļ	GGSLGCR/SMLPASSGPPPAPGPRRLAAGAHTSASARCPPAAAA
j	1	. !	GWOPRRPGFAGRAALPGPPHPPSS*RELGGLPGPGW*TLDPLPA
	i	}	HPAHPPGSAPPWGALGGWAAARASLPWSPSLCLSFPAVTPVAGL
		.	FPPGRG
5700	923	597	NGHKGVWEINIY*RRSNIHKNSKSESHLNQDHSFPPPTPNSARS
			KLHSTGTAKNTGLPLSGAPRQRAVFSGRTICQEFSSCLQCAYLD
			E*CSIASSLIKAILRVSVLSE
5701	59	410	IFEKICSDTQEFISPEINPQICSWLIFDKGAK/NHATGKDSLFN
1			KWSWKNWLSTCR*MRPGPYFTPYTKINSK*IK/DANIRCETVKL
		ı	LEENTGENLHDTGLGNVFLDMTPKTQPTKQK
			TOTAL TANKET WENT TOTAL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A-Alanine, C=Cysteine, D=Aspartic Acid, R=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
j	sequence		\=possible nucleotide insertion)
5702	. 3	1517	BTFVDPSQCGGIPSDSPHPVITPSRASESSASSDGPHPVITPSR
1			ASESSASSDGPHPVITPSRASESSASSDGLHPVITPSRASESSA
1			SSDGPHPVITPSRASESSASSDGPHPVITPSRASESSA
			PVITPSRASESSASSDGPHPVITPSWSPGSDVTLLAEALVTVTN
1		l	IEVINCSITEIETTTSSIPGASDTDLIPTEGVKASSTSDPPALP
j		<b>l</b> ,	DSTEAKPHITEVTASAETLSTAGTTESAAPHATVGTPLPTNSAT
	j		EREVTAPGATTLSGALVTVSRNPLEETSALSVETPSYVKVSGAA
	1		PVSIEAGSAVGKTTSFAGSSASSYSPSEAALKNFTPSETLIMDI
1			TTKGPFPTSRDPLPSVPPTTTNSSRGTNSTLAKITTSAKTTMKP
1	1		PTATPTTARTRPTT\A*VQVKNEVSSSCG*VWLPRKTSLTPEWQ
1	1		KG*CSSSTGNSTPTRLTSRSPYCVSGEANG/PSAAARHVPYAKR
1			GCCP+PGPPPTDCSCVTVLRGTQKVPMKGSMSKPLTPDVATGPS
			LTSTGVYVWGGASPVPRGVLGLTLAHVLCFSKEKT
5703	14	1117	HHKDSRSQGLPRTQECARPELRPLLCPRALWPVTRLSYRCPWQA
1			PKAGIGTKAKPSESHLKLHPGWPSLDRQGEPATLGTGTGHCSDS
1			RILRWHP*HTAAR*PRWRRLPSSHRWTRHLGVLRVQDKS**VSL
			DPSCRPRFLRTC**YGMRSVASSSNPPPGWSGPGASVFPARPVS
ł	1		ALPTGPRCW*APRGRTRQPCGWPRLSSPHATADWGPGCPLSPSR
			GSWETAPGS*WCPWL*AARWTGWRTASGASAGLGRAADRPSAWA
ļ			RRVAGLLPGQGLTVRR*H*TAGAPASVRSSQGATRSPAPGGDQC
			ACGRGPGSC*HPPPWPVSPSSPVPCPSGR*HLRGPLLSAARPRA
			AGWPRHSPHDTOTPEP
5704	23	562	GDYEFDSPYWDDISQAAKDLVTRLMEVEQDQRITAEEAISHEWI
			SGNAASDKNIKDGVCAQIEKNYARAKWKKAVRVTTLMKRLRAPE
1			QSSTAAAQSASATDTATPGAAGGATAAAASGATSAPEGDAARAA
1	ł ł		KSDNVAPRRP*LPPQPQMEVPPQPLMAVSPQPPMEASLQPLMGE
4	f		SPOP
5705	23	562	GDYEFDSPYWDDISQAAKDLVTRLMEVEQDQRITAEEAISHEWI
1	]	·	SGNAASDKNIKDGVCAQIEKNFARAKWKKAVRVTTLMKRLRAPE
1	i i		QSSTAAAQSASATDTATPGAAGGATAAAASGATSAPEGDAARAA
			KSDNVAPRRP*LPPQPQMEVPPQPLMAVSPQPPMEASLQPLMGE
			SPQP
5706	1161	610	OLGRFXAQDTVAIRKVKEVFGTGAMRHVVILFTHKED+GGQALD
	1		DYVANTDNCSLKDLVRECERRYCAFNNWGSVBEQRQQQAELLAV
			IERLGREREGSFHSNDLFLDAQLLQRTGAGACQEDYRQYQAKVE
i	[		WQVEKHKQELRENESNWAYKALLRVKHLMLLHYEIFVFLLLCSI
	i 1		LFFIIFLF
5707	28	609	GSPAPTPGFRRPGRGTPSPGTRHHQGRAEPEPDAPERAPLRR*
1	l		MFAIQPGLAEGGQFLGDPPPGLCQPELQPDSNSNFMASAKDANR
	1		NWHGMPGRVEPILRRSSSESPSDNQAFQAPGSPEEGVRSPPEGA
1	]		EIPGAEPERMGGAGTVCSPLEDNGYASSSLSIDSRSSSPEPACG
<u> </u>			TPRGPGPPDPLLPSVAQA
5708	44	1925	SFSWEETISPCFPKMPAEPWWLSPVSLGAAGWPGQPRPYLDLPA
		c	QASVSRPHDRA+GEAVSLSLSSGDVCGHTDGGGAGSDPQAKPKP
1			PRCPFTAMPSPRTKQKVRNKVCLLIAIRYSDIPSDVSKAP\GPA
			GNPHDRSSTAA*LHRRAGAGSLCLSASLLPPSFSLGAPGAPSPL
] :	ľ		RVSPASGGPRKEGRQGSGG*AGGGGP\ARTHADLPCVGFVCSPP
í í			LLK*SDSPVKQLPA\SGQGSGAGMPPVGSSDILRPRPTSVSGTG
		•	RAAG*CSWQPAACCTPRSQ*WAVARSPSRCSRW*RQSGR*RG*S
( )			SRRRRGP+AAGRSTPAVP+PCS+GGAGRRAYACRTGWGYAPSR+
			LEPSGPTSGSAL*TWASHSTGA**SRLCGTAGTGPLCSQSSRS*
		ĺ	AG*RCCCTAASPCGGGGPSHPGSPSAHCLSWSGGRTQPRAPSAH
[			GRGRAMGSRCVCTCTGLPCPGIPLSGASPGGSGETGAGRSHTLK
	1	ļ	AARSRLSPRPGSGSRGSY*SHNDNWGTWPAPPSAGHLLVGG*NS
	1		QRTSSDH*YTGTRRPWAGPGTRCSTAPSRAAPPVSRCRPPPPPPP
	İ		PPRPPRLPAAAS/SGGASGSPAASCSCSCRAPAKPASS/GEAPA
			PPPRPEPPPPPARRP
5709	2	2031	ITLCPLPQTEKCLNVVTEAATPLGIYLKARVEAGGLKELEISWG
			LHQIVVRWGAVVMRAGMGGCKCWGVMAPFAPK/NALSFLVNDCS
		ļ	LIHNNVCMAAVFVDRAGEWKLGGLDYMYSAQGNGGGPPRKGIPE
	<del></del>		THE TOTAL PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROP

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			LEQYDPPELADSSGRVVREKRSADMWRLGCLIWEVFNGPLPRAA
1		1	ALRNPGKIPKTLVPHYCELVGANPKVRPNPARFLONCRAPGGFM
			SNRFVETNLFLEEIQIKEPAEKQKFFQELSKSLDAFPEDFCRHK
Ì			VLPQLLTAFEFGNAGAVVLTPLFKVGKFLSAEEYQQKIIPVVVK
		İ	MFSSTDRAMRIRLLQQMEQFIQYLDEPTVNTQIFPHVVHGFLDT
	!		NPAIREQTVKSMLLLAPKLNEANLNVELMKHFARLQAKDEQGPI
			RCNTTVCLGKIGSYLSASTRHRVLTSAFSRATRDPFAPSRVAGV
			LGFAATHNLYSMNDCAQKILPVLCGLTVDPEKSVRDQAFKAIRS.
1			FLSKLESVSEDPTQLEEVEKDVHAASSPGMGGAAASWAGWAVTG
			VSSLTSKLIRSHPTTAPTETNIPQRPTPEGVPAPAPTPVPATPT
1	]		TSGHWETQEEDKDTAEDSSTADRWDDEDWGSLEQEAESVLAQQD
1			DWSTGGQVSRASQVS\TPTTNPPNPQSPTGAAGK\RGLLGTGLA
5710	<u> </u>		GAKLPGATS*RYTAGQRV
3/10	1	562	IPGSTISCEVELMARMAKTIDSFTQNQTRLVVIIDGLDACEQDK
i		·	VLQMLDTVRVLFSKGPFIAIFASDPHIIIKAINQNLNSVPSGFK
İ		:	\LNGHDYMRNIVHLPVFLNSRGL/RQ/LQENFS*LQQQMBTFHA
			QILQGYRKMLTEEFHRTALGR*QNLVARQPSIDG*DAIGFELYV
5711	1526	1130	CIAIQFNTNKDDAT
3,11	1320	1130	RRHPFQWTTVTQEAFSHHDVAFTSTPVLFYPDSAQPFIVKSESS SQIAKAVLSQQRPSLFHECAFHFPS*SLQRHTINLDQGIP*LLM
1			LSEERQHLFESS/IWTTPHNLK*/FEIHEHLGSHEGHWTLFFLL
ł			OIL
5712	3	1391	GRKLFQSLDISERLKFLLTLDCVDDTLIVLAEEHGCLDIIKELP
	-	2331	ETVIDIJINKCLTFHPSKRPTPDELMKDKVFSEVSPLYTPFTKPA
1			SLFSSSLRCADLTLPEDISQLCKDINNDYLAERSIEEVYYLWCL
			AGGDLEKELVNKEIIRSKPPICTLPNFLFEDGESFGQGRDRSS/
!			TFR*YHWDIVVMPAKK*IERCWGRSILPITLKMTSLILPYSNSN
			NELSAAATLPLIIREKDTEYQLNRIILFDRLLKAYPYKKNQIWK
			EARVDIPPLMRGLTWAALLGVEGAIHAKYDAIDKDTPIPTDRQI
	1		EVDIPRCHQYDELLSSPEGHAKFRRVLKAWVVSHPDLVYWQGLD
			SLCAPFLYLNFNNEALVYACMSAFIPKYLYNFFLKDNSHVIQEY
1			LTVFSQMIAFHDPELSNHLNEIGFIPDLYAIPWFLTMFTHVFPL
			HKIFHLW\DTLLLGEFLFPILYWE
5713	634	284	PVCAVPVDRWPVLPREDQEGQQL*AKLPRDFRR*FQILGPMEGH
1			TACRCSRRGAQVQHLPREDIRAAE*DPHLREVWPGLPTSSATSP
			*RAVLTSPCSHLGSADAASSHWLCGVSPH
5714	212	613	WGLGLGPTMSSLGGGSQDAGGSSSSSTNGSGGSGSSGPKAGAAD
1			KSAVVAAAAPASVADDTPPPERRNKSGIISEPLNKSLRRSRPLS
	!		HYSSFGSSGGSGGSMMGGESADKATAAAAASLLANGHDLAAA
5715	127	1075	MA
2,12	131	1979	ESASQQKRSKCLILTLKLELSGSAPKKTSARPGSSLWLPPHSQE
			QTPPASKLQGGGGGLQTGWGLHPVPVTAASPLPRWCLFGAVAK\
'			GLPGP+LCPSGAA/GGLQRGPGLSPLGAAGKVSCLHPPSMVENN
Į J	f		DSTCHEHHEGILAARVTPVP\SGKPGRVLKPPGRVCRPPHPAAS
			PRPPGS/SDLDGPRPQMHLRAFPAAHGGPVNTPHGGEEKTFMSS
	}		QIRRKETKPL*RKTPAG\NNYQSNSIPVSQSPQLTVDLLPSAGR
			TQAPSGRGDAGKPTPGHG\LPKASVILTPNCPCSLAGGQ*PPGL
	}		YPKTPKQRRWRRPL/LLGPSQ+GSRQSTC+EV\GALGEPVRIPG
1 1			L*PDLSCILSNGSKHRREGLSFPRSLGPGRRGPAGLQSLGCSPT
	l		PKNTACHSSGHVALQAGHDSARDVGSGHVALQAGHDSTQDVGRP
	ļ		VWRWIPLE*LGLSRETGQATRRGLVWISPGRAAAACVACAQALE EGPLRLPGQDRGAQPCSHCPGRAAGQPBPGAGAPCRE/GG*DPT
}			GLT/GVPGTDPKRGGRKPGQSGQETQGPTVWSGPESPLQPKP+E
	ļ	•	RQE/VGAGASSGVGLSRGRAGGPSSAWEVAAMLLLLRHGSHSEL
		ļ	TDLTEAQTSQH
5716	1711	1370	RVFSLLCEGPGHCYQGAVCREACAAASPGLDSAAEPHRLCEHTD
.		· <del>-</del>	*LPK*GPGYIQHFHCDSNILCILYNISFNLFSYSF*GVARYAC*
			RCPLVL*SGFFTIIVGGYSCCMPLKT
		1489	
5717	44	7403	LPTEALRESEWVSEYGKCGPRGLVPEGESTSPLPSSVDTEDSLD

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, R=
1	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S-Serine, T-Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
<u> </u>	sequence	ł	\=possible nucleotide insertion;
			GDSLGARPGLPYGLSDDESGGGRALSAESEVEEPARGPGEARGE
1			RPGPACQLCGGPTGEGPCCGAGGPGGGPLLPPRLLYSCRLCTRY
1		ŀ	SHYSSHLKRHMQTHSGEKPFRCGRCPYASAOLVNLTRHTRTHTG
			EXPYRCPHCPFACSSLGNLRRHORTHAGPPTPPCPTCGFRCCTP
j	ļ		RPARPPSPTEQEGAVPRRPEDALLLPDLSLHVPPGGASFLPDCG
1	]		Q\CGVKGRASAGLDQNHCQS/SLFPWTCRGCGOELEEGEGSPIG
1			AAMCGRCMRGEAGGGASGGPQGPSDKGFACSLCPFATHYDNHIA
			RHMKTHSGEKPFRCARCPYASAHLDNLKRHQRVHTGEKPYKCPL
5718	120		CPYACGNLANLKRHGRIHSGDKPFRCSLCNYSCNQSMNLIRHM
3/10	120	284	VAHALSLPAESYGNDVSMTHPQLPPTQLAWDLCRTCLPLSYNFT
5719	48	400	S**STADPLHL
	, 10	428	ELNNGPFQMPLCNGGNLAVTGSWADRSPLHRAASQGRLLALRTL
Ī			LSQGYNVNAVTLDHVTPLHEACLGDHVACARTLLEAGANVNAIT
5720	1	1051	IDGVTPLFNACSQGSPSCAELLLEYGAKAQP\ESCLPSP
	· -	1031	LQAFRNASEVPMVLVGTQDAISAA\NPRVYRRTSRARKLSTDLK
ľ	1		\RCT\YYE\TCGGTYGLQMWSVSFQDVAQKVVAL\RKKQQ\LAI
ı			GPCK\SLPN\SPSH\SAVSAASIPARAPINQGHE/SGGSAFSD Y\SSSVPSTPSISQRELRIETIAASSTPTPIRKQSKRRSNIFTS
			RKGADP\DREKKAAGCKVDSIGSGRAIPIKQGILLKRSGKSLNK
	]		EWKKKYVTLCDNGLLTYHPSLHDYMQNIHGKEIDLLRTTVKVPG
i			KRLPRATPATAPGTSPRANGLSVERSNTQLGGGTGAPHSASSAS
1			LHSERPLSSAWAGPRPEGLHQRSCSVSSADQWSEATTSLPPGM
L	<u>L</u> 1		CHPASG
5721	97	192	RHSSPCCSLRRTERSSNAAVST/TTVQQFKRFIENYRRHIGCVA
1			VFYAIAGGLFLERAYYYAFAAHHTGITDTTRVGIILSRGTAASI
			SFMFSYILLTMCRNLITFLRETFLNRYVPFDAAVDFHRLIASTA
5722	88	1043	VALDVLAGSSPGGMAGALLGPRVHGIRAVLRVARGGVOADGAD
1			GSLGVSHAAAPPARPQGAAQSPHRGRRHGGGGAGLPPPRSDRFD
1			QESVPASTSTARGPRRVSRRLPPOHPGPRGRRRRPGAGVGAPRP
			GRARGQAGLLGRQGQGGRGAERERAALOARRGRRPGPEDDOSCG
]			GRPRRAAAAPGRAPADPQPPAPRPAPAPDVRPPADAPAPAPAPA
[	i		PPPPPHLGALTAGSGEERQSQPRAETLRLGRGAPLP\PRAERGG
]			RPKQAEQQQ\PKRPTPPARGPQSSGDPAMLPQRAGLRTGGLAGT
5723	88	1043	KSSTREIPEMI VALDVI AGSENGGOVA GAVE GARAGE
1 1			VALDVLAGSSPGGGMAGALLGPRVHGIRAVLRVARGGVQAPGAP GSLGVSHAAAPPARPQGAAQSPHRGRRHGGGGAGLPPPRSPRFP
! i			QESVPASTSTARGPRRVSRRLPPQHPGPRGRRRPGAGVGAPRR
1			GRARGQAGLLGRQGQGGRGAERERAALQARRGRRPGPEPDQSCG
] ]	.		GRPRRAAAAPGRAPADPQPPAPRPAPADDVRPPADAPAPAPA
j			PPPPPHLGALTAGSGEERQSQPRAETLRLGRGAPLP\PRAERGG
·	1		RPKQAEQQQ\PKRPTPPARGPQSSGDPAMLPQRAGLRTGGLAGT
			KSSTREIPEMI
5724	3	1841	FTNEAPPAPLPDASASPLSPHRRAKSLDRRSTEPSVTPDLLNFK
	1		KGWLTKQYEDGQWKKHWFALADQSLRYYRDSVAERAADLDGRID
	ļ		LSACYDVTEYPVQRNYGFOIHTKEGEPTLSAMTSGIRRNWIOTI
			MKHVHPTTAPDVTSSLPEEKNKSSCSPETCPRPTEKOEAELGED
1			DPEQKRSRARE\RRREGRSKTFDWAEFRPIOOALAOERVGGVGP
-			ADTH\DPWRPEAEHGELERBRARRREERRKRFGMLDATOGDGTF
}	j	j	DAALRMEVDRSPGLPMSDI.KTHNVHVEIEORWHOVETTPLRERK
		Í	QVPIAPVHLSSEDGGDRLSTHELTSLLEKELEOSOKEASDLLEO
ļ		į	NRLLQDQLRVALGREQSAREGYVLQATCERGFAAMEETHQKKIE
1		ĺ	DLQRQHQRELEKLREEKDRLLAEETAATISAIEAMKNAHREEME
			RELEKSQRSQISSVNSDVEALRRQYLEELQSVQRELEVLSEQYS
}		ļ	QKCLENAHLAQALEAERQALRQCQRENQELNAHNQELNNRLAAE
	İ		ITRLRTLLTGDGGGEATGSPLAQGKDAYELEVPSGARPCLTQLC
5725	3	1049	TOEPOGSAAWPLSYRVVGGTDLRQQESQGPGRSKSPEGGEEQ
-	-	1043	VNGHSEBTSQSPNRTEPHDSDCSVDLGISKSTEDLSPQKSGPVG
			SVVKSHSITNMEIGGLKIYDILSDN\DLSSHLQPLK/FTSAVEG
1	i		KNIVRSKAATLLYDOPLOVFTGSSSSSDLISGTKAIFKFDSNHN PE/GAKYNKRPHKWAHNLHLKYMVLHSIISNTVAV\RSQRHFVA
<del></del>	· L.		- D, GIRLLAND AND AND AND AND AND AND AND AND AND

SEO	Predicted	Predicted end	l limino poid
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
Ī	location	corresponding	H-Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L-Leucine, M-Methionine, N-Asparagine,
İ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ŀ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
İ	amino acid	sequence	Codon, /=possible nucleotide deletion,
ļ	sequence		\=possible nucleotide insertion)
i		<del> </del>	LQTKSPNRPCQFSSSAPS/VDQRAQ/INQSYAKHSANMNFSNHN
	1		NVRANTAYHLHQRLGPARHGEMWAISPNDRLIPAVTRSTIQRQS
ŀ			SVSSTASVNLGDPGSTRRAQIPEGDYLSYREFHSAGRTPPMMPG
1			SQRPLSARTYSIDGPNASRPQSARPSINEIPERTMSVSDFNYSR
			TSP
5726	2	486	SRSLSMWWNSGLPASSHSSKLPVTVGFSGCVKRLRLHGRPLGAP
İ	1		TRMAGVTPCILGPLEAGLFFPGSGGVITL/ESVGAGIPGPSRAG
	İ	•	QGSPGGSGEGPPLSSPSQPLPADLPGATLPDVGLELEVRPLAVT
1	ĺ	ļ	GLIFHLGQARTPPYLQLQVTEKQVLLRADDG
5727	21	221	RPILILKETRLPWATGYAEVINAGKSTHNEDQASCEVLTVKKK
1		i	AGAVTSTPNRNSSKRRSSLPNGE
5728	2	877	GTRNGQFEPRRGRAWEGSAGGLRAPGAAAGGPGVQPRGSG/LPG
	[		NAIRAGVNPGRGPASPFWDLSLPWDLWPPPTDHAPGAPDFPAVE
1			GR\PWAGGRPPWPVSGVLGSRVCGPLYSTSPAGPG/SGGLSPSQ
1			GGPAGAGGDAG/LPGRCPSAPWRAGSRPAASCPDWIPGPQGLWL
			HRNPTS/GPPSQIGEGAEQGDEGVADAPQIQCKN/GAEDPPAED
			EPPQVPEAGEEDAVPABEGPGGTPETQADQVRERPEAHLAEGGA
1			KGSPRZLADPQDLPAGQMSLAPPFPPVAAVIRSNK
5729	1	1525	AGGAREVLTLQLGHFAGFVGAHWWNQQDAALGRATDSKEPPGEL
1		2020	CPDVLYRTGRTLHGQETYTPRLILMDLKGSLSSLKEEGGLYRDK
		*	QLDAAIAWQGKLTTHKEBLYPKNPYLQDFLSAEGVLSSDGVWRV
			KSIPNGKGSSPLPTATTPKPLIPTEASIRVWSDFLRVHLHPRSI
			CMIQKYNHDGEAGRLEAFGQGESVLKEPKYQEELEDRLHFYVEE
1 1			CDYLQGFQILCDLHDGFSGVGAKAAELLQDEYSGRGIITWGLLP
1			GPYHRGEAQRNIYRLLNTAFGLVHLTAHSSLVCPLSLGGSLGLR
1 1			PEPPVSFPYLHYDATLPFHCSAILATALDTVTCS\YRLCSSPVS
1 1			MVHL\ADMLSFCGKKVVTAGAIIPFPLAPGQSLPDSLMQFGGAT
1			PWTPLSACGEPSGTRCFAQSVVLRGIDRACHTSQLTPGTPPPSA
			LHACTTGEBILAQYLQQQQPGVMSSSHLLLTPCRVAPPYPHLFS
1	ĺ		SCSPPGMVLDGSPKGAAVESVPVFG
5730	1258	1713	KKPQAPARETCVECQKTVYPMERLLANQQVFHISCFRCSYCNNK
1 . [			LSLGTYASLHGRIYCKPHFNQLFKSKGNYDEGFGHRPHKDLWAT
ľ <b>í</b>			KIETEGFWERPRNFENGGRPLKSPGGEDCPSC*GGCPGSNY*AQ
	•		GSSSREKGGQASWNPKLRVA
5731	122	443	RSHRGELIPKDSCYMRKPPRRPKKRRQG/CALPQGCLTFKDVAI
] .			EPSLEEWKCLNPAQRALYRAVMLENYRNLESVGLTSKDSWYMRK
i i	•		KPGRGRGKQRRQEWFFLRVY
5732	226	772	PPSRSCQSPRRKSRRAHVTVTLVCGFTSFSFSLPLYLCGCLRF
, ,	1		PERTCSQLQQADWAPDFGPSSFVPSWGATATGARKFLIAFNI\N
[ ]		,	LLGTKEQAHRIALNLREQGRGKDQPGRLKKVQGIGWYLDEKNLA
) j	1		QVSTNLLDFEVTALHTVYEETCREAQELSLPVVGSQLVGLVPLK
	. [		ALLDAA
5733	1	460	PALQEVNANALAWGKQYENDARTLFEFTSGVNDTESPIIYRDES
í l	1	<del>-</del>	MRTACSPDGLCSDGNGLELKCPFTSRDFMKFRLGGFEAIKSAYM
	ļ		AQVQYSMWVTRKNANYFANYDPRMKREGLHYVVIERDEKYM\AS
			FDEI/VP/EFIGKMDEVLSRDPM
5734	3	968	RCNSPESLTSLLVLLTTANNLFVLIPAYSKNRAYAIFFIVFTVI
	1	, ,	GSLFLMNLLTAIIYSQFRGYLMKSLQTSLFRRRLGTRAAFEVLS
	.	Ï	SMVGEGGAFPQAVGVKPQNLLQVLQKVQLDSSHKQAMMEKVRSY
[ [	.	İ	GSVLLSAEEFQKLFNELDRSVVKEHPPRPEYQSPFLQSAQFLFG
			HYYFDYLGNLIALANLVSICVFLVLDADVLPAERDDFILGILNC
	1	1	VFIVYYLLEMLLKVFALGLRGYLSYPSNVFDGLLTVVLLVLEIS
[		}	TL/VCTDCHTQAGGRRWW/RLLSLWDMTRMLNMLIVFRFLRIIP
	]		SMKPMAVVASTVLGL
5735	<del></del>	540	
	-	240	PFTPCVARAFNFPDQATVKKANYSLPRVGGGTSCGLPQARRISL
	1		ATPROLYK/SSNMTQRWQRREISNFEYLMFLNTIAGRTYNDLNQ
1	. !	}	YPVFPWVLTNYESEELDLTLPGNFRDLSKPIGALNPKRAVFYAE
Į.		[-	RYETWEDDQSPPYHYNTHYSTATSTLSWLVRIVSIFIELACLWY LKILT
	1	382	GTRPSTKKSGYSPQQVAVIHCKGHQKENTAVAHSNQKADSAAQV
5736	4 1	202 1	GTRPSTKKSGYSPMOVAVTHCKGHOVENMAUAUCAIOKA BOS SON TO

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
ł	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ļ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
		<del> </del>	TARLSVTPPNLLPTVSFPQPDLPDNPVYSTTTEKLASDLRANKN
		İ	QES**ILPDSGIFIP*T*TSYLQSTTHLRRAKLPQLLRR
5737	290	1041	VACUUT CORT TOWER FAIRT T DOG WOUND
1		1031	KACLHLLSSFLTSNFLFNPLLPDSLYSVEARSQRANLGPCRRKR
			LQTLMRLAAGFQYSSHKDPSLSAKEKHTDYHNEARGPWPGWVG*
	ļ		RTADGSCGRGPDGAHHPGPKSSSWRASRLLPGLGGSHHLDAYVG
ŀ			RDLECGTPAPLQLEIPPQPRGHPAPIPTGQAGPRDSGPGASP±V
1			ETRPLTDGRR*PGVRPVGWTPAHPAGTLRPRGAVEPSVSACGKW
5738	8	460	APSPTSQGCCEGRCDAVPKHRAWRTPLCSQ
		""	DTLSLNCTLPETLPMTPSF*LSFL*FPGLARAKSIPTKTYSNEV
1			VTLWYRPPDILLGSTDYSTQIDMW*GQVEVWQGPCGKGGGLVTT
1 :			ATQPAAFLFTVPSLPRGVGCIFYEMAIGRPLFPGSTVEEQLHFI
5739	1	1222	FRILSEEAWALCAVETHR
	_	1222	SFQRRGIRWNVHTLHPHPRAVWAGIGRGHGS*ALLGRARAPALC
1		,	FPTLLEFLESLEPDLPALRAMGLHLWAAGPGTHPAGISDLLAEV
			SAEVDGPVPGYLSSPQSITDTCLYIFTSGTTGLPKAARISHLKI
l i			LQCQGFYQLCGVHQEDVIYLALPLYHMSGSLLGIVGCMGIGATV
1			VLKSKFSAGQFWEDCQQHRVTVFQYIGELCRYLVNQPPSKAERG
1 1			HKVRLAVGSGLRPDTWERFVRRFGPLQVLETYGLTEGNVATINY
i l			TGQRGAVGRASWLYKHIFPFSLIRYDVTTGEFIRDFQGHCMATS
			PGEPGLLVAPVSQQSPFLGYAGGPELAQGKLLKDVFRPGDVFFN
	1		TRDLLVCDDQGFLRFHDRTGDFFRWKGENVATTEVAEVFEALDF LQEVNVYGVTV
5740	265	231	
1 1		231	PAYWLKVPTLCLESKTDLREKASHVSAQLQGEVRGLAGALWM*A
1 1			YVYERVYN*NISRMVHALEQKRHPAGLSSSMALQLNFCLGMLMA
5741	1	650	LQSELHKLYDEETQSWVSGSACGGYP
1 1	_	050	PRKTMRRGVLMTLLQQSAMTLPLWIGKPGDRPPPLCGAIPASGD
1			YVARPGDKVAARVKAVDGDEQWILAEVVSYSHATNKYEVDDIDE
1 1			EGKERHTLSRRRVIPLPQWKANPETDPEALFQKEQLVLALYPQT
1 1	j		TCFYRALIHAPPQRPQDDYSVLFEDTSYADGYSPPLNVAQRYVV
5742	2	362	ACKEPKKK*CRLADSPSPNDTGQDSRGRAGIKHIPPLKKK
1 1			TQSVKEILKRNPNVNLTDKDGNTALMIASKEGHTEIVQDLLDAG TYVNIPDRSGDTVLIGAVRGGHVEIVRALLQKYADIDIRGQDNK
			TALYWAVEKGNATMVRDILQCNPDTEICTKDG
5743	2	415	CYTECTENTERTHEN TENTERTHEN
1	-	320	GKTPEGIDAIEEIEIDLEETEREISPQENGLEEVKPLGEMQTDL
1 1	ļ		KATGREISPREKTPEVIDATEEIDKDLEETGRREISPEENGPEE
1 1		•	VKPVDEMETDLKTTGREGSSREKTREVIDAAEVIETDLEETERE ISPOE
5744	3	703	
} ]	-	,03	TRRTTTTSPTTTRQMTTTPAALPTTVVTTPDLTTGTPLQMTTIA
1 1	f	ĺ	VFTTANTCLSLTPSTLPERATGLLTPEPSKEGPILTAESETVLP
1			SDSWSSAESTSADTVLLTSKESKVWDLPSTSHVSMWKTSDSVSS
1 1			POPGASDTAVPEQNKTTKTGQMDGIPMSMKNEMPISQLLMIIAP
			SLGFVLFALFVAFLLRGKLMETYCSQKHTRLDYIGDSKNVLNDV QHGREDEDGLFTL
5745	1400	599	
			GKSRFVNLMKHSKKTYDSFQDELEDYIKVQKARGLEPKTCFRKM
	1	•	KGDYLETCGYKGEVNSRPTYRMFDQRLPSETIQTYPRSCNIPQT
ļ .		}	VENRLPQWLPAHDSRLRLDSLSYCQFTRDCFSEKPVPLNFNQQE
		İ	YICGSHGVEHRVYKHFSSDNSTSTHQASHKQIHQKRKRHPBEGR
j	İ		EKSEERSKHKRKKSCEEIDLDKHKSIQRKKTEVEIETVHVSTE
	1	Į.	KLKNRKEKKSRDVVSKKEERKRTKKKKEQGQERTEEEMLWDQSI
5746	3	821	
' I	-		SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES
1		İ	RAGERRFPCPVCGKRFRFNSILALHLRTHQPERPRSPAARLLLE
		}	LEERALLREARLGRARSSGGMQATPATEGLARPQAPSSSAFRCP
1			YCKGKFRTSAERERHLHILHRPWKCGLCSFGSSQEEELLHHSLT
j			AHGAPERPLAATSAAPPPQPQPQPPPQPEPRSVPQPEPEPQPER
İ			EATPTPAPAAPEEPPAPPEFRCQVCGQSFTQSWFLKGHMRKHKA
5747			SFDHACPV
İ	-	-340	DRHVETLC1HFLGPSTGSTAKTGGRNWLKTGNCLYGNTCRFVHG
1	[	İ	PSPRGKGYSSNYRRSPERPTGDLRERIKNKRQDVDTEPQKRNTE
	<u>-</u>		ESSSPVRKESSRGRHREKEDIKITKERTPESEEENVEWETNRDD

SEO	Predicted	1 5 31 -6 - 3 5	
ID	beginning	Predicted end	Amino acid segment containing signal peptide
NO:	nucleotide	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1.0.	location	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	corresponding to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
1 .	amino acid		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
}	sequence	sequence	Codon, /=possible nucleotide deletion,
	bequence		\=possible nucleotide insertion)
1	i		SDNGDINYDYVHELSLEMKRQKIQRELMKLEQENMEKREEIIIK
	J	j	KEVSPEVVRSKLSPSPSLRKSSKSPKRKSSPKSSSASKKDRKTS
	•		AVSSPLLDQQRNSKTNQSKKKGPRTPSPPPPPIPEDIALGKKYKE
ļ	*	į	KYKVKDRIEEKTRDGKDRGRDFERQREKRDKPRSTSPAGQHHSP
-1	1		ISSRHHSSSSQSGSSIQRHSPSPRRKRTPSPSYQRTLTPPLRRS
1			ASPYPSHSLSSPQRKQSPPRHRSPMREKGRHDHERTSQSHDRRH
	İ		ERREDTRGKRDREKDSREEREYEQDQSSSRDHRDDREPRDGRDR
5748	934	433	RE
3/40	754	473	SEGPOVFYKGLAPTLIAIFPYAGLQFSCYSSLKHLYKWAIPAEG
}		}	KKNENLQNLLCGSGAGVISKTLTYPLDLFKKRLQVGGFEHARAA
	[		FGQVRRYKGLMDCAKQVLQKEGALGFFKGLSPSLLKAALSTGFM
5749			FFSYEFFCNVFHCMNRTASQR
3/49	552	1	GFPVDPRVRGSTLSLAERPKGMIRSGSFRDPTDDVHGSVLSLAS
}	1		SASSTYSSAEERMQSEQIRKLRRELESSQEKVATLTSQLSANAN
1	1		LVAAFEOSLVNMTSRLRHLAETAEEKDTELLDLRETIDFLKKKN
			SBAQAVIQGALNASETTPKELRIKRQNSSDSISSLNSITSHSSI
5750	22		GSSKDADA
3/50.	22	866	IFISICLWNAHLCFLLLPKDCIDQVMKLQNLFVDDSGRYLAIQF
ı			
		•	QENYVAQLILDVRREGDVLSNCEFTPAPTPQEHLTKNLELNDDT
1			ILNDIKLADCEQFQMPDLCAEEIAIILGICTNFQKNNPVHTLTE
1			VELLAFTSCLLSQPKFWAIQTSALILRTKLEKGSTRRVERAMRQ
1			TQALADQFEDKTTSVLERLKIFYCCQVPPHWAIQRQLASLLFEL
5751			GCTSSALQIFEKLEMWE
3/31	3	751	SCGSALRAWRCGAAALATFPAPALPGLMYRALYAFRSAEPNALA
1		,	FAAGETFLVLERSSAHWWLAARARSGETGYVPPAYLRRLQGLEQ
Į.			DVLQAIDRAIEAVHNTAMRDGGKYSLEQRGVLQKLIHHRKETLS
			RRGPSASSVAVMTSSTSDHHLDAAAARQPNGVCRAGFERQHSLP
1			SSEHLGADGGLFQIPLPSSQIPPQPRRAAPTTPPPPPVKRRDREA
5752	3	409	LMASGSGGHNTMPSGGNSVSSGSSVSSCI
3132	3	471	GPVCGVGLSVAWAGPWRGPVHSVGGGGRAALHGAELPCLSGAAT
1			VEREMELRHKNEMLRVETEARARAKAERENADI IREQIRLKASE
	, '		HRQTVLESIRTAGTLFGEGFRAFVTDRDKVTATVNIFIKQGWQV
5753			AERQHVGASWSPRSCPCRLCTAL
3/33	34	483	DDSXAIPGGVQAPFGAVRNIYTPRTGHRIRKLDQIQSGGNYVAG
			GOEAFKKLNYLDIGEIKKRPMEVVNTEVKPVIHSRINVSARFRK
			PLQEPCTIFLIANGDLINPASRLLIPRKTLNQWDHVLQMVTEKI
5754	14	3.3	TLRSGAVHRLYTLEGRLV
3/34	14	331	TLVHVVEFAGEHAEAIASREQEVLQGWKELLSACEDARLHVSST
	†	•	ADALRFHSQVRDLLSWMDGIASQIGAADKPRCPSSLLGLPASPW
5755	3	000	WPTPATPSPLTAPFSME
.5755	3	888	LGDQFYKEAIEHCRSYNSRLCAERSVRLPFLDSQTGVAQNNCYI
			WMEKRHRGPGLAPGQLYTYPARCWRKKRRLHPPEDPKLRLLEIK
			PEVELPLKKDGFTSESTTLEALLRGEGVEKKVDAREEESIQEIQ
	•		RVLENDENVEEGNEEEDLEEDIPKRKNRTRGRARGSAGGRRRHD
			AASQEDHDKPYVCDICGKRYKNRPGLSYHYAHTHLASEEGDBAQ
	1		DQETRSPPNHRNENHRPQKGPDGTVIPNNYCDFCLGGSNMNKKS
5756			GRPEELVSCADCGRSAHLGGEGRKEKEAAA
3,30	3	621	SSKLQALFAHPLYNVPEEPPLLGAEDSLLASQEALRYYRRKVAR
	ŀ		WNRRHKMYREQMNLTSLDPPLQLRLEASWVQFHLGINRHGLYSR
			SSPVVSKLLQDMRHFPTISADYSQDEKALLGACDCTQIVKPSGV
-	,		HLKLVLRFSDFGKAMFKPMRQQRDEETPVDFFYFIDFQRHNAEI
			AAFHLDRILDFRRVPPTVGRIVNVTKEIL
5757	3	473	YKDALLLPDNHRQVVFENGTLKLTDVQKGMDEGEYLCSVLIQPQ
		ľ	LSISQSVHVAVKVPPLIQPFEFPPASIGQLLYIPCVVSSGDMPI
l l			RITWRKDGQVIISGSGVTIESKEFMSSLQISSVSLKHNGNYTCI
2022			ASNAAATVSRERQLIVRVPPRFVV
5758	1	474	FRRGAGAERGEHREGERGAAGMGEFKVHRVRFFNYVPSGIRCVA
			YNNQSNRLAVSRTDGTVEIYNLSANYFQEKFFPGHESRATEALC
			WAEGQRLFSAGLNGRIMEYDLQALNIKYAMDAFGGPIWSMAASP

ı	SEO	Predicted	Predicted end	
	ID	beginning	nucleotide	Amino acid segment containing signal peptide
	NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
		location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ļ		corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
		to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
		amino acid	residue of	S=Serine, T=Threonine, V=Valine.
-		residue of.	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Ston
-		amino acid	sequence	Codon, /=possible nucleotide deletion
1		sequence		\=possible nucleotide insertion)
ŀ	5759			SGSQLLVGCEDGSVKLFQITPDKIPV
- [	3/59	2	1240	GNAAFAGQGVVYETFHMSDLPSYTTNGTVHVVVNNQIGFTTDPR
1				MARSSPYPTDVARVVNAPIFHVNADDPRAVIVVCSVAARWRNTE
-		•		NKDVGADLVCYRRRGHNEMDEPMFTQPLMYKQIHRQVPVLKKYA
				DKLIAEGTVTLQEFEEEIAKYDRICEEAYGRSKDKKILHIKHWL
-1				DSPWPGFFNVDGEPKSMTCPATGIPEDMLTHIGSVASSVPLEDF
1				KIHTGLSRILRGRADMTKNRTVDWALAEYMAFGSLLKEGIHVRL
				NGQDVERGTFSHRHHVLHDQEVDRRTCVPMNHLWPDQAPYTVCN
-				SSLSEYGVLGFELGYAMASPNALVLWEAQFGDFHNTAQCIIDQF
İ				ISTGQAKWVRHNGIVLLLPHGMEGMGPEHSSARPERFLQMSNDD SDAYPAFTKDFEVSOL
ı	576C	1	1221	
-			- <del></del>	VRDITSDSLSLSWTVPEGQFDHFLVQFKNGDGQPKAVRVPGHED GVTISGLEPDHKYKMNLYGFHGGQRVGPVSAVGLTAPGKDEEMA
	ļ	ļ		PASTEPPTPEPPIKPRLEELTVTDATPDSLSLSWTVPEGGFDHF
		ļ		LVQYKNGDGQPKATRVPGHEDRVTISGLEPDNKYKMNLYGFHGG
1		}		CRVGPVSAIGVTAAEEETPTPTEPSMEAPEPPEEPLIGELTVTC
	J			SSPDSLSLSWTVPQGRFDSFTVQYKDRDGRPOVVRVGGEESEVT
ı	j			VGGLEPGRKYKMHLYGLHEGRRVGPVSTVGVTAPOEDVDETDSD
1	i			TEPGTEAPEPPEEPLLGELTVTGSSPDSLSLSWTVPOGREDSET
1		,		VQYKDRDGRPQAVRVGGQESKVTVRGLEPGRKYXMHLYGLHEGR
⊦	5761	3		RLGPVSAIGVT
1	3,01	• • • • • • • • • • • • • • • • • • •	1275	SCDMAEAAALVWIRGPGFGCKAVRCASGRCTVRDFIHRHCQDQN
				VPVENFFVKCNGALINTSDTVQHGAVYSLEPRLCGGKGGFGSML
ı	ŀ			RALGAQIEKTTNREACRDLSGRRLRDVNHEKAMAEWVKQQAERE
	}	]		AEKEQKRLERLQRKLVEPKHCFTSPDYQQQCHEMAERLEDSVLK
ı		1		GMQAASSKMVSAEISENRKRQWPTKSQTDRGASAGKRRCFWLGM EGLRTAEGSNSESSDDDSEEAPSTSGMGFHAPKIGSNGVEMAAK
				FPSGSQRARVVNTDHGSPEQLQIPVTDSGRHILEDSCAELGESK
	j		•	EHMESRMVTETEETQEKKAESKEPIBEEPTGAGLNKDKETEERT
		ł		DGERVAEVAPEERENVAVAKLQESQPGNAVIDKETIDLLAFTSV
L				AELELLGLEKLKCELMALGLKCGGTLQ
l	5762	2	344	GSTGQTPLHSQGGGGGGGGGRRRTPRGMPKEKYEPPDPRRMYTI
				MSSEEAANGKKSHWAELEISGKVRSLSASLWSLTHLTALHLSDN
L				SLSRIPSDIAKLHNLVYLDLSSNKIR
ı	5763	3	129	LDKDTGLIMLIARLDYELIQRFTLTIIARDGGGERTTGRVRINV
ı				LDVNDNVPTFQKDAYVGALRENEPSVTQLVRLRATDEDSPPNNQ
ŀ	i			ITYSIVSASAFGSYFDISLYEGYGVISVSRPLDYEQISNGLIYL
$\vdash$	5764	19 +		TVMAMDAGN
	-, -,	1.5	441	VCARACGEMRQLLRPIDRQRYDENEDLSDVEEIVSVRGFSLEEK
l	- 1	1	,	LRSQLYQGDFVHAMEGKDFNYEYVQREALRVPLIFREKDGLGIK
		1		MPDPDPTVRDVKLLVGSRRLVDVMDVNTQKGTEMSMSQFVRYYE TPEAORDKL
Н	5765	3	825	
	- 1	-		QKILRLNNSHQPPTSSSNSKDCGGPASSGAGATAALADGLKFAS
				VQASAPQGNSHKETSKSKVKRSKTSKDANKSLPSAALYGIPEIS
				STGKRQEVQGRPGEATGMNSALGQSVSSGGSGNPNSNSTSTSTS AATAGAGSCGKSKEEKPGKSQSSRGAKRDKDAGKSRKDKHDLLQ
				GHQNGSGSQAPSGGHLYGFGAKSNGGGASPFHCGGTGSGSVAAA
	- 1		}	GEVSKSAPDSGLMGNSMLVKKEEEEEESHRRIKKLKTEKVDPLF
			ļ	TVPAPPPHV
	5766	1608	663	SGLFSVDPASSQAMBLSDVTLTEGVGNEVMVVAGVVVLTLALVL
			İ	AWLSTYVADSGSNQLLGAIVSAGDTSVLHLGHVDHLVAGQGNPE
		]		PTELPHPSEGNDEKAEEAGEGRGDSTGEAGAGGGVEPSLEHLLD
	1		i	IQGLPKRQAGAGSSSPEAPLRSEDSTCLPPSPGLITVRLKFLND
		]		TEELAVARPEDTVGALKSKYFFGQESQMKLIYQGRLLQDPARTL
		į	ł	RSLNITDNCVIHCHRSPPGSAVPGPSASLAPSATEPPSLGVNVG
	[			SLMVPVFVVLLGVVWYFRINYRQFFTAPATVSLVGVTVPFSFLV
	F767			FGMYGR
1	5767	2	892	NFRATPRPPTRPELRTGTEVILWYLDWRALMKRKRMKANIKLVG
				SGFPLPSSDLDDSLTEEIDEKIGFRNDANFDWONVADFRDAGGS
			<u> </u>	LTEVKVEEEERDPOSPEFEIEEEEEMLSSVIPDSRRENELPDFP

SEQ	Predicted	1 83333	
ID	beginning	Predicted end	Amino acid segment containing signal peptide
NO:	nucleotide	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ļ		corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
}	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
İ	amino acid	sequence	Codon, /=possible nucleotide deletion
	sequence	Í	\=possible nucleotide insertion)
ļ			HIDEFFTLNSTPSRSAYDEPHLLVNIEKOKLELEKRRIDIEAER
ŀ			LQVEKERLQIEKERLRHLDMEHERLOLEKERLOTEREKLRIOTY
ŀ			NSEKPSLENELGOGEKSMLOPODIETEKLKLERERLOLEKDRLO
L			FLKFESEKLQIEKERLQVEKDRLRIQKEGHLQ
5768	3	476	SSRSRLSVSVSPPPPGIVELGPPFAWEFCSRLGSAVTSQRAGPA
	1		AAMVAKDYPFYLTVKRANCSLELPPASGPAKDABEPSNKRVKPL
			SRVTSLANLIPPVKATPLKRFSQTLQRSISFRSESRPDILAPRP
	1	j	WSRNAAPSSTKRRDSKLWSETFDVC
5769	38	667	
	""	""	TKTKKGVKEKATDQSVKAFAEHCPELQYVGFMGCSVTSKGVIHL
	j	ł	TKLRNLSSLDLRHITELDNETAMEIVKRCKNLISLNLCLNWIIN
			DRCVEVIAKEGQNLKELYLVSCKITDYALIAIGRYSMTIETVDV
ĺ	ĺ	ĺ	GWCKEITDQGATLIAQSSKSLRYLGLMRCDKVNEVTVEQLVQQY
5770	<del></del>		PHITFSTVLQDCKRTLERAYQMGWTPNMSAASS
3770	1	484	DSRRYDVKTRKWSFLLEEHSKLIAKVRCLPQVQLDPLPTTLTLA
1.			FASQLKKTSLSLTPDVPEADLSEVDPKLVSNIMPFORAGVNFAT
			AKGGRLLLADDMGLGKTIQAICIAAFYRKEWPLLVVVPSSVRFT
5771		i	WEQAFLRWLPSLSPDCINVVVTGKDRLTA
3,17	168	741	GLLPSACLRARSWREASEGPSSRACSNGSQDTFEACYSGTSTPS
			FHGSHCSGSDHSSLGLEQLQDYMVTLRSKLGPLEIOOPAMLIRE
1			YRLGLPIQDYCTGLLKLYGDRRKFLLLGMRPFIPDODIGYFEGP
1 1			LEGVGIREGGILTDSFGRIKRSMSSTSASAVRSYDGAAQRPEAQ
L.,			AFHRLLADITHDIE
5772	148	383	EPNLALVSPSHPQIKAEDDQPLPGVLLSLSGGLFRSNLLTQDNG
			ILTFSNLVTCSAIYHLPVFPEREPGCSMRDLRVA
5773	2	723	PRVRSKHNFCFMEMNTRLQVEHPVTEMITGTDLVEWQLRIAAGE
			KIPLSQEEITLQGHAFEARIYAEDPSNNFMPVAGPLVHLSTPRA
1 1			DPSTRIETGVRQGDEVSVHYDPMIAKLVVWAADRQAALTKLRYS
1 1			LROYNIVGLHTNIDFLLNLSGHPEFEAGNVHTDFIPQHHKQLLL
1 1	ł		SRKAAAKESLCQAALGLILKEKAMTDTFTLQAHDQFSPFSSSSG
L_ 1	j		RRLNISYTRNMTLKDGKNSK
5774	. 2	592	FVEBENIRVVRCGGSELNFRRAVFSADSKYIFCVSGDFVKVYST
1 1	J		VTEECVHILHGHRNLVTGIQLNPNNHLQLYSCSLDGTIKLWDYI
1 1			DGILIKTFIVGCKLHALFTLAQAEDSVFVIVNKEKPDIFQLVSV
1 1			KLPKSSSQEVEAKELSFVLDYINQSPKCIAFGNEGVYVAAVREF
1 1	į		YLSVYFFKKETTSRVTLSSS
5775	3	538	SSGCCDPAAPSSLAEAATMPVSKCPKKSESLWKGWDRKAQRNGL
			RSQVYAVNGDYYVGEWKDNVKHGKGTQVWKKKGAIYEGDWKFGK
<u> </u>			RDGYGTLSLPDQQTGKCRRVYSGWWKGDKKSGYGIQFFGPKEYY
			FGDWCGGOBGWGBWGOXGDZIFFGDKKSGYGIQFFGPKEYY
1			EGDWCGSQRSGWGRMYYSNGDIYEGQWENDKPNGEGMLRLSQNP RP
5776	2	484	
1 1	-	704	RLPQDCVCQNLSESLGTLCPSKGLLFVPPDIDRRTVELRLGGNF
1 1	1		IIHISRQDFANMTGLVDLTLSRNTISHIQPFSFLDLESLRSLHL
1 1			DSNRLPSLGEDTLRGLVNLQHLIVNNNQLGGIADEAFEDFLLTL
5777	2	949	EDLDLSYNNLHGPAVGLRGDAWVQPSTS
1	- I	747	GODPEPGQDLFQPEREVDPSWGRGREPRLGKLRFQNDHLSVLKQ
1			VXKLEQALKDGSAGLDPQLPGTCYSPHCPPDKAEAGSTLPENLG
ł i			GGSGSEVSQRVHPSDLEGREPTPELVEDRKGSCRRPWDRSLENV
1. 1	í	1	YRGSEGSPTKPFINPLPKPRRTFKHAGEGDKDGKPGIGFRKEKR
	<b> </b>	İ	NLPPLPSLPPPPLPSSPPPSSVNRRLWTGRQKSSADHRKSYEFE
			DLLQSSSESSRVDWYAQTKLGLTRTLSEENVYEDILDPPMKENP
			YEDIELHGRCLGKKCVLNFPASPTSSIPDTLTKQSLSKPAFFRQ
5770			NSERRNV
5778	1	1210	QRRQSVSRLLLPVFLLEPPAEPGLEPPPEEEGGEPAGVAEEPGS
<b>i</b>		1	GGPCWLQLEEVPGPGPLGGGGPLRSPSSYSSDELSPGEPLTSPP
1			WAPLGAPERPEHLLNRVLERLAGGATRDSAASDILLDDIVLTHS
J		ľ	LFLPTEKFLQELHQYFVRAGGMEGPEGLGRKOACLAMILLHELDT
J			YQGLLQEEEGAGHIIKDLYLLIMKDESLYQGLREDTLRLHQLVE
		j	TVELKIPEENQPPSKQVKPLFRHFRRIDSCLQTRVAFRGSDEIF
l			CRVYMPDHSYVTIRSRLSASVQDILGSVTEXLQYSEEPAGREDS
			LILVAVSSSGEKVLLQPTEDCVFTALGINSHLFACTRDSYEALV
		L	THE THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO THE TABLE TO T

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
1	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
- 1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
)	sequence	sequence	Codon, /=possible nucleotide deletion,
	acdactice		\=possible nucleotide insertion)
	ì		PLPEEIQVSPGDTEIHRVEPEDVANHLTAPHWELFRCVHELEFV
5779	138	1677	DYVFHGE
3,79	138	1671	EAVQVLIKHSADVNARDKNWQTPLHVAAANKAVKCAEVIIPLLS
			SVNVSDRGGRTALHHAALNGHVEMVNLLLAKGANINAFDKKDRR
1			ALHWAAYMGHLDVVALLINHGAEVTCKDKKGYTPLHAAASNGQI
			NVVKHLLNLGVEIDEINVYGNTALHIACYNGQDAVVNELIDYGA
		1	NVNQPNNNGFTPLHFAAASTHGALCLELLVNNGADVNIQSKDGK
1		1	SPLHMTAVHGRFTRSQTLIQNGGEIDCVDKDGNTPLHVAARYGH
ł	1	ł	ELLINTLITSGADTAKCGIHSMFPLHLAALNAHSDCCRKLLSSG
1			QKYSIVSLFSNEHVLSAGFEIDTPDKFGRTCLHAAAAGGNVECI
1		İ	KLLQSSGADFHKKDKCGRTPLHYAAANCHFHCIETLVTTGANVN
ľ			ETDDWGRTALHYAAASDMDRNKTILGNAHDNSEELERARELKEK
•			EATLCLEFLLONDANPSIRDKEGYNSIHYAAAYGHRQCLELLLE
	<u> </u>	<u> </u>	RTNSGFEESDSGATKSPLHLAVSEMP
5780	154	624	QFFRVITCLPFKGPDYRLYKSEPBLTTVAEVDESNGEEKSEPVS
-	]		EIETSVVKGSHFPVGVVPPRAKSPTPESSTIASYVTLRKTKKMM
1			DLRTER?RSAVEQLCLAESTRPRMTVEEQMERIRRHQQACLREK
			KKGLNVIGASDQSPLQSPSNLRDNP
5781	19	941	RGSLGGHPWRPPMRAASOGCLPVSFVTGPHOERAYGGRGPGGAF
ł			PAPPVSGTCPPDLIYAPTPEKAEGGSQKNHQPPPGERAAHRDGE
1			QAPCRAGPTRKVAVAPRPPSCP*GPE\PGEEPRRPLDRSPPLGQ
i			VQPHFTSQDAKSAEDEAPSRHLGKHQPRSAQVGSRLDALQGPKT
1			QHSIHTVTCKSPRQKEDRSPKPPOAPKHPERHGROS\QAPPPI,P
1			VAPSRTCGGC*TWDPALLVSP/PQGDSTPELPAP\QQPTGGPSR
			CRQALPPQG*RQQPRQRPR/PTGASRSHPAKAKGCQGPPKIRNY
	<u></u>		NIMD
5782	5176	1237	DRSMMSMAADSYTDSYTDTYTEAYMVPPLPPEEPPTMPPLPPEE
			PPMTPPLPPEEPPEGPALPTEQSALTAENTWPTEVPSLPSEESV
l i			SQPEPPVSQSEISEPSAVPTDYSVSASDPSVLVSEAAVTVPEPP
		•	PEPESSITLTPVESAVVABEHEVVPERPVTCMVSETPAMSAEPT
			VLASEPPVMSETAETFDSMRASGHVASEVSTSLLVPAVTTPVLA
i [			ESILEPPAMAAPESSAMAVLESSAVTVLESSTVTVLESSTVTVL
1 1			EPSVVTVPEPPVVAEPDYVTI PVPVVSALEPSVPVLEPAVSVLQ
			PSMIVSEPSVSVQESTVTVSEPAVTVSEQTQVIPTEVAIESTPM
!			ILESSIMSSHVMKGINLSSGDQNLAPEIGMQEIALHSGEEPHAE
í l			EHLKGDFYESEHGINIDLNINNHLIAKEMEHNTVCAAGTSPVGE
ł .	1		IGEEKILPTSETKORTVLDTYPGVSEADAGETLSSTGPFALEPD
[			ATG\TSKGIEFTTASTLSLVNKYDVDLSLTTODTEHDMLISTSP
	,		SGGSEADIEGPLPAKDIHLDLPSNINLVSSDTNEPLPVKRD\DQ
	1		TLAALI\SLKESSGGEKEVPPPS*REHLPDSGFSANIEDINEAD
] ]			LVRPVSSPRTWNVLPSPRAGL\EGP\LLASDFGPVONLYSSPVV
ŀ	ĺ		\SSMP\ERASGS\SSGEKGG\YEIFVKVKDTHEKSKYNVNDDVC
[	1	1	EKEKKRDSSLRSRSKRSKSSBHKSRKLTSESRSRARKRSKSKSKS
l l	Į.		HRS\QTRSRSRS/RDRRRRSSRSRSRSRGRRSVSKEKRKPSDKH
}			RSKSRERKRKRSSSRDNRKTVRARSRTPSRRSRSHTPSRRRRSR
			SVGRRRSFSISPSRRSRTPSRRSRTPSRRSRTPSRRS
			RTPSRRSRTPSRRRRSRSVVRRRSFSISPVRLRRSRTPLRRRFS
	,		RSPIRRKRSRSSERGRSPKRLTDLDKAQLLEIAKANAAAMCAKA
1		į	GVPLPPNLKPAPPPTIEEKVAKKSGGATIEELTEKCKQIAQSKE
' 1	1	1	DDDVIVNKPHVSDEBEEEPPFYHHPFKLSEPKPIFFNLNIAAAK
Ī	Į.	1	PTPPKSQVTLTKEFPVSSGSQHRKKEADSVYGEWVPVEKNGEEN
f			KDDDNVFSSNLPSEPVDISTAMSERALAQKRLSENAFDLEAMSM
	1	j	LNRAQERIDAWAQLNSIPGQFTGSTGVQVLTQEQLANTGAQAWI
ļ		ĺ	KKDQFLRAAPVTGGMGAVLMRKNGWREGEGLGKNKEGNKEPILV
1		į	DPKTDRKGLVAVGERAQKRSGNFSAAMKDLSGKHPVSALMEICN
	1	İ	KRRWQPPEFLLVHDSGPDHRKHFLFRVLINGSAYQPNCMFFLNR
		.[	Y
5783	1693	698	DSGLRVAFTMEGISNFKTPSKT,SFKKKGVT,CGTDTTNTDXCDTC
5783	1693	698	DSGLRVAFTMEGISNFKTPSKLSEKKKSVLCSTPTINIPASPFM OKLGFGTGVNVYLMKRSPRGLSHSPWAVKKINDICNDUVPSVVO
5783	1693	1	QKLGFGTGVNVYLMKRSPRGLSHSPWAVKKINPICNDHYRSVYO
5783	1693		DSGLEVAFTMEGISNFKTPSKLSEKKKSVLCSTPTINIPASPFM QKLGFGTGVNVYLMKRSPRGLSHSPWAVKKINPICNDHYRSVYQ KRLMDEAKILKSLHHPNIVGYRAFTEANDGSLCLAMEYGGEKSL NDLIEE/PI*SQ/PKILFQQP/LILKVALNMARGLKYLHQEKKL

Deginning nucleotide location corresponding corresponding corresponding to first amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino a	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Octacion corresponding to first amino acid residue of nation cide of the contemporary of first amino acid residue of amino acid sequence corresponding to first amino acid sequence corresponding to first amino acid sequence corresponding to first amino acid sequence corresponding to first amino acid sequence corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first corresponding to first correspondin				(A=Alanine C-Cyptoine D herestic heid D
corresponding to first amino acid residue of residue of free amino acid residue of amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid acid acid acid acid acid acid acid	NO:	nucleotide	location	Glutamic Acid. Fathenvialanine Gaglicine
Leucine, M-Methonine, M-Asparagine,   First amino acid   residue of   residue of   residue of   residue of   anino acid   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence	1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine
Colitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Calitagine   Cal	1		to first	L=Leucine, M=Methionine, N=Asparagine
sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence seq	1	1		P=Proline, Q=Glutamine, R=Arginine.
maino acid sequence    Martyptophan, Yatyrosine, Kulnknown, "stop   Codon, /possible nuclectide deletion,   Codon, /possible nuclectide deletion,   Codon, /possible nuclectide deletion,   Codon, /possible nuclectide deletion,   Codon, /possible nuclectide insertion,   Codon, /possible nuclectide insertion,   Codon, /possible nuclectide insertion,   Codon, /possible nuclectide insertion,   Codon, /possible nuclectide insertion,     Codon, /possible nuclectide insertion,     Codon, /possible nuclectide insertion,     Codon, /possible nuclectide insertion,     Codon, /possible nuclectide insertion,     Codon, /possible nuclectide insertion,     Codon, /possible nuclectide insertion,     Codon, /possible nuclectide insertion,     Codon, /possible nuclectide insertion,     Codon, /possible nuclectide insertion,     Codon, /possible nuclectide insertion,     Codon, /possible nuclectide     Codon, /possible nuclectide insertion,     Codon, /possible nuclectide insertion,     Codon, /possible nuclectide insertion,     Codon, /possible nuclectide insertion,     Codon, /possible nuclectide insertion,     Codon, /possible nuclectide insertion,     Codon, /possible nuclectide insertion,     Codon, /possible nuclectide insertion,     Codon, /possible nuclectide insertion,     Codon, /possible nuclectide insertion,     Codon, /possible nuclectide insertion,     Codon, /possible nuclectide insertion,     Codon, /possible nuclectide insertion,     Codon, /possible nuclectide insertion,     Codon, /possible nuclectide insertion,     Codon, /possible nuclectide insertion,     Codon, /possible nuclectide insertion,     Codon, /possible nuclectide insertion,     Codon, /possible nuclectide insertion,     Codon, /possible nuclectide insertion,     Codon, /possible nuclectide insertion,     Codon, /possible nuclectide insertion,     Codon, /possible nuclectide ins	1	1	residue of	S=Serine, T=Threonine, V=Valine,
sequence    Coden, /=possible nucleotide deletion,    -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nucleotide insertion   -possible nu	l		amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Sequence	į.		sequence	Codon, /=possible nucleotide deletion.
LHGDIKSSNVIKGDFETKICOVGVSILDLEDNRTYTPERGYT   STERMENEAVERNOVITOKADIPAGNILHAEMITISIPINILS   MODDDEDITTPESOFDDENYYAALOTEPPINMESLDESYGKVIE     LFSWCTNEDPKORPSAAHIVEALETDV		sequence	Ĺ	\=possible nucleotide insertion)
ST84   1888		1		LHGDIKSSNVVIKGDFETIKICDVGVSLPLDENMTVTDPEACYI
S784   1388   PRIVERYENTHUS PROPERS AND THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF THE VALUE OF TH	1	İ	Ì	GTEPWKPKEAVEENGVITDKADIFAFGLTLWEMMTLSIPHINLS
1388   PRVERPURTUHNYYISITYCESDESSERDLWVIDDMERICHYDESTY   GLISHTHROARWISDPEPYGETREITUTAGETYTCEVUW   RMLTATOYLAPLMANFOPEVGETRUETUTAGETYTCEVUW   RMLTATOYLAPLMANFOPEVGETRUETUTAGETYTCEVUW   RMLTATOYLAPLMANFOPEVGETRUETUTAGETYTCEVUW   RMLTATOYLAPLMANFOPEVGETRUETUTAGETYTCEVUW   GLISAPTVUVRIQOTPMUTRAGETYTCHYRWIDMERITYMISTHYPWY   GLISAPTVUVRIQOTPMUTRAGETYTCHYRWIDMERITYMISTHYPWY   VUDSCCEBESKEMCENTEPUTTAFLEPOY* REGPESSIS-LPP   E/DAVTSOPPTSLEPPEDTYLAPLEPOY* REGPESSIS-LPP   E/DAVTSOPPTSLEPPEDTYLAPLEPOY* REGPESSIS-LPP   E/DAVTSOPPTSLEPPEDTYLAPLEPOY* REGPESSIS-LPP   E/DAVTSOPPTSLEPPEDTYLAPLEPOY* REGPESSIS-LPP   E/DAVTSOPPTSLEPPEDTYLAPLEPOY* REGPESSIS-LPP   E/DAVTSOPPTSLEPPEDTYLAPLEPOY* REGPESSIS-LPP   E/DAVTSOPPTSLEPPEDTYLAPLEPOY* REGPESSIS-LPP   E/DAVTSOPPTSLEPPEDTYLAPLEPOY* REGPESSIS-LPP   E/DAVTSOPPTSLEPPEDTYLAPLEPOY* REGPESSIS-LPP   E/DAVTSOPPTSLEPPEDTYLAPLEPOY* REGPESSIS-LPP   E/DAVTSOPPTSLEPPEDTYLAPLENDAGETY REFPER   FPLACESCOPPTSLEPPEDTYLAPLENDAGETY REGPESSIS-LPP   E/DAVTSOPPTSLEPPEDTYLAPLENDAGETY REGPESSIS-LPP   E/DAVTSOPPTSLEPPEDTYLAPLENDAGETY REGPESSIS-LPP   E/DAVTSOPPTSLEPPEDTYLAPLENDAGETY REGPESSIS-LPP   E/DAVTSOPPTSLEPPEDTYLAPLENDAGETY REGPESSIS-LPP   E/DAVTSOPPTSLEPPEDTYLAPLENDAGETY REGPESSIS-LPP   E/DAVTSOPPTSLEPPEDTYLAPLENDAGETY REGPESSIS-LPP   E/DAVTSOPPTSLEPPEDTYLAPLENDAGETY REGPESSIS-LPP   E/DAVTSOPPTSLEPPEDTYLAPLENDAGETY REGPESSIS-LPP   E/DAVTSOPPTSLEPPEDTYLAPLENDAGETY REGPESSIS-LPP   E/DAVTSOPPTSLEPPEDTYLAPLENDAGETY REGPESSIS-LPP   E/DAVTSOPPTSLEPPEDTYLAPLENDAGETY REGPESSIS-LPP   E/DAVTSOPPTSLEPPEDTYLAPLENDAGETY REGPESSIS-LPP   E/DAVTSOPPTSLEPPEDTYLAPLENDAGETY REGPESSIS-LPP   E/DAVTSOPPTSLEPPEDTYLAPLENDAGETY REGPESSIS-LPP   E/DAVTSOPPTSLEPPEDTYLAPLENDAGETY REGPESSIS-LPP   E/DAVTSOPPTSLEPPEDTYLAPLENDAGETY REGPESSIS-LPP   E/DAVTSOPPTSLEPP   E/DAVTSOPPTSLEPP   E/DAVTSOPPTSLEPP   E/DAVTSOPPTSLEPP   E/DAVTSOPPTSLEPP   E/DAVTSOPPTSLEPP   E/DAVTSOPPTSLEPP   E/DAVTSOPPTSLEPP   E/DAVTSOPPTSLEPP   E/DAVTSOPPTSLEPP   E/DAVTSOPPTSLEPP   E/DAVTSOPPTSLEPP   E/DAVTSOPPTSLEPP   E/DAVTSOPPTSLEPP   E/DAVTSOPPTSLEPP   E/D	İ			NDDDDEDKTFDESDFDDEAYYAALGTRPPINMEELDESYQKVIE
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#AGLIVGILIUNILIVATAILUTYYMYHHTSAASIFFIEREPSR #PAMKERRISGCHPANAEVEPUGEKEGFIVESSQC  \$785	}			E/DAVTSOFPTSI.DTRDDTVIALUL YDAGA CTDDGA AUGUSCOTT
### PAMKPRRGSGHPAYAEVEPUGEKEGFIVSEQC    ST85	1	J		HAGIIVGILIIMIIVATATI.VTVVMVUUDTCAACIERIEDDDOD
1388 PRVPRVRTDINTYTISRYGGSDSAGRDLWWNTOMEROKVKIH RNLTANQYIA-DLAMADD PSVSRNSTVRYFDNGTALVVQWDHVHL QDISNTHGARATWLS PDPPPYOHERS IT STYKET PVLVTQTISTSTHMYVK GLSDAFVVVRHIQQI RNVRRRTI TYEYHRVELQMSKITMI SAVEM TPLPTCLQFNRCGFCVSSQIGFNCSWCSKLQRCGSGFDRIRQDW VDSGCPERSKMCENTEPVETY FLEPPP ERPPSSSS'-LPP E/DAVTSQFPTSLPTEDDTKIALHLEDNGASTDDSAAKKGGTL EAGLIVGI LIVLIVATALIVTYWHYHPTAAASIPPIERRPSR WPAMKFRRGSGHPAVAEVEPVGEKGFTVSBQC  5786 2532 1674 SYKLPAAERERSSGSQFPTPTRRWFPARGRTSRGHRQM*SGTF APRPPARSTVSPASPLPKPRAGRCSSRFRSGGSTRFQM*SGTF APRPPARSTVSPASPLPKPRAGRCSSRFRSGGTFRC*SLM*M S'H:KRNLSGRSSSSSGRST*PERFRFQNFORDATP SLAPSSRF/FKGRPQCTWIPSRWPASPTPATT*PADTSSPGGT GRSMMTCTFRATTHYSAARSSRRWETP; SSPGGMPAIP SLAPSSRF/FKGRPQCTWIPSRWPASPTPATT*PADTSSPGGT GRSMMTCTFRATTHYSAARSSRRWETP; SSPGGMPAIP SLAPSSRF/FKGRPQCTWIPSRWPASPTPATT*PADTSSPGGT GRSMMTCTFRATTHYSAARSSRRWETP; SSPGGMPAIP SLAPSSRF/FKGRPQCTWIPSRWPASPTPATPTT*PADTSSPGGT GRSMMTCTFRATTHYSAARSSRRWETP; SSPGGMPAIP SLAPSSRF/FKGRPQCTWIPSRWPAPPTP*WFFPGSFRPWGLANV VENISRLQLWSTLGGEDVCQEHGEKIYFFCGDEMCLVCVC EAGEMATHTMFFLEDAA LAPKRQIHKCLGLIKBREETQETQS RENKRWQULLTQVSTKRQQVISSFAHLEKFLEEQQSILLAQLES QDGDLLRQRDSFPLLVAGGTCFPSALLEELERKNERPABELLTD IRSTLIRCETTRKCRRPVAVSPELGQRRDFPQAAPJCRMMMF LEKLGFELDVEPHISLDFTSHFLLLSDHQRAQPSYKWQMS PNDRQRFDRATCVLAHTGITGGRHTWVVSIDLANGGSCTVGVVS EDVQRKGELBLRPEGVAAVRLANGFVSALGSFPTALIKEOP RQKKGLBLRPEGVAAVRLANGFVSALGSFPTALIKEOP RQKKGLBLRPEGVAAVRLANGFVSALGSFPTALIKEOP RQKKGLBLRPEGVAAVRLANGFVSALGSFPTALIKEOP SGGGGGGTEGDVHTSSRLHMVRAMLLERLLGTLAPLGNAGAW AIPJWQVILLHTDLDGGEBEKKAGNDONLSQLKRA AIPJWQVILLHTDLDGGEBEKKAGNDONLSQLKRA AIPJWQVILLHTDLDGGEBEKKAGNDONLSQLKRA AIPJWQVILLHTDLDGGEBEKKAGNDONLSGLKRA AIPJWQVILLHTDLDGGEBEKKAGNDGFSGXGSSSA SGGARAGAGNDOLLGALGGAKAGNUGALATIH ITTSSPPDWSFFFLQVVKSHAADVFEATLQTLFGMILGGLFG HTSSPPDWSFFLQVVKSHAADVFEATLGGTFRANGVVTA SGGSSSLSS SSPAVAASGGGATTQSKSTKKSKREKEKKBOGETSGGGDD LCTALWGUNNKFADKETLIQCALCGSKVATLAGASGSSSA SSPAVAASGGGLLDLMMSIWPELPAVGRAAAAGSGCATTGGLVENL ITRUSSKSQGBLLDLMMSIWPELPAVGRAAAAFTTOQAVKLL ITRUSSKSQGLLDLLMMSIWPELPAVGRAAAAGVULLGYFSIK TPQTEKKLKENSQAAVEILRCQNIT ILLSINGSVGTATT	1			WPAMKERRGSGHPAVAEVEDVGEKEGETVCEOC
GILSNTHRQARVALS PDFPYGHFLREITVATGSTYTGEVYH RMLTATQYTAPIMAMPDFSUSRINTY YRYDNOTALVVQWDHYAL QDWYNLGSSTFQATLLMDGRIIFGYKEIPVLYTQISSTNHPVKV GLSDAFVVVRIQQIPWVRRTIYEYHRVELDMSKITNISAWE TPLPTCLOFNRCGCVSSQIGFNCSWCKQCSSGPDRRCQDW VDSSCPEESKEKMCENTEPVET\FLEPPQP\PEQPPSSGS\LPP E/DAVISQFPTSLYBEIDTKIALHKOKQCSSGPDRRCQDW VDSSCPEESKEKMCENTEPVET\FLEPPQP\PEQPPSSGS\LPP E/DAVISQFPTSLYBEIDTKIALHKOKQCSSGPTDRAKGGL HAGLIVGILILVILVATALLVYWYHHPPTSAASIFPIERRPSR WPAMKERGSGHPAYARVEPVGEKEGT HAGRIVGILILVILVATALLVYWYHHPPTSAASIFPIERRPSR WPAMKERGSGHPAYARVEPVGEKEGT APRPPARETVSPASPLDKERAGGSSKPRSACSTFRC\SLN**M SYPLKENISQRSSMSMSRRSLSCAPHR***RQGITVARALPTY**WK SPPLACSTCQAAQKSQSLSSGRSTR**PERMSFRP\SPPGMPAIP SLAPSSRP\PKGRPCCTUFTSFRWAPAFFTT**APTSPGST GRSMMTCPTRHTATFWSAAASSRRNNPTP***RPSGRLSTV**RA TGGSTATADPKPPPRWAMPMMAB  5787 2 1460 MASAASVTSLADEVNCP\TCQGTLKEAGSLSNCG/HKNFCRACL T\RYCEIP\GPD\LEBSP\TCP\LCKEPPRP\GSFRNMQLANV VENIERLGLVSTLGLEGEDVOCHGEKITYFCEDDEMQLCVVCR EAGEHATHTWRFLEDAA\APYREQIHKCLKCLIKEREIQEIOS SRINKMQULLTOVSTKRQVSUSBERLHEEQOSILLAQUES QODDLLRQRBEFDLLVAGEICRFSALIEBLEEKMERPARELLTD IRSTLIRCETRKCKKPVAVSPELGQRIRGFPQALPLQREMEMP LEKLCPELDVEPHISLDFOTSHFKLLISEDORGAPSYKMONS PONDRORFDRATCVLAHTGITGGRTTWVSILLAGGSCTVGWSV SENVENGULLTOVSTKRQVVSEBAHANGSCTVGWSV SENVENGULLTOVSTKRQVSVSLAGSFP\TRITLKEOP RQVWSLDYSVGWTFTNAVTREPIYTFTASFTRKVIPPFGLWG RGSSFSLS  5788 2 6860 EHSVSGRSSAYGDATAEGHPAGPGSVSSSTGAISTTTGHQEGDG SEGGGGEETEGDVHTSNRLHMVRLIMLERLLQTLPQLRNVGGVR ATAPALLSSGAATYCLHVLKSLLEVKKSQANBEPVATSGLKS HTTSSPPDMSPFFLRQVYKGHAADVBAYTJULTEMVLRLPYQI KKITDTNSRIPPPPPDHSWFYFLSEYLMIQGTPRRGVYRLLL FICCSKEKYRQLROLHTLDS\HVGIKKLLEEGGIFLARVVTA SPOSALGYDTLISIMEHLKACABIAQRTIMKQRFCHODSVLY FILLOVSFLUVDEGVSFVLULISLACLGGSTGSSSAS SSPAPVAASSGQATTQSKSSTKKSKKEEKEKEDGTGSGSGDG LCTALVWOLMKFADKETLIDPLCFULLSSLCCSSSSVRWQACLLTH IYRNSKSQQELLLDLMWSIWPELPAYGRKAAQFVDLLGYFSKK TPQTEKKLKSYSGKAVEILKTQMHITTHNPNSHITTGGLVWEL GSHTISKVTVXKIGDLKATKWNRTIMLYYNNRTVQAIVELKKKAR RWHAKKVQLTROGTFWCLTBOTEVCLTUREPTYTTQVVKLI GSHTISKVTVXKIGDLKATKWNRTIMLYYNNRTVQAIVELKKARA	5785	2669	1388	PRVRPRVRTDHNYYTSRTVGPSDSASPDLWATDOMPVDVUVTU
RMLTATQYIAPLMANFDPSUSRNSTVAYPENGTALVQWDHVALL QDYNINGSFTEGATLMORGI I FGYKEVUTOTISSTNHYVKY GLSDAFVVVHRIQQI PNVRRTIYYEYHRVELQMSKITNI SAVEM TPLPTCLQFINKGGFVSSQIGFNCSWCSKLQKCSSGFDRRRQDW VDSSCPEESKEKMEENTE PVETY TLEPOPERQPPSSSS* LPP E/DAVISQFFTSLPTEDDTKIALHKONGSTDDSAAEKKGGTL EAGLIVGLILVATLVATALLVTVWHHHPTSAASIFPIERRPSR WPAMKFRRGSGHPAYAEVEPVGEKEGFIVSEQC  SYKLPAAERRASSCGPPTFTRRWFAPGRTSRGHRPQW*SGTP APRPARSTVSPASPLPKFRAGRGSGRPSAGSTFRRC* SLM*M S*H*KRNLSQRSSSMSRRPLSCARPHK**RQGLTVAARLPTWAK S*H*KRNLSQRSSSMSRRPLSCARPHK**RQGLTVAARLPTWAK S*H*KRNLSQRSSSMSRRPLSCARPHK**RQGLTVAARLPTWAK S*H*KRNLSQRSSSMSRRPLSCARPHK**RQGLTVAARLPTWAK S*H*KRNLSQRSSMSRRPLSCARPHK**RQGLTVAARLPTWAK S*H*KRNLSQRSSMSRRPLSCARPHK**RQGLTVAARLPTWAK S*H*KRNLSQRSSMSTRPRSPTSPPTT**APTSSPGGT GRSMMTCPTFWTATPWSABASSRPNWPTP**WPSGRLSTV**RA TGGSTATAPPKRFPRNWNPMAB  5787  2 1460 MASAASVTSLADEVNCP\TCQGTTLKEAGSLSMCG/HKNFCRACL T\SYCEILYGPD\LEBESPTCP\LCKEPFRP\GSFRPNMOLANV VENIBRLQLVSTIGLGEBDVCCPHIGEKIYFFCEDDEMQLCVVCR EAGEHATHMR*FLEDAA\PAPREGILKFRCEDCOSILLAQLSS QGGDLLRQRBSFPLLVAGEICRFSALIEELERKREPARELLTD IRSTLIRCETTRCKREVAVSSELQQRIRGFPQADLPQLREMMF LEKLCFELDVSPAHISLDPQTSHFKLLLSEDDQASPSXWONS PDNPQRFBRATCVLAHIGTTGRGHTVVYSIDLARGGSCTVGVVS EDVQRRGGLRLRDEBGVWAVRLAWGFVSALGSFP\TRLILKEQP RQVRVSLDYBVGWFTRAVTREPITTTASFTRKVIPFFGLMG SSSSSLSS DNPQRFBRATCVLAHIGTTGRGHTVVYSIDLARGGSCTVGVVS EDVQRRGGLRLRDEBGVWAVRLAWGFVSALGSFP\TRLILKEQP RQVRVSLDYBVGWFTRAVTREPITTTASFTRKVIPFFGLMG SGSGEGEGEFTGDVHTSNLHWNIKHLIRELLQTLPDLORGVRA AFPWQVILMLTTDLDGEDEKDKGALDNLLSQLIAELGMDKXDV SKKNERSALWSHLVVMRLLSSLEVMSGNBEPVATSGLKB HTTSSPPMSPFFLRQYVKGHAADVFRAYTQLIFEWLRLPYQI KKITDTNSRTPPPVENSWYFFLSSVGNGTFRODSVLV FILLQVSFLVDEGVSFVLQLLSCALCGSKVLRALAASSGSSAS SSPAVAASGGATTQSKSSTKKSKKEEKKERDGFTGSGGDQ LCTALVWQLMKFADKETLIOPLRCFILLSSSVFRQARLTTH IYRNSKSQQELLLDLMMSI WPSLPAYGRKAAQFVDLLGYFSLK TPOTEKKLKEYSQKAVEILRTQMHLITHNNSNI TYTLIGGUVEL LCTALVWQLMKFADKETLIOPLRCFILLSKVTARQFTTTTQCVVKLI GSHTISKVTVKLGDLKTRKWNRT INLYYNNETVQARVKLOA RWHAKKVCQLTFGOTFOVKLDLEPLYVARGFADAS	-	ł .		GILSNTHROAARVNLSPDFPFYGHFLRRITVATGGFTVTGFUNG
ODNYNLGSFTFQATLMOGRIJFGYKEIPYUTTGISSTNHPVKV GLSDAFVVVRRQIJFGYKRRITIFSYKEUMSKITHISAVEM TPLDTCLOPNRCGCVSSQIGFNCSMCSKLQRCSSGPDRHRQDW VDSGCPESKEKMCENTEPVET\FLEPPQP*ERQPPSSGS*LPP E/DAVISQFPTSLPTEDDTKIALHLKORSTDDSAAEKKGCTL HAGLIVGILILVILVATAILVTYWYHHPTSAASIFFIERRER MPAMKERRGSCHPAYAEVPVCEKEGTUSGC  5786  2532  1674  SYKIPARERRASGCSQPPTPTTRRWFAPGGTSRGHRQDM*SGTP APPEPARTVSPASPLDKFRARGCSSPARSCSTFRPC*SLN*M S*H*KRNLSQRSSSMSRRPLSCARPHR**RQGIVTARALPTWAK SPLACSFCQAAKKGGLSGSSTR*PERMSFTP*SPSGTTGGRAPH SAAPSFRP*FRGRPCTWTFSRWAPAFAPTT*APTSSPGST GRSMMTCFTRWTATTFWSARASSFRNNPTP*MRPSGRISTV*RA TGGSTATAPPKFPFRWMPMMAB  5787  2 1460  MASAASVTSLADEWNCP*,CCQGTLKEEAGSLSNCG/HKNFCRACL T\RYCEIP\GPD\LEESP\TCP\LCKEPFRP\GSFRPNMCLNV VENIBRIQLUSTIGLEEDVCQHIGKITYFCEDDEMQLCVVCR EAGERATHTWFFLDAA\APYREQIHKCLKCLIKEREIQEIQS RENKRWQULITOVSTRGQVISEPAHREEQOSILLAQLIS QDGDILRQRDEFDLLVAGEICRFSALIEBLEKKMERPARELLTD IRSTLIRCETTRKCRKBVAVSEDLGQRIFKEEQOSILLAQLIS QDGDILRQRDEFDLLVAGEICRFSALIEBLEKKMERPARELLTD IRSTLIRCETTRKCRKBVAVSEDLGQRIFKEEQOSILLAQLIS DVQRKGGLELREESVVAVAKLAAGGVSALGSFF\TRLTLKEOP RQVRVSLDYSVGWVFTTNAVTREIYTFTASFTRKVIPPFGLWG SGSSFSLS  5788  2 6860  EHSVSGRSSAYGDATAECHPAGPGSVSSSTGAISTTTGURGDGD SKKMERSALMEVHLVVMRLLSJEVMSKTKGGKSEICRSSLISS ATAAALLSSGAAVTCLHVKSLLEFWKSCQNEEPVATSCLKP HTTSSPPDMSPFFLRQYVKGHAADVERAYTOLLTEMVLRLEFVQI KKITOTNSRTPPPVDHSWFYFLSEVIMIQQTPFVRRQVRKLLL FICGSKEKKPQLRDLHTLDS\HVGIKKLEEGGIFLARSVVTA SPQSALGYDTLISIMEHLKACABIAAQRTIMQKPCIKDDSVIJ FILLAVSFILVDEVSVFLVGLISCALCGSVLRALAASSGSSAS SSPAPVAASSGQATTQSKSSTKKSKKEEKKEKDGTSGSORDQ LCTALVWQLMKFADKETLIDPLECHLESSSVFRQAHCLTH LYRNSSKSQQELLLDLMWSIWPELPAYGRKAAQPVDLLGFYSKK TPOTKKKLKEYSGKAVETLENDMILITHNPNSNITYTGGLVVKLI GSHTISKVTVKLGDLKKENSSTKRAAQPVDLLGFYSKK TPOTKKKLKEYSGKAVETLENDMILITHNPNSNITYTGGVVKLI GSHTISKVTVKLGDLKATKRAVRTIMLYYNNETVQAIVELKLER GSHTISKVTVKLGDLKATKRAVRTIMLYYNNETVQAIVELKLER GSHTISKVTVKLGDLKATKRAVRTIMLYYNNETVATLTSGLVVKLI GSHTISKVTVKLGDLKATKRAVRTIMLYYNNETVQAIVELKLER GSHTISKVTVKLGDLKATKRAVRTIMLYYNNETVQAIVELKLER GSHTISKVTVKLGDLKATRRAVRTIMLYYNNETVAAUELKRAA	1	1		RMLTATQYIAPLMANFDPSVSRNSTVRYFDNGTALVVOWDHVHI.
GLSDAFVVVHRIQGIPNVRRTITYEHREUDMSKITNISAVEM TPLPTICLORNICGS-CVSSQCISHCSNCSKLORCSSGPRIRGOM VDSGCEBESKEMCENTEPUET\FLEPPQP*ERGPPSGS*LPP R/DAVTSQPPTSLPTEDDTKIALHLKDNGASTDDSAAEKKGGTL EAGLIVGILILVLIVATALILVTVYMHHPTSAASIPPIERRESR WPAMKERGSGHPAYAEVEPVGEKEGFIVSEQC  5786  2532  1674  SYKLPABERRASSCSQPPTFTRENPGPRTSGGHRPOM*SGTP APRPARSTVSPAGPLEKPRAGRCGSRPRSACSTFRFC*SLN*M S*H*KRNLSQRSSSMSRPLSCARPHR**RGGIVARARLPTWAK S*PLACSFCQAAQKSGSLSSGRST*PERMSFRP\SPPORPATP GRAMMCTPTWTATTWSARASSSFRWTP**WTP*WTP*SPGSTT*GRAMMCTPTWTATTWSARASSFRPWTP**WTP**WTATSSPGST GRAMMCTPTWTATTWSARASSFRWTP**WTP**WTATSSPGST GRAMMCTPTWTATTWSARASSFRWTP**WTP**WTATSSPGST GRAMMCTPTWTATTWSARASSFRWTP**WTP**WTSFGRLSTV*RA TGGSTATAPPKFFPNNNPPMAP  5787  2 1460  MASAASVTSLADEVNCP\CQGTLKEAGSLSNCG/HKNFCRACL T\RYCEIP\GPD\LEESP\TCP\LCKEPFR\GSFRPNMQLANV VENIERLQLVSTLGEBEDVCGHGEKIYFFCEDDEMQLCVVCR EAGEHAHTHMFFLEDAA\APPKEGHLKCKLLKEREEREGETGS RENKMOVLLTOVSTKRQOVISEFAHLEKFLEBQGSILLAQLES QDCDILRQRDEFDLLVAGEICRFSALIEBLEEKEREPARELLID IRSTLIRCETRKCKREVAVSPELGGRINDFPQQALPLQREMMF LEKLCFELDYBPHISLDPGTSHFKLLLSCHQRAGFSYKMONS PDNORGFRATCVLAHTGITGGRHVVSILLAKLKEDP ROVRYSLDYBUGWVTPTNAVTREPIYTFTASFTRKVIPFFGLMG RGSSFSLSS  5788  2 6860  EHSVSGRSSAYGDATAEGHPAGGSVSSSTGAISTTTGHQEGDG SGEGEGETECDVHTSNRLHMVRIMLLERILJOTLPGLRNVGGVR AIPYMQVILMLTDLGCEBEKKGALDNILLSQLIALLGMDKKDV SKKNERSALNEVHLVVMRLLSVFMSGRNSSSICESSSLISS ATAAALBSGAVDYCLHVLKSLLEYMKGQNDEEEVATSGLLKE HTTSSPPDMSPFFLRQYVKGHADVPRATYGLLTEMVLRLPYQI KKITDTNSRTPPPFFDHSMFFFLSCHKGQTFFKRQVRKLLL FICGSKEKYRQLKDLHTLDS\HVRGIKKLLEEGGIFLRASVVTA SPQSALQYDTLISLMEHLKACAEIAAQRTINMCPCIKDDSVLY FILLQVSFLVDEGVSFVLLQLISCALGGSKVLRALAASSGSSSAS SSPAPVAASSGQATTGSKSTKKSKKEEKEKECGETSGSGEDQ LCTALVAGLKKFAKKETLIGFLEGFLESNSSVKMOANCLITH IYRNSKSQQELLLDLMMSIMPELPAYGRKAAQPVDLLGYFSLK TPOTEKKLKEYSQKAVEILIPQHNILTNIPNNNIYNTISGLVBF DGYYLESDPCLVCMBPEVPFCYIKLSSIKVDRYTTTQVVKKIKPA RWHAKKVQLTPGQTEVKILDLERKRUMMEFFAKDFSKVKA RWHAKKVQLTPGQTEVKILDLERKNUMMEFFAKPTFFENOA	1			QDNYNLGSFTFQATLLMDGRIIFGYKEIPVLVTOISSTNHPVKV
TPLPTCLQFNRGSPCVSSQTGFNCSNCSKQRCSGSPDRRGOW VDSGCPESKERMCENTEPUET\PLEPPOPP EROPPSSGS*LBP B/DAVTSQPPTSLPTEDTKIALHLKDNGASTDDSAAEKKGGTL EAGLIVGILILVLIVATAILLVTYYMTHHTEASAIFPIERRSR WPAMKFRGSGHPAYAEVEPUGKEGFIVSRQC SYKLPAAERRASGSQPPTFTRRWBAPGRTSGGHRPQM*SGTP APRPPARSTYSPASPIBPEKPRAGRCGSRPRACSTFRFC*SLN*M S*H*KRNLSQRSSSMSRRPLSCARPHR**RGGLTVAARLPTMAK SPPLACSTCQAAQKSQSLSSGRST*PERMSPRAGSTFRFC*SLN*M S*H*KRNLSQRSSSMSRRPLSCARPHR**RGGLTVAARLPTMAK SPPLACSTCQAAQKSQSLSSGRST*PERMSPRASFPOENPAIP SLAPSSRF/PKGRPCQTWIPSRWPASPTAPPTTT*APTSPGGT GRSMMTCPTRWTATWSARASSPRNWPTP*WRPSGRLSTV*RA TGGSTATAPPKFFPENNPMMAMAS TGGSTATAPPKFFPENNPMMAMAS VENIRRLQLVSTLGLGEBUCQLGHEKIYFPGEDDEMQLCVVCR EAGEHATHTMFPLEDAA\APYREQIHKCLKCLIKEREEIQEIQS RENKRMQVLLTQVSTKRQQVISEFAHLRKFLEEQQSILLAQLES QGGDILRGRBFDLLVAGEICRFSAHLRKFLEEQQSILLAQLES QGGDILRGRBFDLLVAGEICRFSAHLBLLSGDHQRAPPRAGLLTD IRSTLIRCETRKCRKDVAVSPELGGRINDFQQALFLGREMMF LEELCFELDYSPAHISLDPQTSHFHLLLSGDHQRAPPSKWGNS PONPQRFDRATCVLAHTGITGGRHTWVVSIDLAHGGSCTVGVVS EDVQRKGELRLRPESGVWAVLAWGFVSALGSFY\RUITLEQP RQVRVSLDYSVGWWTTNAVTREPIYTTTAFTFRVIPFFGLWG RGSSFSLSS SEGEGEGETEGDVHTSNRLHMVRLLLERLLGTLPQLENVGGW AIFYMQVILMLTDLDGEDEKKGADINLLSQLIAELGMDKKDV SKKNERSALMEVHLVWRRLLSVFNEXGSKSSICESSSLISS ATAAALLSSGAVDYCLHVLKSLLEYWKSQGNDEEPVATSQLIKP HTTSSPPDMSPFFIRQYVKGHAADVFRATYQLIEMVLRLPYQI KKITDTNSRIPPPVFDHSMFFYLSEYMIQGTFFVRROYRKLLL FICGSKEKYRQLBDLHTLDS\JVRGIKKLEEGGIFLASVVTA SPOSALGVDTHISLBMHKACAETARGSKSSICESSLISS SSPAVAASSGQATTQSKSSTKKSKKEKEKSEKEDETSGSQEDQ LCTALVWGLNKFARKETLIQFLCFLLESSSSVKWGHCLITHH IYRNSKSQOGLLLDLMMSIMPELPAYGRRAAQFVDLLGYFSLK TPOTEKKLKEYSGKAVELIKTONHILTNNYNINTICGLVBF DGYYLESDPCLVCNNPEVPFCYIKLSSIKVDRYTTTQQVVKLI GSHTISKVTVKLGDLKRYRMYTINLYYNNRTVQAIVELKNRPA RWHARKVQLTPQGTVEKULDLERVKRIMLHEFALDFYFRYOAK		]		GLSDAFVVVHRIQQIPNVRRRTIYEYHRVELOMSKITNISAVEM
VDSCCPESKEMCENTEPUET\FLEPEOP PEROPPSSCS+LPP  8/DAVTSOPTSLEPTEDTATIALHLEMORASTDDSAARKGGTL  EAGLIVGILIULTVATAILVTVYMYHHPTSAASIFFIERRSR WAMKFRCSGHPAYABVBPVGEKEGTIVSBC  5786  2532  1674  SYKLPABERRASSCSQPTPTTRRWPAPGRTSGGHPPOW*SGTP APRPPARSTVSPASPLEVERBAGRCGSRPSRACSFRRPC*SLN*M S"H*KRILSQRSSSMSRRPLSCARGFRYSRCSPRPSCSTPP APRPPARSTVSPASPLEVERBAGRCGSRPSRACSFRRPC*SLN*M S"H*KRILSQRSSSMSRRPLSCARGFRY*P**CSGTP APRPPARSTVSPASPLEVERP**CSGTPTPAPTTT**APTSSPGST GRSMMTCPTRWTATWBARASSRPRUP**P**MRSCHITV**RA TGGSTATAPPKFPPNNNPMMAB  5787  2 1460  MASAASVTSLADENUTO** 1000GTLKEAGGLSNCG/HKNFCRACL T\RYCEIP\GPD\LEESP\TCP\LCKEPFR\GSFPNWQLNV VENIBRLQLVSTLGEEDVCQEHGEKIYFFCEDDEMQLCVVCR EAGHANTHMFLEDAA\APPREGITECKICKLIKEREBIQEIOS RENKHMQVILIVQVSTKRQQVISSFAHLBKFLEBQOSILLAQLSS QGGDILGROBEPHLUAGGLECPSLCKCLKLIKEREBIQEIOS RENKHMQVILIVQVSTKRQQVISSFAHLBKFLEBQOSILLAQLSS QGGDILGROBEPHLUAGGLECPSLEUELENENERPARELLTD INSTIIRCETBKCKKPVAVSPELGQRIRDFPQGAPPSVKWONS PDNPQRFPRATCVLAHTGITGGRHTWVVSIDLAHGSCTVGVVS EDVQRKGELRIRPEGGWAVRILAWGFVSALGSFP\RTLILKEDOP RQVRVSLDYEVGWTFTNAVTREPIYTFTASFTRKVIPPFGLWG RGSSFSLSS  5788  2 6860  EHSVSGRSSAYGDATAEGHPAGGSVSSSTALSTTTCHQEGDG SGGGEGEFTEDVHTSNRLHMYRIMLLERILOTLPQLRNVGGVR AIPYMQVILMITDLDCEDEKKGALDNILSQLIALGMDKKDV SKKHRSALBEVHLUVMRLLSVFMSQNDEEVATSGLIKB HTTSSPPDMSPFFLRQVVKGHAADVPBAYTQLIEMVLRLPYQOI KKITTINSTPPPVFPHSMFFYLESVIMIQQTPFVRGVRKLL FICGSKEKYRQLKDLHTLDS\JVRGIKKLLEEQGIFLBASVVTA SPOSALQVDTLISLMEHKACAEIAAQRTINMQKPCIKDDSVLY FILLQVSFLVDEGVSFVLLQLISCALGGSKVLRALAASSGSSSAS SSPAPVAASSGQATTQSKSSTKKSKKREKKEKEKEKECTSGSOEDQ LCTALVMQLNKFARKETLIGPLECFLLESNSSVROAHCLITH IYRNSKSQOELLLDLMMSIUPELPPAYGRAAQPVDLLGYFSLK TPOTEKKLKEYSQKAVEILTQPLRCFLLESNSSVROAHCLITH IYRNSKSQOELLLDLMMSIUPELPAYGRAAQPVOLLGYFSLK TPOTEKKLKEYSQKAVEILTQPLRTYLNYNNITYTLSGLVBF DOYYLESDPCLVCMBPEVPFCYIKLSIKVDRYTTYQJVVKIKPA RWHAKKVQLTMQGTVENLIDDLWILMEFALDYFNYDQVVKIL		1		TPLPTCLQFNRCGPCVSSQIGFNCSWCSKLQRCSSGFDRHRODW
FAGLIVGILILVITVATALITVTYMYHHPTSAASIPPIERRPSR WPAMKERGSGHPVATAEVEPUCEKEG IVSEQC  SYKLPAAERRASSCSQPPTPTRRWFAPGRTSKGHRPOM*SGTP APRPPARSTVSPASPLPKPRAGRGSKPRPGC*SLM*M S*1**KRNLSQRSSSMSRPLSCARPH***RQGLTVARHPTWAK S*PLACSFCOAOASGSLSGGSTR**PERMSFRPSPGNDAIP SLAPSSRP/FKGRPQCTWIPSRWPASPTAPTT**APTSSPGST GRSMMTCPTRWTATTWSARASSRPNNPTT**MRPSGRLSTV*RA TGGSTATAPPKFPRNWMPMAB  5787  2 1460  MASAASVTSLADEVNCP\1CQGTLKEAGSLSNGG/HKNFCRACL T\RYCEIP\GPD\LEESP\TCP\1CKEPFKP\GSFRPWQLLNV VENIBRLQLVSTLGIGEBDVCQFIGEKIYFFCEDDEMQLCVVCR EAGEHATHMR*LEDAA\APYREGIKKCLKCLKEREBIQEIQS RENKRMQVLLTQVSTKRQQVISEFAHLRKFLEEQQSILLAQLES QGGDLLRGRBFDLLVAGGICRFSALLEELBEKNERPARBELLTD IRSTLITRCETRKGREPVAVSPELGGRIRDFPQOALPLQREMMP LEKLCFELDYBPAHISLDPQTSHFKLLLSEDHQRAQFSYKWONS PDNPQRFDRATCVLAHTGITGGHTMVVSJULAHGGSCTVGVVS BEVQRKGELRILPBESGWAVRLAWGFVSALGSFP\TRUTLKEQP RQVRVSLDYEVGWVTFTNAVTREPIYTFTASFTRKVIPFFGLWG RGSFSLSS  5788  2 6860  EHSVSGRSSAYGDATAEGHPAGPGSVSSSTGAISTTTCHQEGDG SEGEGEGETECDVHTSNRLHMVRIMLIERLIGTLPQLENVGGVR ALPYMQVILMLTDLDCEDEKDKGALDNILLSQLLAELMDKKDV SKKNERSALNEVHLVVMRLLSVFMSRTKSGSKSSICESSSLISS ATAAALISSGAVDYCLHVLKSLLEYMKSQONDEFPVATSQLLKR HTISSPPMSFFFLRQVVKGHADVEATYGLLKEQIFFLAWVRTAVILL FICGSKEKYRQLRDLHTLDS\APVRGIKKLEEQGIFLRASVVTA SPQSALQYDTLISLMEHLKAQAEJARQRTIMOQYTPFVRQVKKLL FICGSKEKYRQLRDLHTLDS\APVRGIKKLEEQGIFLRASVVTA SPQSALQYDTLISLMEHLKAQAEJARQRTIMOQYTFVRQVKKLL FILQVSFLVDGGVSPVLLQLLSCALGGSKVLRALAASSGSSA3 SSPAPVAASSGQATTQSKSTKKSKKEKKEKEKDGETSGSQBDQ LCTALVNQLMKFADKETLIQFLRCFLLESNSSVMOAHCLTH- IYRNSSKSQGELLDLMWSIWPPLPAYGRKAAQFVDLLGYFSLK TPOTEKKLKEYSGKAVEILRTQMITHNPNNSTIYNTISGUVEF DGYYLESDPCLVCNNPEVPFCYIKLSIKVDTRYTTTQQVVKLI GSHTISKVTVKIGDLKRVIKNITHLYNNTNTVQAIVELKIKPA RWHARKKVQLTPZGTKVKIGDLKVKDALMLESCLIKRPA	1			VDSGCPEESKEKMCENTEPVET\FLEPPQP*EROPPSSGS*LPP
######################################				B/DAVTSQFPTSLPTEDDTKIALHLKDNGASTDDSAAEKKGGTL
SYKIPAAERRASSCSQPTPTTRRRWEAPGRTSRGHRPQW-SGTP APRPPARSTYSPASPIPKPRAGGSRPRASCTFRFC*SLN*M S*H*KNLSQRSSSMSRRISCARPHR**RQCLITVAARLPYWAK SPELACSFCQAAQKSQSLSGRST*PEPEMSFRP\SPEMDRAIP SLAPSRP/RKRPQCTWTPTT*APTTSPPGST GRSMMTCPTRWTATPWSARASSRPRNWPTP*WRPSGRISTV*RA TGGSTATAPPKRFPRNWNDMMAB  5787 2 1460 MASAASVTSLABEVNCP\TCQGTLKEAGSLSNCG/HKNFCRACL T\RYCEIP\GPD\LEESP\TCP\LCKEPFRP\GSFRPNWQLANV VENIERLQLVSTLGIGEBOVCQEHGEKIYFFCEDDEMQLCVVCR EAGENATHTMRFLEDAA\APPKGHIKCLKCLIKEREBIGIOS RENKMWQVLLTOVSTKRQQVISEFAHLRKFLEEQQSILLAQLES QDGDILRQRDEFDLLVAGEICRFSALIEELERKWERPARBLLITD IRSTLIRGETRKCRKPVAVSPELGQRINDFPQOALPLORRNKMF LEKLCFELDYEPAHISLDFOTHFKLLISEDHORAOPSYKWQNS PONPGRFDRATCVLAHTGITGGRHTWVVSIDLAHGGSCTVGVVS EDVQRKGELRLRPEEGVWAVRLANGFVSALGSFF\TRLIKECPP RQVRVSLDYEVGWVTFTRAVTREPIYTFTASFTRKVIPFFGLWG RGSSFSLSS  5788 2 6860 EHSVSGRSSAYGDATAEGHPAGPGSVSSTGAISTTTGHQEGDG SGGBGGGTEGDVHTSNRLHHVURLLERLQTIPQLRRNGGVR APPYMQVILMITDLDGEDERGADINLLSQLIAELGMKKDV SKKNERSALNEVHLVVWRLLSVFMSRTKSGSKSSICESSSLISS ATAAALLSSGAVDYCLHVUKSLLEFWRSQONDEEPVATSGLLERP HTTSSPPDMSPFFLRQYVKGHADDVFRAYTQLITEMVKLRPYI KKITDTNSRIPPPVBDHSWFYFLSEVLMIQQTPFVRRQVRKLLL FICGSKEYRQLRDLHTLDS\HVRGIKKLEEQGIFLRASVVTA SPQSALQYDTLISLMEHLKACABETAAQRTINMQKFCIKDDSVLY FILQVSFLVDEGVSPVLLQLLSCALCGSKVLRALAASGSSSAS SSPAPAASSGQATTQSKSSTKKSKEEKEKEKDGETSGSQBDQ LCTALVNQLNKFADKETLIOPLRCFLLESNSSSVRQAHCLTIH IYRNSSKSQQELLDLLWSLMSTWPELPAYGRKAAGPVDLLGYFSLK PTOTEKKLKEYSGCAVEIRTOPLITINHNNINTIYNTICGLVEF DGYYLESDPCLVCNNPEVPPCYIKLSSIKVDTRYTTTQQVVKLI GSHTISKVTVKIGGLKRTAVRTINLYYNRRTVQALVELKNFA RWHRAKKVQLTPGGTEVKIDLPJFIVASNLMIEFADPYRNYQAS	1			HAGLIVGILILVLIVATAILVTVYMYHHPTSAASIFFIERRPSR
APPPPARSTYSPASPIPERFAGRCGSRPRSACSTFRFC'SIN'M S'H'KRNLSGRSSMSRPILSCARPHR'*RQGLTVAARLPYWAK SPPLACSFCQAQKSQSLSSGRST*PT*PERMSFRP\SPPGNPAIP SLAPSSRP/KGRPQCTWIPSWPASPTAPPTTT*APTSSTGGT GRSMMTCPTRWTATTWSARASSRPRWPTP*WRPSGRLSTV*RA TGGSTATAPPKRPPRWNPWPB*WRPSGRLSTV*RA TGGSTATAPPKRPPRWNPWPB*WRPSGRLSTV*RA TGGSTATAPPKRPPRWNPWPB*WRPSGRLSTV*RA TGSTATAPPKRPPRWNPWPB*WRPSGRLSTV*RA TGSTATAPPKRPPRWNPWPB*  MASASVTSLADEVNCP\\CQGTLKEAGSLSNCG/HKNFCRACL T\RYCEIP\GPP\\LEESP\TCP\\LCKEPFRP\GSFRPWOLANV VENIERLGLUSTLIGLGEEDVCHGEKLYFFCEDDEMQLCVVCR EAGEHATHTMRFLEDAA\APYREQIHKCLKCLIKEREEIQEIQS RENKHMQVULUTOVSTKRQQVISEFAHLEKFLEEQQSILLAQLES QCGDLIRQRDEFPLLVAGEICFSALIEELEREKERPARRELLTD IRSTLIRCETRKCRKPVAYSPELQRIRGFPQQALPLQREMKMP LEKLCFELDYEPAHISLDPQTSHRILLISEDHQRAQFSYKWQNS EDVQRKGELRLRPESVWAVRLAWGFVSALGSFP\TRLTLKEQP RQVRVSLDYEVGWVTFTNAVTREPIYTTASFTRKVIPFFGLMG RGSSFSLSS SEGGEGETEGDVHTSNRLHMVRLLLERLLQTLPQLRNVGGW AIFYMQVILMITTDLDGEDEKDKGALDNILSQLIAELGMKKDV SKKNRRSSAYGDATAEGHPAGPGSVSSSTGAISTTTGHQEGDG SEGGEGETEGDVHTSNRLHMVRLLLERLLQTLPQLRNVGKW SKKNRRSALNEVHLVVWRLLSVFMSRTKSGSKSSICESSSLISS ATAALLSSGADYCLHVLKSLLEYMKSQQNDEEPVATSQLKP HTTSSPPDMSPFFLRQVYKGHAADVFRAYTQLLTEMVLRPYQI KKITDTNSRIPPPVPBHSWFYFLSEYLMIQQTPFVRRQVKKLLL FICSKEKYRQLRDLHTLDS\HVGIKKLLEEQGIFLARSVVTA SPQSALQYDTLISLMEHLKACABTAAQRTINMQKFCIKDDSVLY FILLQVSFLVDEGVSPVLLQLLSCALCGSVLRALAASGSSSAS SSPAPAASSGQATTQGKSSKKKKEKEKEKEKDGTTSGSQBDQ LCTALVNQLNKFADKETLIOPLRCFLLESNSSVRWQAHCLTLH IYRNSKSQGELLLDLHWSIWPELPAYGRRAAQFVDLLGYFSLK PTQTEKKLKEKSGQATTQGKSSYKKSKKEKEKEKENGETSGSQBDQ LCTALVNQLNKFADKETLIOPLRCFLLESNSSVRWQAHCLTLH IYRNSSKSQGELLLDLHWSIWPELPAYGRRAAQFVDLLGYFSLK PTQTEKKLKEKSGAVELTLROPLITINHPNNI IYNTLSGLVEF DGYYLESDPCLVCNNPEVPPCYIKLSSIKVDTRYTTTQQVVKLI GSHTISKVTVKIGGLKKRAVRTINKIYYNRTVQAIVELKNKPA RWHRAKKVQUTPGGTEVKIDLPLFVASNIMTYNGTYCALVELKNKPA	5786	2532	3.694	WPAMKFRRGSGHPAYAEVEPVGEKEGFIVSEQC
S*#*KRNLSQRSSSMSRRPLSCAPPH***RGGLTVAARLPTWAK SPPLACSFCQAAQKSQSLSSGSTR*PERMSFRP\SPPGNPAIP SLAPSSRP/PKGRPQCTWIPSRWPASPTAPPTTT*APTSSPGST GRSMMTCPTRWTATPWSARASSRPRNWFTP*WRPSGRLSTV*RA TGGSTATAPPKRFPRNWNPMMAE  5787  2 1460 MASAASVTSLADEVNCP\LCGGTLKEAGSLSNCG/HKNFCRACL T\RYCEIP\GPD\LEBSP\TCP\LCKEPFRP\GSFRPNWQLANV VENIERLQLVSTLGLEEDVCQEHEGKIYFFCEDDEMQLCVVCR EAGEHATHTWRFLEDAA\APYREGIHKCKLLKEREEIQEIQS RENKRMQVLLTQVSTKRQQVISEFAHLRKFLEEQQSILLAQLES QDGDLLRQRDEFDLLVAGEICRFSALIEBLBERKNERPARBLLITD IRSTLIRCETRKCRKPVAVSPELGQRIRDFQQAIPLQRENKMF LEKLCFELDYEPAHISLDPQTSHPKLLLSEDHQRAQFSYKWQNS PDNPQRFDDRATCVLAHTGITGGHRHTWVSIDLAHGGSCTVGVVS EDVQRKGELRLRPEEGVWAVRLAWGFVSALGSFP\TRUIKEQDF RQVRVSLDYEVGWVTFTNAVTREPIYTFTASFTRKVIPFFGLMG RGSSFSLSS  5788  2 6860 EHSVSGRSSAYGDATAEGHPAGFGSVSSSTGAISTTTGHQEGDG SEGEGEGETEGDVHTSNRLHMVRLMLLERLLQTLPQLRNVGGVR ALPYMQVILMLTTDLDGEDEKDKGALDNLLSQLIABLGMDKKDV SKKNERSALNEVHLVVMRLLSVFMSRTKSGSKSSICESSSLISS ATAAALLSSGAVDYCLHVLKSLLEVMKSQONDEEPVATSGLLKF HTTSSPPDMSPFFLRQYVKGHAADVFRATVOLLTEMVLRLPYQI KKITDTNSRIPPPVFDSWFYFLSEYLMIQQTPFVRRQVRKLLL FICGSKEKYRQLRDLHTLDS\JVNGIKKLLEEQGIFLRASVVTA SPQSALQYDTLISLMEHLKACABIAAQRTINMQKPCIKDDSVLY FLLQVSFLVDEGVSPVLLGLSCALCGSKVLRALAASSGSSSA SSPAPVAASSGQATTQSKSSTKKSKKEEKEKENDETSGGSDQ LCTALVNQLNKRADKETLIQPLRCFILESNSSVRWQAHCLTLH IYRNSSKSQQELLLDLIMMSIWPELBAYGRKAAQPVDLLGYFSLK TPQCTEKKLKEYSQKAVEILRTQNHILTNIPNNIVNTLSGLVEF DGYYLESDPCLVCNNPEVPFCYIKLSSIKVDTRYTTTQQVVKLI GSHTISKVTVKIGDLKRTKMVRTINLYYNNRTVQAIVELKKRA RWHRAKKVQLTPGGTEVKIDLPLPTVASMLMEFADFTENYQAS	1	-552	10/4	SIKLPAAERRASSCSQPPTPTRRRWPAPGRTSRGHRPQM*SGTP
SPILACSFCQAAOKSGSLSSGRSTR*PERMSFRP\SPPGNPAIP SLAPSSRP/PKGRPQCTWIPSRPASPTAPPTTT*APTSSPGST GRSMMTCPTRWTATPWSARASSRPRNWPTP*WRPSGRISTV*RA TGGSTATAPPKRFPRNNNPMMAE  ***MASASVTSLADEVNCP\ICQGTLKEAGSLSNCG/HKNFCRACL T\RYCEIP\QPD\LEESP\TCP\LCKEPFRP\GSFRPNWQLANV VENIERLQLVSTLGLGEDVCQEHGEKIYFFCEDDEMQLCVVCR EAGEHATHTMRFLEDAA\APPYREQIHKCLKCLIKEREEIQEIQS RENKHMQVULTQVSTKRQQVISEFAHLRKFLEEQOSTLLAQLES QCGDLLRQRDEFDLLVAGEICRFSALIEBLEEKNERPARRLLTD IRSTLIRCETRKCRKPVAVSPELGQRIRDFPQQALPLQREMKMF LEKLCFELDYBPAHISLDPQTSHFKLLLSDHQRADGFSYMQNS PDNPQRFDRATCVLAHTGITGGRHTWVSIDLAHGGSCTVGVVS EDVQRKGELRLRPEEGVWAVRLAWGFVSALGSFP\TRLTLKEOP RQVRVSLDVEVGWVTFTNAVTREPIYTFTASFTRKVIPFFGLWG RGSSFSLSS  **SGSEGEGETEGDVHTSNRHMWRLMLLERLQTLPQEGDG** SEGEGEGETEGDVHTSNRHMWRLMLLERLQTLPQLRNVGGVR ALPYMQVILMLTTDLDGEDEKDKGALDNLLSQLIAELGMDKKDV SKKNERSALNEVLLVVWRLLSVFMSRTKSGSKSSICESSSLISS ATAAALLSSGAVDYCLHVLKSLLEYMKSQQNDEEPVATSGLLKP HTTSSPPDMSPFFLRQVVKGHAADVBEAYTQLLTEMVLRUPQI KKITDTNSRIPPPVFDHSWFYFLSEYLMIQQTFPKRQVVKLL FTCGSKEXYRQLRDHTLDS\HVGGIKKLLEEQGIFLRASVVTA SPOSALQYDTLISLMHLKACABIAAGRTINWQKPCIKDDSVLY FLLQVSFLVDEGVSFPLULGLISCALCGSKVLRALAASSGSSSSAS SSPAPVAASSGQATTQSKSSTKKSKBEEKEKDGBTSGGBDQ LCTALVNQLNKRADKETLIQPLRCFBLESNSSVRWQAHCLTLH IYRNSKSQQELLLDLMSIBPELPAYGRKAAQFVDLLGYFSLK TPQTEKKLKEYSQKAVEILRTQNHTLINNPNNIVNTLSGLVEF DGYYLESDPCLVCNNPEVPFCYIKLSSIKVDTRYTTTQQVVKLI GSHTISKVTVKIGGLKRTKMVRTINLIYYNNRTVQAIVELKKRA RWHKAKKVQLTPGGTEVKIDLPLYDAIMLEFADFTNYQAS	1	1		Stutken Sorgener of Stutken Stranger
SLAPSSRP/PKGRPQCTVIPSRWPASPTAPPTTT*APTSSGGT GRSMMTCPTRWTATPWSARSRPRNWPTP*WRPSGRLSTV*RA TGGSTATAPPKRFPRNMWPMMAE  5787  2 1460 MASAASVTSLADEVNCP\ICQGTLKEAGSLSNCG/HKNFCRACL T\RYCEIP\GPD\LEESP\TCP\LCKEPPRP\GSFRPNMQLANV VENIERLQLVSTLGLGEBVVCQFHGEKIVFFCEDDEMQLCVVCR EAGEHATHTMRFLEDAA\APYREQIHKCLKCLIKEREBIQEIQS RENKRMQVLLTQVSTKRQQVISEFAHLRKFLEEQQSILLAQLES QDGDILKRGNEFFDLLVAGEICRFSALIEBLBERKNEPARELLTD IRSTLIRCETRKCRKPVAVSPELGQRIRDFPQOADPLQREMKMP LEKLCFELDVEPAHISLDFQTSHFKLLSEDHQRAGFSVKWONS PDNPQRFDRATCVLAHTQITGGRHTWVVSIDLAHGGSCTVGVVS EDVQRKGELRLRPEEGVWAVRLANGFVSALGSFP\TRLTLKEOP RQVRVSLDTYGWTFTNAVTREPIYTFTASFTRKVIPFFGLNG RGSSFSLSS  5788  2 6860 EHSVSGRSSAYGDATAEGHPAGPGSVSSSTGAISTTTGHQEGDG SGEGEGETTEGDVHTSNRLHHVRLMLLERLLQTLPQLRNVGGVR AIPYMQVILMLTTDLDGEDEKDKADINLSQLIAELGMDKKDV SKKNERSALNEVHLVVMRLLSVFMSRTKSGGKSI CESSSLISS ATAAALLSSGAVDYCLHVLKSLLEYWKSQQNDEEPVATSQLLKP HTTSSPPDMSPFFLRQYVKCHAADVFRAYTQLLTEMVLRLPYQI KKITDTNSRIPPPVFDNSWFYFLSEYLMQQOFFVRRQVKKLLL FICGSKEKYRQLRDLHTLDS\HVRGIKKLLEEQGIFLRASVVTA SPQSALQYDTLISLMEHLKACABTAAQRTINMQKFCINDSVLY FLLQVSFLVDEGVSPVLLQLLSCALCGSKVLRALAASSGSSSAS SSPAFVAASSGQATTQSKSSTKKSKKEEKEKDGETSGSGBDQ LCTALVNQLNKFADKETLJOPLRCFLLESNSSVRWQAHCLTLH IYRNSKSQQELLLDLMWSIWPELPAYGRKAAQFVDLLLGYFSLK TPQTEKKLKEYSGKAVEILRTQNHILTNHPNSNIYNTLSGLVEF DGYYLESDPCLVCNNPEVPCYIKLSSIKVDTRYTTTQQVVKLI GSHTISKVTVKIGDLKRTKWTRINLYYNNRTVQAIVELKKKPA RWHRAKKVQLTFGQTFVKKJDLPLPIVASNLMIEFADYFENYOAS	1			SPPLACSFCOAAOKSOSI.sccpcrp+proverppl.copcupa.rp
GRSMMTCPTRWTATPWSARASSRPRNWPTP*WRPSGRLSTV*RA TGGSTATAPPKRFPRNWNPMAE  MASAASVTSLADEWICP\ICQGTLKEAGSLSNCG/HKNFCRACL T\RYCEIP\GPD\LEESP\TCP\LCKEPFRP\GSFRPNWQLANV VENIERLQLVSTLGLGEEDVCQEHGEKIYFFCEDDEWQLCVVCR EAGGHATHTMR FLEDAA\APYREQIHKCLKCLIKEREEIQEIQS RENKRMQVLLTQVSTKRQQVISEFAHLRKFLEEQQSILLAQLSS QOGDILRQRDEFDLLVAGEICRFSALIEELBEKMERPARELLTD IRSTLIRCETRKCRKPVAVSPELQQRIRDFPQAPFLQKEMKMF LEKLCFELDYEPAHISLDPQTSHFKLLLSEDHQRAQFSYKWQNS PDNPQRFDRATCVLAHTGITGGRHTWVVSIDLAHGGSCTVGVVS EDVQRKGELRLREPEGWWAVKLAWGFVSALGSFP\TRLTLKEOP RQVRVSLDVBVGWVFTNAVTREPIYFFASFTRKVIPPFGLMG RGSSFSLSS  SEGGEGETEGDVHTSNRLHLERLLQTLPQLRNVGGVR AIPYMQVILMLTTDLDCEDEKDKGALDNLLSQLIAELGMDKKDV SKKNERSALNEVHLVVMRLLSVFMSRTKSGSKSSICESSSLISS ATAAALLSSGAVDYCLHVLKSLLEYWSQQNDEEPVATSQLKP HTTSSPPDNSPFPLRQVYKGHAADVPEAYTQLLTEMVLRLPYQI KKITDTNSRIPPPVFDHSWFYFLSEYLMIQQTPFVRROVRKLLL FICGSKEKYRQLRDLHTLDS\HVBIKKLLEEQGIFLRASVVTA SPQSALQYDTLISLMEHLKACHAARQTIMQKPCINDDSVLY FLLQVSFLVDEGVSPVLLQLISCALCGSKVLRALAASSGSSSAS SSPAPVAASSGQATTQSKSTKKSKKEEKEKEKDGETSGSQEDQ LCTALVNQLNKFADKSTLIOFLRCFLLESNSSVRWQAHCLTLH IYRNSKSQOELLDLMNSIWPELPAYGRKAAQPVDLLGYFSLK TPQTEKKLKEYSOKAVEILRTQNHILINNPRNSNIYNTLSGLVEF DGYYLESDPCLVCNNPEVPFCYIKLSSIKVDTRYTTTQQIVELKKKPA RWHRAKKVQLTPGQTFVKIDLPLFIVASNLWIEFAPPYENYQAS	1			SLAPSSRP/PKGRPOCTWIPSRWPASPTAPPTTT*APTCCPGGT
TGGSTATAPPKRFPRNWNPMAE  MASAASVTSLADEVNCP/ICQGTLKEAGSLSNCG/HKNFCRACL T\RYCEIP\GPD\LEESP\TCP\LCKEFFRP\GSFRPNWGLAVV VENIERLQLVSTLGIGEEDVCQEHGEKIYFFCEDDEMQLCVVCR EAGEHATHTMRFLEDAA\APYREQIHKCLKKCLIKEREEIQEIQS RENKRMQVLITOVSTKRQQVISEFAHLEKFLEEQGSILLAQLES QDGDILRQRDEFDLLVAGEICRFSALIEELEKMERPARELLTD IRSTLIRCETKKCRKPVAVSPELGQRIRDFPQAADPLQREMMAP LEKLCFELDYEPAHISLDPQTSHPKLLLSEDHQRAQFSYKWQNS PDNPQRFDRATCVLAHTGITGGRHTWVVSIDLAHGGSCTVGVVS EDVQRKGELRLRPEEGVWAVRLAWGFVSALGSFP\TRLTLKEQP RQVRVSLDYEVGWVTFTNAVTREPIYTFTASFTRKVIPFFGLWG RGSSFSLSS  5788  2 6860 EHSVSGRSSAYGDATAEGHPAGPGSVSSSTGAISTTTGHQEGDG SGGEGEGTEGDVMTSNRLHWNRIMLLERLLQTLPQLRNVGGVR AIPYMQVILMLTTDLDGEDEKDKGALDNLLSQLIAELGMDKKDV SKKNERSALNEVHLVVWRLLSVFMSRTKSGSKSSICESSSLISS ATAAALLSGGAVDYCLHVLKSLLEYWKSQQNDEEPVATSQLLKP HTTSSPPDMSPFFLRQYVKGHAADVPEAYTQLLTEMVLRLPYQI KKITDTNSRIPPPVFDHSWFYFLSEVIMIQQTPFVRRQVRKLL FICGSKEKYRQLRDLHTLDS\HVRGIKKLLEEQGIFLRASVVTA SPQSALQYDTLISLMEHLKACAEIAAQRTINMCKFCIKDDSVLY FILLQVSFLVDEGVSPVLQLLSLCSLAGSKVLRALAASSGSSSAS SSPAFVAASSGQATTQSKSSTKKSKKEEKEKENGETSGSGDDQ LCTALVNQLNKFADKETLIQFLRCFILESNSSVRWQAHCLTLH IYRNSSKSQQELLLDLMWSIWPELPAYGRKAAQFVDLLGYFSLK TPQTEKKLKEYSGKAVEILRTQNHILITNIPNSNIYNTLSGLVEF DGYYLESDPCLVCNNPEVPFCTIKLSSIKUDTRYTTTQQVVKLI GSHTISKVTVKIGDLKRTKWVRTINLYYNNRTVQAIVELKKKPA RWHRAKKVQLTPSQTEVKIDLPLPIVASNIMMEFADPYENYQAS	1			GRSMMTCPTRWTATPWSARASSRPRNWPTP*WRPSGRLSTV*RA
TRYCEIP/GPD/LEESP/TCP/LCKEPFRP/GSFRPNWQLANV VENIERLQLVSTLGIGEEDVCQEHGEKIYFFCEDDEMQLCVVCR EAGEHATHTMRFLEDAA\APPREQIHKCLKKLIKEREEIQEIQS RENKRMQVLLTQVSTKRQQVISEFAHLRKFLEEQQSILLAQLES QCGDILRQRDEFDLLVAGEICRFSALIEELERKNERPARELITD IRSTLIRCETRKCRKPVAVSPELGQRIRDFPQQALPLQREMKMF LEKLCFELDYEPAHHSLDPQTSHFKLLLSEDHQRAQFSYKWOMS PDNPQRFDRATCVLAHTGITGGRHTWVVSIDLAHGGSCTVGVVS EDVQRKGELRLRPEEGVWAVRLAWGFVSALGSFP\TRILIKEOP RQVRVSLDYEVGWVTFTNAVTREPIYTFTASFTRKVIPFFGLWG RGSSFSLSS SEGEGEGETEGDVHTSNRLHMVRLMLLERLLQTLPQLRNVGGVR AIPYMQVILMLTTDLDGEDEKKGALDNLLSQLIAELGMDKKDV SKKNERSALNEVHLVVNRLLSVFMSRTKSGSKSSICESSSLISS ATAAALLSSGAVDYCLHVLKSLLEYWKSQQNDEEPVATSQLLKP HTTSSPPDMSPFFLRQYVKGHAADVPEAYTQLLTEMVLRLPYQI KKITDTNSRIPPPVFDHSWFYFLSEYLMIQQTPFVRQVRKLLL FICGSKEKYRQLRDLHTLDS\HVRGIKKLEEGGIFLRASVVTA SPQSALQYDTLISIMEHLKACAEIAAQRTINWQKPCIKDDSVLY FLLQVSFLVDEGVSPVLLQLLSCALCGSKVLRALAASSGSSSAS SSPAPVAASSGQATTQSKSSTKKSKKEEKSKEDGETSGSQBDQ LCTALVNQLNKFADKETLIQPLRCFILLESNSSSVRWOAGHCITLHH IYRNSKSQQELLLDLMWSIWPELPAYGRKAAQPVDLLGYFSLK TPQTEKKLKEYSQKAVEILRTQNHILTNHPNSNIYNTLSGLVEF DGYYLESDPCLVCNNPEVPPCYIKLSSIKVDTRYTTTQQVVKLI GSHTISKVTVKIGDLKRTKWVRTINLYYNNRTVQAIVELKNKPA RWHRAKKVQLTPSQTEVKIDLPLPTVASNLMHEFADPYENYQAS				TGGSTATAPPKRFPRNWNPMMAE
VENIERLQLVSTLGLGEBUVCQEHGEKLYFFCEDDEMQLCVVCR EAGEHATHTMR FLEDAA\APYREQIHKCLKCLIKEREHQEIQS RENKRMQVLLTQVSTKRQQVISEFAHLRKFLEEQQSILLAQLES QDGDILRQRDEFDLLVAGEICRFSALIEELEERKREPARELLTD IRSTLIRCETHKCRKEPVAVSPELGQRIRDFPQOALPLQREMKMF LEKLCFELDYEPAHISLDPQTSHPKLLLSEDHQRAQFSYKWONS PDNPQRFDRATCVLAHTGITGGRHTWVVSIDLAHGGSCTVGVVS EDVQRKGELRLRPEEGVWAVRLAWGFVSALGSFP\TRLTLKEOP RQVRVSLDYEVGWVTFTNAVTREPIYTFTASFTRKVIPFFGLWG RGSSFSLSS  5788 2 6860 EHSVSGRSSAYGDATAEGHPAGPGSVSSSTGAISTTTGHQEGDG SEGEGEGETEGDVHTSNRLHMVRLMLLERLLQTLPQLRNVGGVR AIPYMQVILMLTTDLDGEDEKDKGALDNLLSQLIAELGMDKKDV SKKNERSALNEVHLVVMRLLSVFMSRTKSGSKSSICESSSLISS ATAAALLSSGAVDYCLHVLKSLLEYWKSQONDEEPVATSQLLKP HTTSSPPDMSPFFLRQVVKGHAADVFEAYTQLLTEMVLRLPYQI KKITDTNSRIPPPVFDHSWFYFLSEYLMIQQTPFVRRQVRKLLL FICGSKEKYRQLRDLHTJSLWFHLKACAEIAAQRTINMQKFCIKDDSVLY FLLQVSFLVDEGVSPVLLQLLSCALCGSKVLRALAASSGSSSAS SSPAVAASSGQATTQSKSSTKKSKKEEKEKEDGETSGSQEDQ LCTALVNQLNKFADKETLIQFLRCFLLESNSSSVRWQAHCLITLH IYRNSSKSQQELLLDLMMSIWPELPAYGRKAAQFVDLLGYFSLK TPQTEKKLKEYSQKAVEILRTQNHILTNHPNSNIYNTLSGLVEF DGYYLESDPCLVCNNPEVPFCYIKLSSIKVDTRYTTTQQVVKLI GSHTISKVTVKIGDLKRTKMVRTINLYYNNRTVQAIVELKNKPA RWHKAKKVQLTPGGTEVKIDLPLPIVASNLMIEFADPYENYOAS	5787	2	1460	MASAASVTSLADEVNCP\ICQGTLKEAGSLSNCG/HKNFCRACL
EAGEHATHTMR FLEDAA (APYREQIHKCLKCLIKEREBIQEIQS RENKRMQVLLTQVSTRQQVISBFAHLRKFLEBQQSILLAQLES QCGDILRQRDBFDLLVAGEI CRPSALIEBLEBKNERPARBLLTD IRSTLIRCETRKCRKPVAVSPELGQRIRDFPQQALPLQREMKMF LEKLCFELDYBPAHISLDPQTSHPKLLLSEDHQRAQFSYKWQNS PDNPQRFDRATCVLAHTGITGGRHTWVVSIDLAHGGSCTVGVVS EDVQRKGELRLRPEEGVWAVRLAWGFVSALGSFP\TRLTLKEQP RQVRVSLDYBEVGWVTFTNAVTREPIYTFTASFTRKVIPFFGLWG RGSSFSLSS  5788 2 6860 EHSVSGRSSAYGDATAEGHPAGPGSVSSTGAISTTTGHQEGDG SEGEGEGETEGDVHTSRHHMVRIMLLERLLQTIPQLRNVGGVR AIPYMQVILMITTDLDGEDEKDKGALDNLLSQLIAELGMDKKDV SKKNERSALNEVHLVVMRLLSVFMSRTKSGSKSSICESSSLISS ATAAALLSSGAVDYCLHVLKSLLEYWKSQQNDEEPVATSQLLKP HTTSSPPDMSPFFLRQVYKGHAADVPEAYTQLLTEMVLRLPYQI KKITDTNSRIPPPVFDHSWFYFLSEYLMIQQTPFVRQVRKLLL FICGSKEKYRQLRDLHTLDS\HVRGIKKLLEEQGIFLRASVVTA SPQSALQYDTLISLMEHLKACAEIAAQRTINWQKPCIKDDSVLY FLLQVSFLVDEGVSPVLLQLLSCALGSKVLRALAASSGSSSAS SSPAPVAASSGQATTQSKSTKKSKKEEKEKEKDGETSGSQEDQ LCTALVNQLNKFADKETLIOPLRCFLLESNSSVRWQAHCLTLH IYRNSSKSQQELLLDLMWSIWPELPAYGRKAAQFVDLLGYFSLK TPQTEKKLKEYSQKAVEILRTQNHILTNHPNSNIYNTLSGLVEF DGYYLESDPCLVCNNPEVPRCYIKLSSIKVDTRYTTTQQVVKLI GSHTISKVTVKIGDLKRTKMVRTINLYYNNRTVQAIVELKNKPA RWHRAKKVQLTPGGTEVKIDLPLPIVASNLMIEFADFYENYQAS				T\RYCEIP\GPD\LEESP\TCP\LCKEPFRP\GSFRPNWQLANV
RENKRMQVLLTQVSTKRQQVISEFAHLRKFLBEQQSILLAQLES QDGDILRQRDEFDLLVAGEICRFSALIEBLBEKNERPARBLITD IRSTLIRCETRKCRKPVAVSPELGQRIRDFFQQALPLQREMKMF LEKLCFELDYBPAHISLDFQTSHFKLLLSEDHQRAQFSYKWONS PDNPQRFDRATCVLAHTGITGGRHTWVVSIDLAHGGSCTVGVVS EDVQRKGELRRPEEGWAVRLANGFVSALGSFP\TRLTLKEOP RQVRVSLDYEVGWVTFTNAVTREPIYTFTASFTRKVIPFFGLWG RGSSFSLSS  5788 2 6860 EHSVSGRSSAYGDATAEGHPAGPGSVSSSTGAISTTTGHQEGDG SEGEGEGETEGDVHTSNRLHMVRIMLLERLLOTLPQLRNVGGVR AIPYMQVILMLTTDLDGEDEKDKGALDNLLSQLIAELGMDKKDV SKKNBRSALNEVHLVVVNRLLSVFMSRTKSGSKSSICESSSLISS ATAAALLSSGAVDYCLHVLKSLLEYWKSQQNDEEPVATSQLLKP HTTSSFPDMSPFFLRQYVKGHAADVFEATTQLLTEMVLRLPYQI KKITDTNSRIPPPVFDHSWFYFLSEYLMIQQTFFVRRQVRKLLL FICGSKEKYRQLRDLHTLDS\HVRGIKKLLEEQGIFLRASVVTA SPQSALQYDTLISLMEHLKACAEIAAQRTINMQKPCIKDDSVLY FLLQVSFLVDEGVSPVLLQLLSCALCGSKVLRALAASSGSSSAS SSPAPVAASSGQATTGSKSSTKKSKKEEKKEGETSGSQEDQ LCTALVNQLNKFADKETLIQPLRCFLLESNSSVRWQAHCLTLH IYRNSSKSQQELLLDLMWSIWPELPAYGRKAAQFVDLLGYFSLK TPQTEKKLKEYSQKAVEILRTQNHILTNHPNSNIYNTLSGLVEF DGYYLESDPCLVCNNPSVPPCYIKLSSIKVDTRYTTTQQVVKLI GSHTISKVTVKIGDLKRTKMVRTINLYYNNRTVQAIVELKNKPA RWHKAKKVQLTPGQTFVKIDLPLIPIVASNLMIEFADPYENYQAS				VENIERLQLVSTLGLGEEDVCQEHGEKIYFFCEDDEMQLCVVCR
QGGDILRQRDEFDLLVAGEICRFSALIEELBEKNERPARBLLTD IRSTLIRCETRKCRKPVAVSPELGQRIRDFFQQALPLQRBMEMF LEKLCFELDYBPAHISLDPQTSHPKLLLSEDHQRAQFSYKWONS PDNPQRFDRATCVLAHTGITGGRHTWVSIDLAHGGSCTVGVVS EDVQRKGELRLRPEEGVWAVRLAWGFVSALGSFP\TRLTLKEQP RQVRVSLDYEVGWVTFTNAVTREPIYTFTASFTRKVIPFFGLWG RGSSFSLSS  5788 2 6860 EHSVSGRSSAYGDATAEGHPAGPGSVSSSTGAISTTTGHQEGDG SEGEGEGETEGDVHTSNRLHMVRLMLLERLLQTLPQLRNVGGVR AIPYMQVILMLTTDLDGEDEKDKGALDNLLSQLIAELGMDKKDV SKKNERSALNEVHLVVWRLLSVFMSRTKSGSKSSICESSSLISS ATAAALLSGAVDYCLHVLKSLLEYWKSQQNDEBEVATSQLLKP HTTSSPPDMSPFFLRQYVKGHAADVFEAYTQLLTEMVLRLPYQI KKITDTNSRIPPPVFDHSWFYFLSEYLMIQQTFFVRRQVRKLLL FICGSKEKYRQLRDLHTLDS\HVRGIKKLLEEQGIFLRASVVTA SPQSALQYDTLISLMEHLKACAEIAAQRTINWQKFCIKDDSVLY FLLQVSFLVDEGVSPVLIQLLSCALCGSKVLRALAASSGSSSAS SSPAPVAASSGQATTQSKSSTKKSKKBEKEKEKEKDGETSGSQEDQ LCTALVNQLNKFADKETLIQFLRCFLLESNSSSVRWQAHCLTLH IYRNSSKSQQELLLDLMWSIWPELPAYGRKAQPVDLLGYFSLK TPQTEKKLKEYSQKAVEILRTQNHILTNHPNSNIYNTLSGLVEF DGYYLESDPCLVCNNPEVPFCYIKLSSIKVDTRYTTTQQVVKLI GSHTISKVTVKIGDLKRTKMVRTINLYYNNRTVQAIVELKNKPA RWHKAKKVQLTPGQTEVKIDLPPLYPSNIMMEFADPYENYQAS	1	1		EAGEHATHTMRFLEDAA\APYREQIHKCLKCLIKEREBIQEIQS
IRSTLIRCETRKCRKPVAVSPELGQRIRDFPQQALPLQREMKMF LEKLCFELDYBPAHISLDPQTSHPKLLLSEDHQRAQFSYKWQNS PDNPQRFDRATCVLAHTGITGGRHTWVVSIDLAHGGSCTVGVVS EDVQRKGELRLRPEESVWAVRLAWGFVSALGSFP\TRLTLKEQP RQVRVSLDYEVGWVTFTNAVTREPIYTFTASFTRKVIPFFGLWG RGSSFSLSS  5788 2 6860 EHSVSGRSSAYGDATAEGHPAGPGSVSSSTGAISTTTGHQEGDG SEGEGEGETEGDVHTSNRLHMVRLMLERLLQTLPQLRNVGGVR AIPYMQVILMLTTDLDGEDEKDKGALDNLLSQLIAELGMDKKDV SKKNERSALNEVHLVVMRLLSVFMSRTKSGSKSSICESSSLISS ATAAALLSSGAVDYCLHVLKSLLEYWKSQQNDEEPVATSQLLKP HTTSSPPDMSPPFLRQYVKGHAADVPEAYTQLLTEMVLRLPYQI KKITDTNSRIPPPVFDHSWFYFLSEYLMIQQTFFVRRQVRKLLL FICGSKEKYRQLRDLHTLDS\HVRGIKKLLEEQGIFLRASVVTA SPQSALQYDTLISLMEHLKACAEIAAQRTINWQKPCIKDDSVLY FLLQVSFLVDEGVSPVLLQLLSCALCGSKVLRALASSGSSSAS SSPAFVAASSGQATTQSKSSTKKSKKEEKEKDGETSGSQEDQ LCTALVNQLNKFADKETLIQFLRCFLLESNSSSVRWQAHCLITH IYRNSSKSQQELLLDLMWSIWPELPAYGRKAAQPVDLLGYFSLK TPQTEKKLKEYSGKAVEILRTQNHILITNHPNSNIYNTLSGLVEF DGYYLESDPCLVCNNPEVPFCYIKLSSIKVDTRYTTTQQVVKLI GSHTISKVTVNKIGDLKRTKMVRTINLYYNNRTVQAIVELKNKPA RWHKAKKVQLTPGQTEVKIDLPLPIVASNLMIEFADFYENYOAS	1			RENKRMQVLLTQVSTKRQQVISEFAHLRKFLEEQQSILLAQLES
LEKLCFELDYBPAHISLDPQTSHPKLLLSEDHQRAQFSYKWQNS PDNPQRFDRATCVLAHTGITGGRHTWVVSIDLAHGSCTVGVVS EDVQRKGELRRPEEGVWAVRLAWGFVSALGSFP\TRLTLKEOP RQVRVSLDYEVGWVTFTNAVTREPIYTFTASFTRKVIPFFGLWG RGSSFSLSS  5788 2 6860 EHSVSGRSSAYGDATAEGHPAGPGSVSSSTGAISTTTGHQEGDG SEGEGEGETEGDVHTSNRLHMVRLMLLERLLQTLPQLRNVGGVR AIPYMQVILMLTTDLDGEDEKDKGALDNLLSQLIAELGMDKKDV SKKNERSALNEVHLVVMRLLSVFMSRTKSGSKSSICESSSLISS ATAAALLSSGAVDYCLHVLKSLLEYWKSQONDEEPVATSQLLKP HTTSSPPDMSPFFLRQYVKGHAADVPEAYTQLLTEMVLRLPYQI KKITDTNSRIPPPVFDHSWFYFLSEYLMIQQTPFVRRQVRKLLL FICGSKEKYRQLRDLHTLDS\HVRGIKKLLEEQGIFLRASVVTA SPQSALQYDTLISLMEHLKACAEIAAQRTINWQKFCIKDDSVLY FLLQVSFLVDEGVSPVLLQLLSCALCGSKVLRALAASSGSSSAS SSPAEVAASSGQATTQSKSSTKKSKKEEKEKEKDGETSGSQEDQ LCTALVNQLNKFADKETLIOPLRCFLLESNSSSVRWQAHCLTLH IYRNSSKSQQELLLDLMWSIWPELPAYGRKAAQFVDLLGYFSLK TPQTEKKLKEYSGKAVEILRTQNHILTNHPNSNIYNTLSGLVEF DGYYLESDPCLVCNNPEVPPCYIKLSSIKVDTRYTTTQQVVKLI GSHTISKVTVKIGDLKRTKMVRTINLYYNNRTVQAIVELKNKPA RWHKAKKVQLTPGQTEVKJDLPLIVASNIMIEFFADFYENYQAS	1 1			TPSTLIPGETBYCRYDYAIGDELCONTERPROCATE PLANTING
PDNPQRFDRATCVLAHTGITGGRHTWVSIDLAHGGSCTVGVVS EDVQRKGELRLRPEEGVWAVRLAWGFVSALGSFP\TRLTILKEQP RQVRVSLDYEVGWVTFTNAVTREPIYTFTASFTRKVIPPFGLWG RGSSFSLSS  5788 2 6860 EHSVSGRSSAYGDATAEGHPAGPGSVSSSTGAISTTTGHQEGDG SEGEGEGETEGDVHTSNRLHMVRLMLLERLLQTLPQLRNVGGVR AIPYMQVILMLTTDLDGEDEKDKGALDNILSQLIAELGMDKKDV SKKNERSALNEVHLVVMRLLSVFMSRTKSGSKSSICESSSLISS ATAAALLSSGAVDYCLHVLKSLLEYWKSQQNDEEPVATSQLLKP HTTSSPPDMSPFFLRQYVKGHAADVFEAYTQLLTEMVLRLPYQI KKITDTNSRIPPPVFDHSWFYFLSEYLMIQOTPFVRRQVRKLLL FICGSKEKYRQLRDLHTLDS\HVRGIKKLLEEQGIFLRASVVTA SPQSALQYDTLISIMEHLKACAEIAAQRTINWQKFCIKDDSVLY FLLQVSFLVDEGVSPVLLQLLSCALCGSKVLRALAASSGSSSAS SSPAPVAASGQATTQSKSSTKKSKKEKEKEKEKDGETSGSQBDQ LCTALVNQLNKFADKETLIOPLRCFLLESNSSVRWQAHCLTLH IYRNSSKSQQELLLDLMWSIWPELPAYGRKAAQFVDLLGYFSLK TPQTEKKLKEYSQKAVEILRTQNHILTNHPNSNIYNTLSGLVEF DGYYLESDPCLVCNNPEVPPCYIKLSSIKVDTRYTTTQQVVKKI GSHTISKVTVKIGDLKRTKMVRTINLYYNNRTVQAIVELKNKPA RWHKAKKVQLTFGQTEVKJDLPLIVASNLMIEFFADFYENYQAS	] ]			LEKI CEEL DYERANTSI DROTSURVI I CERUCAR ARGUMANA
EDVQRKGELRLRPEGWAVRLAWGFVSALGSFP\TRLTLKEQP RQVRVSLDYEVGWVTFTNAVTREPIYTFTASFTRKVIPFFGLWG RGSSFSLSS  EHSVSGRSSAYGDATAEGHPAGPGSVSSSTGAISTTTGHQEGDG SEGEGEGETEGDVHTSNRLHMVRLMLLERLLQTLPQLRNVGGVR AIPYMQVILMLTTDLDGEDEKDKGALDNLLSQLIAELGMDKKDV SKKNERSALNEVHLVVMRLLSVFMSRTKSGSKSICESSSLISS ATAAALLSSGAVDYCLHVLKSLLEYWKSQONDEEPVATSQLLKP HTTSSPPDMSPFFLRQYVKGHAADVFEAYTQLLTEMVLRLPYQI KKITDTNSRIPPPVFDHSWFYFLSEYLMIQQTPFVRRQVRKLLL FICGSKEKYRQLRDLHTLDS\HVRGIKKLLEEQGIFLRASVVTA SPQSALQYDTLISLMEHLKACAEIAAQRTINWQKPCIKDDSVLY FLLQVSFLVDEGVSPVLLQLLSCALCGSKVLRALAASSGSSSAS SSPAPVAASSGQATTQSKSSTKKSKKEKEKEKDGETSGSQBDQ LCTALVNQLNKFADKETLIOPLRCFFLLESNSSVRWQAHCLTLH IYRNSSKSQQELLLDLMWSIWPELPAYGRKAAQFVDLLGYFSLK TPQTEKKLKEYSQKAVEILRTQNHILTNHPNSNIYNTLSGLVEF DGYYLESDPCLVCNNPEVPFCYIKLSSIKVDTRYTTTQQVVKLI GSHTISKVTVKIGDLKRTKMVRTINLYYNNRTVQAIVELKNKPA RWHKAKKVQLTFGQTEVKJDLPLIVASNLMIEFFADFYENYQAS	1 1	ĺ	•	PDNPOR FDRATCVI.AHTGITGGBUTDANGTDI AUGGGGTTGIAG
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HNDMPIYEAADKALKTFQEEFMPVETFSEFLDVAGLLSEITDPE  SFLKDLLNSVP  LPLHAVEKTGRPGQPALKMPGKLRSDAGLESDTAMKKGETLRKQ  TEEKEKKEKPKSDKTEEIAEEEETVPPKAKQVKKKAEPSEVDMN SPKSKKAKK,KEEPSGODISPKTKSLRKKKEPIEKKVVSSKTKK VTKNEEPSEEIDAPKPKKKKKEKEMNGETREKS PKLKNGFPHP EPDCDRSEAASEESNSEIEGEIPVEQKEG\AFSMFPISEETIKL LKGRGVTFLFPIQAKTFHHVYSGKDLIAQARTGTGKTFSFAIPL IEKLHG\ELQDRKRGRAPQVLVLAPTRELANQVSKDFSDITKKL SVACFYGGTPYGGQFEMMRNGIDILVGTPGRIKDHIQNGKLDLT KLMHVVLDEVDQMLDMGFADQVEEILSVAYKKDSEDNPQTLLFS ATCPHWVFNVAKKYMKSTYEQVDLIGKKTQKTAITVEHLAIKCH WYQRAAVIGDVIRVYSGHQGRTIIFCETKKEAQELSONSAIKQD AQSLHGDIPQKQREITLKGFRNGSFGVLVATNVARARGLDIPEVD LVIQSSPPKDVESYIHRSGRTGRAGRTGVCICFYQHKEEYQLVQ VEQKAGIKFKRIGVPSATEIIKASSKDAIRLLDSVPPTAISHFK QSAEKLIEEKGAVEALAAALAHISGATSVDQRSLINSNVGFVTM ILQCSIEMPNISYAWKELKEQLGEEIDSKVKGMVFLKGKLGVCF DVPTASVTEIQEKMIDSRRWQLSVATEQPELEGPREGYGGFRGQ REGSRGFRGQRDGNRRFRGQREGSRGPRGRSGGGNKSNRSQNK GQKRSFSKAFGQ  5790 3786 1585 ARRQRDFLQALRRENQELKQQVDSLLSESQLKEALEPNKRQHIY QRCIQLKQAIDENNALQKLSKADESAPVANNNQRKEEEHTLLD KLTQQLQGLAVTISRENITEVGAPTEEEBESESEDSDGGEEB DAEEEBERKEENESHKWSTGEEYIAVGDFTAQQVGDLTFKKGEI LLVIEKKPDGWWIAKDAKGNEGLVPRTYLEPYSEEEEGQESSEE GSEEDVEAVDETADGAEVK\QRTDPHNSAVQKAISEAGIFCLVN	1			KDYSAYRSSIJ.FWALUDI.TVNMPVVVDTENTPOGNOGGI ABUTA
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1 2407  LPLHAVEKTGRPGQPALKMPGKLRSDAGLESDTAMKKGETLRKQ TEEKEKKEKPKSDKTEEIAEEEETVPPKAKQVKKKAEPSEVDMN SPKSKKAKK\KEEPSQMDISPKTKSLRKKKEPIEKKVVSSKTKK VTKNEEPSEEEIDAPKPKKMKKEKEMNGETREKSPKLKNGFPHP EPDCNPSEAASEESNSSIEGEIPVEQKEG\AFSNFPISEETIKL LKGRGVTFLFPIQAKTFHHVYSGKDLIAQARTGTGKTFSFAIPL IRKLHG\ELQDRKRGRAPQVLVLAPTRELANQVSKDFSDITKKL SVACFYGGTPYGGQFERMRNGIDILVGTPGRIKDHIQNGKLDLT KLNHVVLDEVDQMLDMGFADQVEEILSVAYKKDSEDNPQTLLFS ATCPHWYFNVAKKYMKSTYEQVDLIGKKTQKTAITVEHLAIKCH WTQRAAVIGDVIRVYSGHQGRTIIFCETKKEAQELSQNSAIKQD AQSLKGDIPQKQREITLKGFRNGSFGVLVATNVAARGLDIPEVD LVVQSSPPKOVESYHRSGRTGRAGRTGVCICFYQHKEEYQLVQ VEQKAGIKFKRIGVPSATEIIKASSKDAIRLLDSVPPTAISHFK QSAEKLIEEKGAVEALAAALAHISGATSVDQRSLINSNVGFVTM ILQCSIEMPNISYAWKELKEQLGEEIDSKVKGMVFLKGKLGVCF DVPTASVTEIQEKWHDSRRWQLSVATEQPELEGPREGYGGFRGQ REGSRGFRGQRDGNRRFRGQREGSRGPRGQRSGGGNKSNRSQNK GQKRSFSKAFGQ GGKRSFSKAFGQ ARRQRDFLQALRRRNQELKQQVDSLLSESQLKEALEPNKRQHIY QRCIQLKQAIDENKNALQKLSKADESAPVANYNQRKEEEHTLLD KLTQQLGGLAVTISRENITEVGAPTEEEBESESEDSEDSGGEEE DAEEEEBEKEENESHKWSTGEEYIAVGDFTAQQVGDLTFKKGEII LLVIEKKPDGWWIAKDAKGNEGLVPRTYLEPYSEEEEGQESSEE	1 1	1		SFLKDLLNSVD
TEEKEKKEKPKSDKTEIAEEEETVFPKAKQVKKKAEPSEVDMN SPKSKKAKKKEPSQNIISPKTKSLRKKKEPIEKKVVSSKTKK VTKNEEPSEEIDAPKPKKMKKEKEMNGETREKSPKLKNGPPHP EPDCNPSEAASEESNSEIRQEIPVEQKEG\AFSNFPISEETIKL LKGRGVTFLFPIQAKTFHHVYSGKDLIAQARTGTGKTFSFAIPL IEKLHG\ELQDRKRGRAPQVLVLAPTRELANQVSKDFSDITKKL SVACFYGGTPYGGQFERMNGIDILVGTPGRIKDHTQNGKLDLT KLNHVVLDEVDQMLDMGFADQVEEILSVAYKKDSEDNPQTLLFS ATCPHWYFNVAKKYMKSTYEQVDLIGKKTQKTAITVEHLAIKCH WTQRAAVIGDVIRVYSGHQGRTIIFCETKKEAQELSQNSAIKQD AQSLHGDIPQKOREITLKGFRNGSFGVLVATNVAARGLDIPEVD LVIQSSPPKDVESYIHRSGRTGRAGRTGVCICFYQHKEEYQLVQ VEQKAGIKFKRIGVPSATEIIKASSKDAIRLLDSVPPTAISHFK QSAEKLIEEKGAVEALAAALAHTSGATSVDQRSLINSNVGFVTM ILQCSIEMPNISYAWKELKEQLGEEIDSKVKGMVFLKGKLGVCF DVPTASVTEIQEKWHDSRRWQLSVATEQPELEGPREGYGGFRGQ REGSRGFRGQRDGNRFFRGQREGSRGPRGQRSGGNKSNRSQNK GQKRSFSKAFGQ  5790 3786 1585 ARRQRDPLQALRRRNQELKQQVDSLLSESQLKEALEPNKRQHIY QRCIQLKQAIDENKNALQKLSKADESAPVANYNQRKEEEHTLLD KLTQQLQGLAVTISRENITEVGAPTEEEBESESEDSEDSGGEEE DAEEEEBEKEENESHKWSTGEEYIAVGDFTAQQVGDLTFKKGEII LLVIEKKPDGWWIAKDAKGNEGLVPRTYLEPYSEEEBEGQESSEE GSEEDVEAVDETADGAEVK\QRTDPHMSAVQKAISEAGIFCLVN	5789	1	2407	
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VTKNEEPSEEIDAPKPKKMKKEKEMNGETREKS PKLKNGPPHP EPDCNPSEAASEESNSEIEGEIPVEQKEG\AFSNFPISEETIKL LKGRGVTFLFPIQAKTFHHVYSGKDLIAQARTGTGKTFSFAIPL IEKLHG\LQDRKRGRAPQVLVLAPTRELANQVSKDFSDITKKL SVACFYGGTPYGGOFERMRNGIDILVGTPGRIKDHIQNGKLDLT KLNHVVLDEVDQMLDMGFADQVEEILSVAYKKDSEDNPQTLLFS ATCPHWYFNVAKKYMKSTYEQVDLIGKKTQKTAITVEHLAIKCH WTQRAAVIGDVIRVYSGHQGRTIIFCETKKEAGELSQNSAIKQD AQSLHGDIPQKQREITLKGFRNGSFGVLVATNVAARGLDIPEVD LVIQSSPFKDVESYIHRSGRTGRAGRTGVCICFYQHKEEYQLVQ VEQKAGIKFKRIGVPSATEIIKASSKDAIRLLDSVPPTAISHFK QSAEKLIEEKGAVEALAAALAHISGATSVDQRSLINSNVGFVTM ILQCSIEMPNISYAWKELKEQLGEEIDSKVKGMVFLKGKLGVCF DVPTASVTEIQEKWHDSRRWQLSVATEQPELEGPREGYGFRGQ REGSRGFRGQROGNRRFRGQREGSRGPRGQRSGGGNKSNRSQNK GQKRSFSKAFGQ  5790 3786 1585 ARRQRDPLQALRRRNQELKQQVDSLLSESQLKEALEPNKRQHIY QRCIQLKQAIDENKNALQKLSKADESAPVANYNQRKEEEHTLLD KLTQQLQGLAVTISRENITEVGAPTEEEBESESEDSEDSGGEEE DAEEEBEKEENESHKWSTGEEYIAVGDFTAQQVGDITFKKGEI LLVIEKKPDGWWIAKDAKGNEGLVPRTYLEPYSEEEBGGESSEE				SPKSKKAKK KERRSONDI SPYTKSI PYKKERTERKOKOKOKOK
EPDCNPSEAASEESNSEIEQEIPVEQKEG\AFSNFPISEETIKL  LKGRGVTFLFPIQAKTFHHVYSGKDLIAQARTGTGKTFSFAIPL  IEKLHG\ELQDRKRGRAPQVLVLAPTRELANQVSKDFSDITKKL  SVACFYGGTPYGGQFERMRNGIDILVGTPGRIKDHIQNGKLDLT  KLNHVVLDEVDQMLDMGFADQVEEILSVAYKKDSEDNPQTLLFS  ATCPHWVFNVAKKYMKSTYEQVDLIGKKTQKTAITVEHLAIKCH  WTQRAAVIGDVIRVYSGHQGRTIIFCETKKEAQELSQNSAIKQD  AQSLHGDIPQKQRRITLKGFRNGSFGVLVATNVAARGLDIPEVD  LVIQSSPPKDVESYIHRSGHTGRAGRTGVCICFYQHKEEYQLVQ  VEQKAGIKFKRIGVPSATEIIKASSKDAIRLLDSVPPTAISHFK  QSAEKLIEEKGAVEALAAALAHISGATSVDQRSLINSNVGFVTM  ILQCSIEMPNISYAWKELKEQLGEEIDSKVKGMVPLKGKLGVCF  DVPTASVTEIQEKWHDSRRWQLSVATEQPELEGPREGYGGFRGQ  REGSRGFRGQRDGNRRFRGQREGSRGPRGQRSGGNKSNRSQNK  GQKRSFSKAFGQ  5790  3786  1585  ARRQRDPLQALRRRNQELKQQVDSLLSESQLKEALEPNKRQHIY  QRCIQLKQAIDENKNALQKLSKADESAPVANYNQRKEEEHTLLD  KLTQQLQGLAVTISRENITEVGAPTEEEBESESEDSEDSGGEEE  DAEEEBEKEENESHKWSTGEEYIAVGDFTAQQVGDLTFKKGEI  LLVIEKKPDGWWIAKDAKGNEGLVPRTYLEPYSEEEBGQESSEE  GSEEDVEAVOETADGAEVK\QRTDPHWSAVQKAISEAGIFCLVN	1			VTKNEEPSEERIDAPKPKKKKEKEMMGETBERG DEL VMGPDUD
LKGRGVTFLFPIQAKTFHHVYSGKDLIAQARTGTGKTFSFAIPL  IEKLHG\ELQDRKRGRAPQVIVIAPTRELANQVSKDFSDITKKL  SVACFYGGTPYGGQFERMRNGIDILVGTPGRIKDHIQNGKLDLT  KLMHVVLDEVDQMLDMGFADQVEEILSVAYKKDSEDNPQTLLFS  ATCPHWVFNVAKKYMKSTYEQVDLIGKKTQKTAITVEHLAIKCH  WTQRAAVIGDVIRVYSGHQGRTIIFCETKKEAQELSQNSAIKQD  AQSLHGDIPQKOREITLKGFRNGSFGTUVATNVAARGLDIPEVD  LVIQSSPPKDVESYIHRSGRTGRAGRTGVCICFYQHKEEYQLVQ  VEQKAGIKFKRIGVPSATEIIKASSKDAIRLLDSVPPTAISHFK  QSAEKLIEEKGAVEALAAALAHISGATSVDQRSLINSNVGFVTM  ILQCSIEMPNISYAWKELKEQLGEEIDSKVKGMVFLKGKLGVCF  DVPTASVTEIQEKWHDSRRWQLSVATEQPELEGPREGYGGFRGQ  REGSRGFRGQROGNRRFRGQREGSRGFRGQRSGGNKSNRSQNK  GQKRSFSKAFGQ  5790  3786  1585  ARRQRDFLQALRRRNQELKQQVDSLLSESQLKEALEPNKRQHIY  QRCIQLKQAIDENKNALQKLSKADESAPVANYNQRKEEEHTLLD  KLTQQLQGLAVTISRENITEVGAPTEEEBESESEDSEDSGGEEB  DAEEEEBEKEENESHKWSTGEEYIAVGDFTAQQVGDLTFKKGEI  LLVIEKKPDGWWIAKDAKGNEGLVPRTYLEPYSEEEBGQESSEE  GSEEDVEAVOETADGAEVK\QRTDPHWSAVQKAISEAGIFCLVN	1			EPDCNPSEAASRESNSETROET DUFOKEG \ APCNEDT CERTIFIC
IRKLHG\ELQDRKRGRAPQVLVLAPTRELANQVSKDFSDITKKL  SVACFYGGTPYGGGFERMRNGIDILVGTPGRIKDHIQNGKLDLT  KLNHVVLDEVDQMLDMGFADQVEEILSVAYKKDSBDNPQTLLFS  ATCPHWVFNVAKKYMKSTYEQVDLIGKKTQKTAITVEHLAIKCH  WTQRAPYIGDVIRVYSGHQGRTIIFCETKKEAQELSQNSAIKQD  AQSLHGDIPQKQREITLKGFRNGSFGVLVATNVAARGLDIPEVD  LVIQSSPPKDVESYIHRSGRTGRAGRTGVCICFYQHKEEYQLVQ  VEQKAGIKFKRIGVPSATEIIKASSKDAIRLLDSVPPTAISHFK  QSAEKLIEEKGAVVBALAAAALAHISGATSVDQRSLINSNVGFVTM  ILQCSIEMPNISYAWKELKEQLGEEIDSKVKGMVFLKGKLGVCF  DVPTASVTEIQEKWHDSRRWQLSVATEQPELEGPREGYGGFRGQ  REGSRGFRGQROONRRFRGQREGSRGPRGQRSGGNKSNRSQNK  GQKRSFSKAFGQ  5790  3786  1585  ARRQRDPLQALRRRNQELKQQVDSLLSESQLKEALEPNKRQHIY  QRCIQLKQAIDENKNALQKLSKADESAPVANYNQRKEEEHTLLD  KLTQQLQGLAVTISRENITEVGAPTEEEBESESEDSBDSGGEEB  DAEEEBEKEENESHKWSTGEEYIAVGDFTAQQVGDLTFKKGEI  LLVIEKKPDGWNIAKDAKGNEGLVPRTYLEPYSEEEBGGESSEE  GSEEDVEAVDETADGAEVK\QRTDPHWSAVQKAISEAGIFCLVN	ļ .			LKGRGVTFLFPIOAKTEHHUVSGKDI.TAOADTCTCVTDCCATAT
SVACFYGGTPYGGQFERMRNGIDILVGTPGRIKDHIQNGKLDLT KLNHVVLDEVDQMLDMGFADQVEEILSVAYKKDSEDNPQTLLFS ATCPHWVFNVAKKYMKSTYEQVDLIGKKTQKTAITVEHLAIKCH WTQRAVIGDVIRVYSGHQGRTIIFCETKKEAQELSQNSAIKQD AQSLHGDIPQKORBITLKGFRNGSFGVLVATNVAARGLDIPEVD LVIQSSPPKDVESYIHRSGRTGRAGRTGVCICFYQHKEEYQLVQ VEQKAGIKFKRIGVPSATEIIKASSKDAIRLLDSVPPTAISHFK QSAEKLIEEKGAVEALAAALAHISGATSVDQRSLINSNVGFVTM ILQCSIEMPNISYAWKELKEQLGEEIDSKVKGMVFLKGKLGVCF DVPTASVTEIQEKWHDSRRWQLSVATEQPELEGPREGYGGFRGQ REGSRGFRGQROGNRRFRGQREGSRGPRGQRSGGMKSNRSQNK GQKRSFSKAFGQ  5790 3786 1585 ARRQRDPLQALRRRNQELKQQVDSLLSESQLKEALEPNKRQHIY QRCIQLKQAIDENKNALQKLSKADESAPVANYNQRKEEEHTLLD KLTQQLQGLAVTISRENITEVGAPTEEEBESESEDSBDSGGEEB DAEEEEBEKEENESHKWSTGEEYIAVGDFTAQQVGDLTFKKGEI LLVIEKKPDGWMIAKDAKGNEGLVPRTYLEPYSEEEBGGESSEE GSEEDVEAVDETADGAEVK\QRTDPHWSAVQKAISEAGIFCLVN	1 1	j		IEKI-HG\ELODRKPGPADOVI-VI-ADTRELANOVEVDEDTTWVV
KLNHVVLDEVDQMLDMGFADQVEEILSVAYKKDSEDNPQTLLFS ATCPHWYFNVAKKYMKSTYEQVDLIGKKTQKTAITVEHLAIKCH WTQRAAVIGDVIRVYSGHQGRTIIFCETKKEAQELSQNSAIKQD AQSLHGDIPQKQREITLKGFRNGSFGVLVATNVAARGLDIPEVD LVJQSSPPKDVESYIHRSGRTGRAGRTGVCICFYQHKEEYQLVQ VEQKAGIKFKRIGVPSATEIIKASSKDAIRLLDSVPPTAISHFK QSAEKLIEEKGAVEALAAALAHISGATSVDQRSLINSNVGFVTM ILQCSIEMPNISVAWKELKEQLGEEIDSKVKGMVFLKGKLGVCF DVPTASVTEIQEKWHDSRRWQLSVATEQPELEGPREGYGGFRGQ REGSRGFRGQRDGNRRFRGQREGSRGPRGQRSGGNKSNRSQNK GQKRSFSKAFGQ  5790 3786 1585 ARRQRDFLQALRRRNQELKQQVDSLLSESQLKEALEPNKRQHIY QRCIQLKQAIDENKNALQKLSKADESAPVANYNQRKEEEHTLLD KLTQQLQGLAVTISRENITEVGAPTEEEBESESEDSEDSGGEEE DAEEEBEKEENESHKWSTGEEYIAVGDFTAQQVGDITFKKGEI LLVIEKKPDGWWIAKDAKGNEGLVPRTYLEPYSEEEBGGESSEE GSEEDVEAVVDETADGAEVK\QRTDPHWSAVQKAISEAGIFCLVN	[			
ATCPHWYPNAKKYMKSTYEQVDLIGKKTQKTAITVEHLAIKCH WTQRAAVIGDVIRVYSGHQGRTIIFCETKKEAQELSQNSAIKQD AQSLHGDIPQKQREITLKGFRNGSFGVLVATNVAARGLDIPEVD LVIQSSPPKDVESYIHRSGRTGRAGRTGVCICFYQHKEEYQLVQ VEQKAGIKFKRIGVPSATEIIKASSKDAIRLLDSVPPTAISHFK QSAEKLIEEKGAVEALAAALAHISGATSVDQRSLINSNVGFVTM ILQCSIEMPNISYAWKELKEQLGEEIDSKVKGMVFLKGKLGVCF DVPTASVTEIQEKWHDSRRWQLSVATEQPELEGPREGYGGFRGQ REGSRGFRGQRDGNRRFRGQREGSRGPRGQRSGGNKSNRSQNK GQKRSFSKAFGQ  5790 3786 1585 ARRQRDFLQALRRRNQELKQQVDSLLSESQLKEALEPNKRQHIY QRCIQLKQAIDENKNALQKLSKADESAPVANYNQRKEEEHTLLD KLTQQLQGLAVTISRENITEVGAPTEEEBESESEDSEDSGGEEE DAEEEBEKEENESHKWSTGEEYIAVGDFTAQQVGDITFKKGEI LLVIEKKPDGWWIAKDAKGNEGLVPRTYLEPYSEEEBGGESSEE GSEEDVEAVOETADGAEVK\QRTDPHWSAVQKAISEAGIFCLVN		}		
WTQRAAVIGDVIRVYSGHQGRTIIFCETKKEAQELSQNSAIKQD AQSLHGDIPQKQREIITKGFRNGSFGYLVATNVAARGLDIPEVD LVIQSSPPKDVESYIHRSGHTGKAGRTGVCICFYQHKEEYQLVQ VEQKAGIKFKRIGVPSATEIIKASSKDAIRLLDSVPPTAISHFK QSAEKLIEEKGAVEALAAALAHISGATSVDQRSLINSNVGFVTM ILQCSIEMPNISYAWKELKEQLGEEIDSKVKGMVFLKGKLGVCF DVPTASVTEIQEKWHDSRRWQLSVATEQPELEGPREGYGGFRGQ REGSRGFRGQRDGNRRFRGQREGSRGPRGQRSGGNKSNRSQNK GQKRSFSKAFGQ  5790 3786 1585 ARRQRDFLQALRRRNQELKQQVDSLLSESQLKEALEPNKRQHIY QRCIQLKQAIDENKNALQKLSKADESAPVANYNQRKEEEHTLLD KLTQQLQGLAVTISRENITEVGAPTEEEBESESEDSEDSGGEEE DAEEEEBEKEENESHKWSTGEEYIAVGDFTAQQVGDLTFKKGEI LLVIEKKPDGWWIAKDAKGNEGLVPRTYLEPYSEEEBGQESSEE GSEEDVEAVDETADGAEVK\QRTDPHWSAVQKAISEAGIFCLVN		Ī		ATCPHWYFNVAKKYMKSTYFOVDI TCKKTOKOKOK TOUBUR A TOOL
AQSLHGDIPQKQREITLKGFRNGSFGVLVATNVAARGLDIPEVD LVIQSSPKDVESYIHRSGRTGRAGRTGVCICFYQHKEEYQLVQ VEQKAGIKFKRIGVPSATEIIKASSKDAIRLLDSVPPTAISHFK QSAEKLIEEKGAVEALAAALAHISGATSVDQRSLINSNVGFVTM ILQCSIEMPNISYAWKELKEQLGEEIDSKVKGMVPLKGKLGVCF DVPTASVTEIQEKWHDSRRWQLSVATEQPELEGPREGYGGFRGQ REGSRGFRGQRDGNRRFRGQREGSRGPRGQRSGGGNKSNRSQNK GQKRSFSKAFGQ  5790 3786 1585 ARRQRDPLQALRRRNQELKQQVDSLLSESQLKEALEPNKRQHIY QRCIQLKQAIDENKNALQKLSKADESAPVANYNQRKEEEHTLLD KLTQQLQGLAVTISRENITEVGAPTEEEBESESEDSBDSGGEEE DAEEEEBEKEENESHKWSTGEEYIAVGDFTAQQVGDLTPKKGEI LLVIEKKPDGWHIAKDAKGNEGLVPRTYLEPYSEEEBGGESSEE GSEEDVEAVDETADGAEVK\QRTDPHWSAVQKAISEAGIFCLVN				WTORAAVIGDVIRVYSGHOGRTIIECETVVENOET CONG-
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GPLGPPGLPGFAGNPGPPGLPGMKGDPG FPGIPGTPGPPGLPGLQGPVGPPGFTGI GLSFQGPKGDKGDQGVSGPPGVPGQAGY BPGFQGMPGVGEKGEPGKPGPRGKPGKF YPGLIGRQGP\QCEKGEAGPPGPPGIVI	/QEKGDFATKGEKGQKG OGDKGEKGSPGFPGEPG IGTGPLGEKGERGYPGT
GPLGPPGLPGFAGNPGPPGLPGMKGDPC FPG1PGTPGPPGLPGLQGPVGPPGFTGI GLSFQGPKGDKGDQGVSGPPGVPGQAQY EPGFQGMPGVGEKGEPGKPGRPGKPGKP YPGL1GRQGP\QGEKGEAGPPGPPGIV1 PGPRGEPGPKGFPGLPGQPCGPPGLPVPC	VQEKGDFATKGEKGQKG DGDKGEKGSPGFPGEPG KGTGPLGEKGERGYPGT GQAGAPGFPGERGEKGD
GPLGPPGLPGFAGNPGPPGLPGMKGDPC FPG1PGTPGPPGLPGLQGPVGPPGFTGI GLSFQGPKGDKGDQGVSGPPGPPGAQQV EPGFQGMPGVGEKGEPGKPGRFGKPGKL YPGL1GRQGP\QGEKGEAGPPGPPGIV1 PGPRGEPGPKGFFGLPGQPGPPGLPVPC RGFPGTSLPGPSGRDGLPGPPGSPGPPG	VQEKGDFATKGEKGQKG DGDKGEKGSPGFPGEPG KGTGPLGEKGERGYPGT SQAGAPGFPGERGEKGD SQPGYTNGIVECOPGPP
GPLGPPGLPGFAGNPGPPGLPGMKGDPC FPG1PGTPGPPGLPGLQGPVGPPGFTGI GLSFQGPKGDKGDQGVSGPPGVPGQAQY EPGFQGMPGVGEKGEPGKPGRPGKPGKP YPGL1GRQGP\QGEKGEAGPPGPPGIV1 PGPRGEPGPKGFPGLPGQPCGPPGLPVPC	/QEKGDFATKGEKGQKG DODKGEKGSPGFPGEPG GTGPLGEKGERGYPGT EQAGAPGFPGERGEKGD EQPGYTNGIVECQPGPP ELICDIDGYRGPPGPOG

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ļ	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
Ĭ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
J	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence	•	\=possible nucleotide insertion)
			GEPGEFYFDLRLKGDKGDPGFPGQPGMPGRAGSPGRDGHPGLPG
ĺ			PKGSPGSVGLKGERGPPGGVGFPGSRGDTGPPGPPGYGPAGPIG
1	1		DKGQAGFPGGPGSPGLPGPKGEPGKIVPLPGPPGAEGLPGSPGF
1			PGPQGDRGFPGTPGR\PGL\PGBKGAVG\QPGIGFPGPPGPKGV
1			DGLPGDMGPPGTPGRPGFNGLPGNPGVQGQKGEPGVGLPGLKGL
			PGLPGIPGTPGEKGSIGVPGVPGEHGAIGPPGLQGIRGEPGPPG
			LPGSVGSPGVPGIGPPGARGPPGGOGPPGLSGPPGIKGEKGFPG
1	1		FPGLDMPGPKGDKGAQGLPGITGOSGLPGLPGOOGAPGTPGFPG
			SKGEMGVMGTPGQPGSPGPWGAPGLPGEKGD\HGFPGSSGPPGD
		•	PGLKGDKGDVGLPGKPGSMDKVYMGSMKGOKGDOGEKGOTGDTG
	1		EKGSRGDPGTPGVPGKDGQAGQPGQPGPKGDPGISGTPGAPGIP
	1		GPKGSVGGMGLPGTPGEKGVPGIPGPOGSPGLPGDKGAKGEKGO
Ī			AGPPGIGIPGLRGEKGDQGIAGFPGSPGEKGEKGSIGIPGMPGS
		+	PGLKGSPGSVGYPGSPGLPGEKGDKGLPGLDG1PGVKGEAGL2G
			TPGPTGPAGQKGEPGSDGIPGSAGEKGEPGLPGRGFPGFPGAKG
			DKGSKGEVGFPGLAGSPGIPGSKGEQGFMGPPGPQGQPGLPGSP GHATEGPKGDRGPQGQPGLPGLPGPMGPPGLPGIDGVKGDKGNP
1			GWPGAPGVPGPKGDPGFQGMPGIGGSPGITGSKGDMGPPGVPGF
i	1		QGPKGLPGLQGIKGDQGDQGVPGAKGLPGPPGPPGPYDIIKGEP
	ľ		GLPGPEGPPGLKGLQGLPGPKGQQGVTGLVGIPGPPGFIDIIKGEP
	İ		PGQKGEMGPAGPTGPRGFPGPPGPDGLPGSMGPPGTPSVDHGFL
			VTRHSQTIDDPQCPSGTKILYHGYSLLYVOGNERAHGODLGTAG
			SCLRKFSTMPFLFCNINNVCNFASRNDYSYWLSTPEPMPMSMAD
			ITGENIRPFISRCAVCEAPAMVMAVHSOTIOTPPCPSGWSSIWT
			GYSFVMHTSAGAEGSGQALASPGSCLEEFRSAPFIECHGRGTCN
1			YYANAYSFWLATIERSEMFKKPTPSTLKAGELRTHVSRCQVCMR
5795	1192	61	STRSPTVEYISAHPHILFMLLKGYEAPQIALRCGIMLRECIRHE
			PLAKIILFSNQFRDFFKYVELSTFDIASDAFATFKDLLTRHKVL
1	1.		VADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDRHN
			FAIMTKYISKPENLKLMMNLLRDKSPNIOFEAFHVFKVFVASDH
1 1			KTQPIVEILLKNQPKLIEFLSSFQKERTDDEOFADEKNYLIKOI
5796			RDLKKTAP*RALRDSKR
3/96	2	1078	GRVGWELWCMYISPPKDWWDAGDPSLPIRTPAMIGCSFVVNRKF
1			FGEIGLLDPGMDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIE
1 1			RKKKPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENP
1 • 1			GIDIGDVSERRALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGE LRNNKAKDVCLDQGPLENHTAILYPCHGWGPQLARYTKEGFLHL
1	ł		GALGTTILLPDTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQ
1 1			NGAIMNKGTGRCLEVENRGLAGIDLILRSCTGQRWTIKNSIK*R
	j		EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASPG
5305			QHRDPG
5797	2	891	PRVRQKTLVDVTLENSNIKDQIRNLQQTYEASMDKLREKQRQLE
			VAQVENQLLKMKVESSQEANAEVMREMTKKLYSQYEEKI.OFFOR
] ]			KHSAEKEALLEETNSFLKAIERANKKMQAAEISLEEKDQRIGEL
. 1			DRLIERMEKERHQLQLLEHETEMSGELTDSDKERYQQLEEAS
			ASLRERIRHLNDMVHCQQKKVKQMVEEIESLKKKLQQKQLLILQ
l: I			LLEKISFLEGENNELQSRLDYLTETQAKTEVETREIGVGCDLLP
5798	644	115	SQTGRTREIVMPSRNYTPYTRVLELTMKKTLT KILGSRWKSMSNQEKQPYYEEQARLSKIHLEKYPNYKYKPRPKR
1 1			TCIVDGKKLRIGEYKQLMRSRRQEMRQFFTVGQQPQIPITTGTG
			VVYPGAITMATTTPSPQMTSDCSSTSASPEPSLPVIQSTYGMKT
ليييا		·	DGGSLAGNEMINGEDEMEMYDDYEDDPKSDYSSENEAPEAVSAN
5799	2679	1435	LLSTYIKFINLFPETKATIQGVLRAGSOLRNADVELOORAVRYI.
	1		TLSSVASTDVLATVLEEMPPFPERESSILAKLKRKKGPGAGSAL
	ľ	ſ	DDGRRDPSSNDINGGMEPTPSTVSTPSPSADLLGLRAAPPPAAP
١. [		•	PASAGAGNLLVDVFDGPAAQPSLGPTPEEAFLSPGPRDTGPPTP
	1	j	EADELLNKFVCKNNGVLFENOLLOIGVKSEFRONLGRMYLFYCN
	1	l	KTSVQFQNFSPTVVHPGDLQTQLAVQTKRVAAQVDGGAQVQQVI.
		ŀ	NIECLRDFLTPPLLSVRFRYGGAPQALTLKLPVTINKFFQPTEM
	<u>-</u> <u>.</u>		AAQDFFQRWKQLSLPQQEAQKIFKANHPMDAEVTKAKLLGFGSA

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ł	corresponding	to first	L-Leucinc, M=Methionine, N=Asparagine,
1	to first	amino acid	P-Proline, Q-Glutamine, R-Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
i	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion.
	sequence	_	\=possible nucleotide insertion)
			LLDNVDPNPENFVGAGIIQTKALQVGCLLRLEPNAQAQMYRLTL
ļ		į	RTSKEPVSRHLCELLAQQF
5800	2679	1435	LLSTYIKFINLFPETKATIQGVLRAGSQLRNADVELQQRAVEYL
-			TLSSVASTDVLATVLEEMPPFPERESSILAKLKRKKGPGAGSAL
			DDGRRDPSSNDINGGMEPTPSTVSTPSPSADLLGLRAAPPPAAP
1		ļ	PASAGAGNLLVDVFDGPAAQPSLGPTPBEAFLSPGPEDIGPPIP
1		ĺ	EADELLNKFVCKNNGVLFENQLLQIGVKSEFRQNLGRMYLFYGN
		ĺ	KTSVQFQNFSPTVVHPGDLQTQLAVQTKRVAAQVDGGAQVQQVL
			NIECLRDFLTPPLLSVRFRYGGAPQALTLKLPVTINKFFQPTEM
		•	AAQDFFQRWKQLSLPQQEAQKIFKANHPMDAEVTKAKLLGFGSA
.	Į.	ĺ	LLDNVDPNPENFVGAGIIQTKALQVGCLLRLEPNAQAQMYRLTL
			RTSKEPVSRHLCELLAQOF
5801	3	1413	FPRLYHLIPDGEITSIKINRVDPSESLSIRLVGGSETPLVHIII
1			QHIYRDGVIARDGRLLPGDIILKVNGMDISNVPHNYAVRLLRQP
1	1		CQVLWLTVMREQKFRSRNNGQAPDAYRPRDDSFHVILNKSSPEE
1			QLGIKLVRKVDEPGVFIFNVLDGGVAYRHGQLEENDRVLAINGH
ſ	<b>i</b>		DLRYGSPESAAHLIQASERRVHLVVSRQVRQRSPDIFQEAGWNS
1	1		NGSWSPGPGERSNTPKPLHPTITCHEKVVNIQKDPGESLGMTVA
1			GGASHREWDLPIYVISVEPGGVISRDGRIKTGDILLNVDGVELT
l			BVSRSEAVALLKRTSSSIVLKALEVKEYEPQEDCSSPAALDSNH
ŀ			NMAPPSDWSPSWVMWLELPRCLYNCKDIVLRRNTAGSLGFCIVG
ļ	,		GYEEYNGNKPFFIKSIVEGTPAYNDGRIRCGDILLAVNGRSTSG
l			MIHACLARLLKELKGRITLTIVSWPGTFL
5802	3	290	CFSLYQIMERIMDLPTLLRHAFREMFSVGGLFWMFRIRIILCLM
1			GAFFYLISPLDFVPEALFGILGFLDDFFVIFLLIYISIMYREV
	l		ITQRLTR
5803	2234	1299	EAQFGTTAEIYAYREEQDFGIEIVKVKAIGRQRFKVLELRTQSD
			GIQQAKVQILPECVLPSTMSAVQLESLNKCQIFPSKPVSREDQC
			SYKWWQKYQKRKFHCANLTSWPRWLYSLYDAETLMDRIKKQLRE
i .			WDENLKDDSLPSNPIDFSYRVAACLPIDDVLRIQLLKIGSAIQR
			LRCELDIMNKCTSLCCKQCQETEITTKNEIFSLSLCGPMAAYVN
			PHGYVHETLTVYKACNLNLIGRPSTEHSWFPGYAWTVAQCKICA
1	}		SHIGWKFTATKKDMSPQKFWGLTRSALLPTIPDTEDEISPDKVI
			rcr ·
5804	2	1707	EMEKQRQEEQRKRTEEERKRRIEQDMLEKRKIQRELAKRAEQIE
ŀ			DINNTGTESASEEGDDSLLITVVPVKSYKTSGKMKKNFEDLEKE
i i			REBKERIKYEEDKRIRYEEQRPSLKEAKCLSLVMDDEIESEAKK
ł			ESLSPGKLKLTFEELERQRQENRKKQAEEEARKRLEEEKRAFEE
			ARROMVNEDEENODTAKIFKGYRPGKLKLSFEEMERORREDEKR
			KAEEEARRRIEEEKKAFAEARRNMVVDDDSPEMYKTISQEFLTP
	ļ		GKLEINFEELLKOKMEEEKRRTEEERKHKLENEKOEFEOLROEM
į l	1		GEEEEENETFGLSREYEELIKLKRSGSIOAKNLKSKFRKIGOLS
1	ì		EKEIQKKIEEERARRRAIDLEIKEREAENFHEEDDVDVRPARKS
	1		EAPFTHKVNMKARFEQMAKAREEEEGRRIBEOKLLRMOPEOREI
]	. [		DAALQKKREEEEEEGSIMNGSTAEDEEQTRSGAPWFKKPLKNT
]	ĺ		SVVDSEPVRFTVKVTGEPKPEITWWFEGEILQDGEDYQYIERGE
لسيجيا			TYCLYLPETFPEDGGEYMCKAVNNKGSAASTCILTIESKN
5805	3	776	YISDTLGQVYKSKIRWWIEENGGNGNISVDDLTALLDLAEHASS
1			AFKESQQQSBDREYEVKERLYPKSKRRYDTYNIAGYQGEIEVGL
		ļ	YTIQILQLIPFFDNKNELSKRYMVNFVSGSSDIPGDPNNBYKLA
		ļ	LKNYIPYLTKLKFSLKKSFDFFDEYFVLLKPRNNIKQNEEAKTR
ļ l	]		RKVAGYFKKYVDIFCLLEESQNNTGLGSKFSBPLQVERCRRNLV
<u></u> -	·		ALKADKFSGLLEYLIKSQEDAISTMKCIVNEYTFLLK
5806	1257	877	AVFTFHNHGRTANLYSLHSWLGITTVFLFACQRFLGFAVFLLPW
			ASMWLRSLLKPIHVFFGAAILSLSIASVISGINEKLFFSLKNTT
			RPYHSLPSEAVFANSTGMLVVAFGLLVLYILLASSWKRP
5807	2267	1302	RFSKKTFRRPMAVDIQPACLGLYCGKTLLFKNGSTEIYGECGVC
	1		PRGQRTNAQKYCQPCTESPELYDWLYLGFMAMLPLVLHWFFIEW
		ł	YSGKKSSSALFQHITALFECSMAAIITLLVSDPVGVLYIRSCRV
			LMLSDWYTMLYNPSPDYVTTVHCTHEAVYPLYTIVFIYYAFCLV

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(AmAlanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H-Histidine, I=Isoleucine, K-Lysine,
	corresponding	to first	Lalousing Manhieria & Ralysine,
ĺ	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
Ī	amino acid	residue of	P-Proline, Q-Glutamine, R-Arginine,
	residue of		S=Serine, T=Threonine, V=Valine,
1	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ŀ	1	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
1			LMMLLRPLLVKKIACGLGKSDRFKSIYAALYFFPILTVLQAVGG
į.	j	}	GLLYYAFPYIILVLSLVTLAVYMSASBIENCYDLLVRKKRLIVL
		1	FSHWLLHAYGIISISRVDKLEQDLPLLALVPTPALFYLFTAKFT
L	<u></u>		EPSRILSEGANGH
5808	2	433	SLPDSGVVEYLSNGGVADNHKDFGELRYNECLMNFSCNGKNGSS
1			EGRITHGFQLKSAYENNLMPYTNYTFDFKGVIDYIFYSKTHMNV
ı	İ		LGVLGPLDPQWLVENNITGCPHPHIPSDHFSLLTQLELHPPLLP
1			LVNGVHLPNRR
5809	464	2422	ILVPGFQG1LHPGVYCALQSQHQAQELVADIDECEVSGLCRHGG
j		1	RCVNTHG9FECYCMDGYLPRNGPEPFHPTTDATSCTEIDCGTPP
{	ĺ	(	PURDOUTION TO COMPANY OF THE TOTAL CONTROL OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF THE PURDOUTION OF TH
1			EVPDGYIIGNYTSSLGSQVRYACREGFFSVPEDTVSSCTGLGTW
1			ESPKLHCQEINCGNPPEMRHAILVGNHSSRLGGVARYVCQEGFE
			SPGGKITSVCTEKGTWRESTLTCTEILTKINDVSLFNDTCVRWQ
			INSRRINPKISYVISIKGORLDPMESVREETVNLTTDSRTPEVC
	]		LALYPGTNYTVNISTAPPRRSMPAVIGFQTAEVDLLEDDGSFNI
]			SIFNETCLKLNRRSRKVGSEHMYQFTVLGQRWYLANFSHATSFN
]			FTTREQVPVVCLDLYPTTDYTVNVTLLRSPKRHSVQITIATPPA
			VKQTISNISGFNETCLRWRSIKTADMEEMYLFHIWGQRWYQKEF
1			AQEMTFNISSSSRDPEVCLDLRPGTNYNVSLRALSSELPVVISL
1 .			TTQITEPPLPEVEFFTVHRGPLPRLRLRKAKEKNGPISSYQVLV
			LPLALQSTFSCDSEGASSFFSNASDADGYVAAELLAKDVPDDAM
1 1			EIPIGDRLYYGEYYNAPLKRGSDYCIILRITSEWNKVRRHSCAV
			WAQVKDSSLMLLQMAGVGLGSLAVVIILTFLSFSAV
5810	3	1641	KVFGTHKDHEVSTLDTAISAVKVQLAEFLENLQEKSLRIEAFVS
l i			BIESFFNTIEENCSKNEKRLEEQNEEMMKKVLAQYDEKAQSFEE
			VKKKKMEFLHEQMVHFLQSMDTAKDTLETIVREAEELDEAVFLT
i I			SFEEINERLLSAMESTASLEKMPAAFSLFEHYDDSSARSDOMLK
1 :1			QVAVPQPPRLEPQEPNSATSTTIAVYWSMNKEDVIDSFQVYCME
1 1			EPQDDQEVNELVEEYRLTVKESYCIFEDLEPDRCYQVWVMAVNF
1 1			TGCSLPSERAIFRTAPSTPVIRAEDCTVCWNTATIRWRPTTPBA
			TETYTLEYCRQHSPEGEGLRSFSGIKGLQLKVNLQPNDNYFFYV
1 1			RAINAFGTSEQSEAALISTRGTRFLLLRETAHPALHISSSGTVI
1 1	}		SFGERRRLTEIPSVLGEELPSCGQHYWETTVTDCPAYRLGICSS
1 1	· 1		SAVOAGALGOCETCHUMIGOEDORUMETIVIDCPAYRLGICSS
1	i		SAVQAGALGQGETSWYMHCSEPQRYTFFYSGIVSDVHVTERPAR
1			VGILLDYNNQRLIFINAESEQLLFIIRHRFNEGVHPAFALEKPG
5811	1918	851	KCTLHLGIRPPDSVRHK
	-5-0	931	AAALADPLPEDKWSAEKRRPLKSSLGYEITFSLLNPDPKSHDVY
ł I	I		WDIEGAVRRYVQPFLNALGAAGNFSVDSQILYYAMLGVNPRFDS
1 1	ł	1	ASSSYYLDMHSLPHVINPVESRLGSSAASLYPVLNFLLYVPELA
j [	1	ļ	HSPLYIQDKDGAPVATNAFHSPRWGGIMVYNVDSKTYNASVLPV
		ì	RVEVDMVRVMEVFLAQLRLLFGIAQPQLPPKCLLSGPTSEGLMT
[ }			WELDRLLWARSVENLATATTTLTSLAQLLGKISNIVIKDDVASE
j !	1		VYKAVAAVQKSAEELASGHLASAFVASQEAVTSSELAFFDPSLL
, ,	ļ		HLLYFPDDQKFAIYIPLFLPMAVPILLSLVKIFLETRKSWRKPE
J-6077			KTD
5812	5204	2744	GGRQRCQRGRSCGAREBEVEPGTARPPPAASAMDASLEKIADPT
[		1	LAEMGKNLKEAVKMLEDSQRRTEEENGKKLISGDIPGPLOGSGO
		1	DMVSILQLVQNLMHGDEDEEPQSPRIQNIGECGHMALLGHSLGA
j ĺ		1	YISTLDKEKLRKLTTRILSDTTLWLCRIFRYENGCAYFHREERE
	1		GLAKICRLAIHSRYEDFVVDGFNVLYNKKPVIYLSAAARPGLGO
	ł		YLCNQLGLPFPCLCRVPCNTVFGSQHQMDVAFLEKLIKDDIERG
			RLPLLLVANAGTAAVGHTDKIGRLKELCEQYGIWLHVEGVNLAT
	1		LALGYVSSSVLAAAKCDSMTMTPGPWLGLPAVPAVTLYKHDDPA
<b>!</b>	1	}	LTLVAGLTSNKPTDKLRALPLWLSLQYLGLDGPVERIKHACQLS
1	1	1	QRLQESLKKVNYIKILVEDELSSPVVVFRFFQELPGSDPVFKAV
			PVPNMTPSGVGRERHSCDALNRWLGEQLKQLVPASGLTVMDLEA
1	1		EGTCLRFSPLMTAAVLGTRGEDVDQLVACIESKLPVLCCTLQLR
1	İ		ERFKOEVEATAGLI.VUDDDNUGGTOURDVEURADDVAGA
1			EEFKQEVEATAGLLYVDDPNWSGIGVVRYEHANDDKSSLKSYPQ
ŀ	ł	1	GENIHAGLLKKLNELESDLTFKIGPEYKSMKSCLYVGMASDNVH
		1	AAELVETIAATAREIEDNSRLLENMTEVVRKGIQEAQVELQKAS
			EERLLEEGVLRQIPVVGSVLNWFSPVQALQKGRTFNLTAGSLES

SEQ	Predicted	Predicted end	Design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and design and
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
ţ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W-Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence	-	\=possible nucleotide insertion)
			TEPIYVYKAQGAGVTLPPTPSGSRTKQRLPGQKPFKRSLRGSDA
		}	LSETSSVSHIEDLEKVERLSSGPEQITLEASSTEGHPGAPSPQH
L			TDQTEAFQKGVPHPEDDHSQVEGPESLR
5813	2936	699	HRDGVSGSLERPLTDRSRTGAFAQQRGKMATAGGGSGADPGSRG
1		ļ	LLRLLSPCVLLAGLCRGNSVERKIYIPLNKTAPCVRLLNATHQI
İ		ĺ	GCQSSISGDTGVIHVVEKEEDLQWVLTDGPNPPYMVLLESKHFT
	•		RDLMEKLKGRTSRIAGLAVSLTKPSPASGFSPSVQCPNDGFGVY
ł			SNSYGPEFAHCREIQWNSLGNGLAYEDFSFPIFLLEDENETWYT
i			KQCYQDHNLSQNGSAPTFPLCAMQLFSHMAWLSFSTAT\CMRRS
Į			SIQSTFSINPKIVCDPLSDYNVWSMLKPINTTGTLKPDDPLAGA
ľ	i		ATRLDSRSFFWNV\APGAESAVASFVTOLAAAEALOKAPDUTTI.
1	1		PRNVMFVFFQGETFDYIGSSRMVYDMEKGKFPVQLENVDSFVEL
1			GQVALRTSLELWMHTDPVSQKNESVRNOVEDLLATLEKSGAGUP
			AVILRRPNQSQPLPPSSLQRFLRARNISGVVLADHSGAFHNKVV
			QSIYDTAENINVSYPEWLEPLKE/ETWNFG*ODTAKALADVATV
1	l		LGRALYELAGGTNFSDTVQADPOTVTRLLYG\FLIKANNSWEGG
1	l i		ILQGRDLRSYLG*RGLFQH\YLAV\SSPTNTIYV/VI.OYALANI.
			TGTVVNLTREQCQDPSKVPSENKDLYEYSWVOGPLHSNETDRID
1			RCVRSTARLARALSPAFELSQWSSTEYSTWTESRWKDIRARIRI
j j	ļ		IASKELELITLTVGFGILIFSLIVTYCINAKADVLFIAPREPGA
5814	8500		VSY
1	0500	432	ALKCRPRRVLAILVGPVQPDRMAEEGAVAVCVRVRPLMSREESL
i			GETAQVYWKTHNNVIYPVDGSKSFNFDRVLHGNETPKNVYEA\I
1 1			AAPIIDSAIQGYNGTIFA\YGQT\ASGKTYTMMGSEDHLGVIPQ
	ł		GQFHGHPSQKI+EVFLDREFLLRVSYMEIYNBTITDLLCGTQKM
1 1			KPLIIREDVNRNVYVADLTEEVVYTSEMALKWITKGEKSRHYGE
			TKMNQRSSRSHTIFRMILESREKGEPSNCEGSVKVSHLNLVDLA
1			GSERAAQTGAAGVRLKEGCNINRSLFILGQVIKKLSDGQVGGFI
1 [	·		NYRDSKLTRILQNSLGGNPKTRIICTITPVSFDETLTALQFAST
			AKYMKNTPYVNEVSTDEALLKRYRKEIMDLKKQLEEVSLETRAQ AMEKDQLAQLLEEKDLLQKVQNEKIENLTRMLVTSSSLTLQQEL
1 1			KAKRKRRVTWCLGKINKMKNSNYADQFNIPTNITTKTHKLSINL
1 1			LREIDESVCSESDVFSNTLDTLSEIEWNPATKLLNQENIESELN
			SLRADYDNLVLDYEQLRTEKEEMELKLKEKNDLDEFEALERKTK
1 1	•		KDQEMQLIHEISNLKNLVKHREVYNQDLENELSSKVELLREKED
	i		QIKKLQEYIDSQKLENIKMDLSYSLBSIEDPKQMKQTLFDAETV
1 1	•		ALDAKRESAFLRSENLELKEKMKELATTYKOMENDIOLYOSOLE
1 1	1		AKKKMQVDLEKELQSAFNEITKLTSLIDGKVPKDLLCNLFLEGK
]	1		ITDLQKELNKEVEENEALREEVILLSELKSLPSEVERLEKETOD
1			KSEELHIITSEKDKLFSEVVHKESRVOGLLEEIGKTKDDLATTO
1 1		į	SNYKSTDQEFQNFKTLHMDFEQKYKMVLEENERMNOEIVNLSKE
1 [			AQKFDSSLGALKTELSYKTOELOEKTREVOERINEMEOLUROLE
	1		NRDSPLQTVEREKTLITEKLOOTLEEVKTLTOEKDDI.KOLOFGI.
] !	1		Q1ERDQLKSDIHDTVNMNIDTQEOLRNALESLKOHOETINTLKS
		İ	KISEEVSRNLHMEENTGETKDEFQQKMVGIDKKQDLEAKNTQTL
1 1		1	TADVKDNEI I EQQRKIFSLIQEKNELQQMLESVIAEKEQLKTDL
1 1			KENIEMTIENQEELRLLGDELKKQQEIVAQEKNHAIKKEGELSR
i	1	ł	TCDRLAEVEEKLKEKSQQLQEKQQQLLNVQEEMSEMQKKINEIE
1		1	NLKNELKNKELTLEHMETERLELAQKLNENYEEVKSITKERKVL
1			KELQKSFETERDHLRGYIREIEATGLQTKEELKIAHIHLKEHQE
	1	}	TIDELRRSVSEKTAQI INTQDLEKSHTKLQEEIPVLHEEQELLP
/ 1			NVKKVSETQETMNELELLTEQSTTKDSTTLARIEMERLRLNEKF
	<b>!</b>	Í	QESQEEIKSLTKERDNLKTIKEALEVKHDQLKEHIRETLAKIQE
i i	İ		SQSKQEQSLNMKEKDNETTKIVSEMEQFKPKDSALLRIEIEMLG
	l		LSKRLQESHDEMKSVAKEKDDLQRLQEVLQSESDQLKENIKEIV
ſ			AKHLETEELKVAHCCLKEQEETINELRVNLSEKETEISTIQKQ
			LEAINDKLQNKIQEIYEKEEQLNIKQISEVQEKVNELKQFKEHR
	ł	i	KAKDSALQSIESKMLELTNRLQESQEEIQIMIKEKEEMKRVQEA
			LQIERDQLKENTKEIVAKMKESQEKEYQFLKMTAVNETQEKMCE
	•	l.	IEHLKEQFETQKLNLENIETENIRLTQILHENLEEMRSVTKERD DLRSVBETLKVERDQLKENLRETITRDLBKQEBLKIVHMHLKEH

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
Ī	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine.
į	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ŀ	amino acid	sequence	Codon, /=possible nucleotide deletion.
L	sequence		\=possible nucleotide insertion)
			QETIDKLRGIVSEKTNEISNMQKDLEHSNDALKAQDLKIQEELR
			IAHMHLKEQQETIDKLRGIVSEKTDKLSNMOKDLENSNAKLOEK
1			IQELKANEHQLITLKKOVNETQKKVSEMEQLKKOIKDOSLTLSK
1			LEIENLNLAQKLHENLEEMKSVMKERDNLRRVEETLKLERDOLK
1			ESLQETKARDLEIQQELKTARMLSKEHKETVDKLREKISEKTIQ
		1	ISDIQKDLDKSKDELQKKIQELQKKELQLLRVKEDVNMSHKKIN
	İ		EMEQLKKQFEPNYLCKCEMDNFQLTKKLHESLEEIRIVAKERDE
1		1	LRRIKESLKMERDQFIATLREMIARDRQNHQVKPEKRLLSDGQQ
			HLMESLREKCSRIKELLKRYSEMDDHYECLNRLSLDLEKEIEFH
1	ĺ	ĺ	RIMKKLKYVLSYVTKIKEEQHECINKFEMDFIDEVBKQKELLIK
		ĺ	IQHLQQDCDVPSRBLRDLKLNQNMDLHIEEILKDFSESEFPSIK
			TEFQQVLSNRKEMTQFLEEWLNTRFDIEKLKNGIQKENDRICQV
	•		NNFFNNRIIAIMNESTEFEERSATISKEWEQDLKSLKEKNEKLF KNYQTLKTSLASGAQVNPTTQDNKNPHVTSRATQLTTEKIRELE
1			NSLHEAKESAMHKESKIIKMQKELEVINDIIAKLQAKVHESNKC
1			LEKTKETIQVLQDKVALGAKPYKEBIEDLKMKLGKIDLEKMKNA
			KEFEKEISATKATVEYQKEVIRLLRENLRRSQQAQDTSVISEHT
1			DPQPSNKPLTCGGGSGIVQNTKALILKSEHIRLEKEISKLKQQN
i i			RQLIKQKNELLSNNQHLSNEVKTWKERTLKREAHKOVTCENSPK
ł			SPKVTGTASKKKQITPSQCKERNLODPVPKESPKSCPFDSRSKS
1			LPSPHPVRYFDNSSLGLCPEVQNAGAESVDSQP\GPWARLFQGK
5815	23		DVP\ECKTQ
3013	ده	1460	SELVMWTVQNRESLGLLSFPVMITMVCCAHSTNEPSNMSYVKET
ļ			VDRLLKGYDIRLRPDFGGPPVDVGMRIDVASIDMVSEVNMDYTL
			TMYFQQSWKDKRLSYSGIPLNLTLDNRVADQLWVPDTYFLNDKK SFVHGVTVKNRMIRLHPDGTVLYGLRITTTAACMMDLRRYPLDE
			CNCTLEIESYGYTTDDIEFYWNGGEGAVTGVNKIELPQFSIVDY
			KMVSKKVEFTTGAYPRLSLSFRLKRNIGYFILQTYMPSTLITIL
			SWVSFWINYDASAARVALGITTVLTMTTISTHLRETLPKIPYVK
			AIDIYLMGCFVFVFLALLEYAFVNYIFFGKGPOKKGASKODOSA
1		•	NEKNKLEMNKVQVDAHGNILLSTLEIRNETSGSKVLTSVSDPKA
1 1	ļ		TMYSYDSASIQYRKPLSSRE\A*GRAPDRHGVPSKGRIRRRAS\
5816	861	707	QLKVKIPDLTDVNSIDKWSRMFFPITFSLFNVVYWLYYVH
	1	191	TSSRSRAAQEGDAETPGSVERRGRRAGAEDGMSQAPGAQPSPP
			TVYHERORLELCAVHALNNVLQQQLFSQEAADHICKRLAPDSRL NPHRSLLGTGNYDVNVIMAALQGLGLAAVWWDRRRPLSQLALPQ
•	i		VLGLILNLPSPVSLGLLSLPLRRRHLRWPCARL/VTVSYYNLDS
!!!			K\LRAPEGPGGLRTE*GPFLAAALAQGLCEVLLVVTKEVEEKG
			SWLRTD
5817	851	118	RLFRGPGANRGRSCRGCSGGREPSGGALPKRHCPC*PPSPPAAD
l l			VMSNTTVPNAPQANSDSMVGYVLGPFFLITLVGVVVAVVMYVOK
	Į		KKRVDRLRHHLLPMYSYDPAEELHEAEQELLSDMGDPKVV\QAG
	i		RVATSTSGCHCWMSRRDLTPLPHPSEPGVLDCLGPCHLLPLLSP
i j			GSPCWVLGLHFSLHPPSAASASHALTITSLPPGLLPFVGVELTA
5818	3	3918	HPQALMGRGFPSGMAAAGRHLCFL
	Ĭ	3916	QALRDKLWIFLVQSFYAVRHTESWKLMSTDDQQKIQAAAFDKGD
		•	DRRIGKKPIFSSSQQRKQVSDSGDIKIKSWRGNNKKECWSYLST
			NKKMKSDGLGASGHSSSTNRNSINKTLKQDDVKEKDGTKIASKI TKELKTGGKNVSGKPKTVTKSKTENGDKARLENMSPRQVVERSA
.[	l		TAAAAATGQKNLLNGKGVRNQEGQISGARPKVLTGNLNVQAKAK
		1	PLKKATGKDSPCLSIAGPSSRSTDSSMEFSISTECLDEPKENGS
J			TEEEKPSGHKLSFCDSPGQMMKNSVDSVKNSTVAIKSRPVSRVT
			NGTSNKKSIHEQDTNVNNSVLKKVSGKGCSEPVPQAILKKRGTS
			NGCTAAQQRTKSTPSNLTKTQGSQGESPNSVKSSVSSRQSDENV
- 1			AKLDHNTTTEKQAPKRKMVKQVHTALPKVNAKIVAMPKNLNOSK
	1	}	KGETLNNKDSKQKMPPGQVISKTQPSSQRPLKHETSTVQKSMPH
			DVRDNNNKDSVSEQKPHKPLINLASEISDAEALOSSCRP\DPOK
[			PLNDQEKEKLALECQNISKLDKSLKHELESKQICLDKSETKFPN
}	ŀ	1	HKETDDCDAANICCHSVGSDNVNSKFYSTTALKYMVSNPNENSL
}			NSNPVCDLDSTSAGQIHLISDRENQVGRKDTNKQSSIKCVEDVS
			LCNPERTNGTLNSAQEDKKSKVPVEGLTIPSKLSDESAMDEDKH

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lvsine
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine
	amino acid residue of	residue of	S=Serine, T=Threonine, V=Valine,
	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	sequence	Codon, /=possible nucleotice deletion,
<b></b>		<del></del>	\=possible nucleotide insertion)
ļ			ATADSDVSSKCFSGQLSEKNSPKNMETSESPESHETPETPFVGH WNLSTGVLHQRESPESDTGSATTSSDDIKPRSEDYDAGGSQDDD
i			GSNDRGISKCGTMLCHDFLGRSSSDTSTPEELKIYDSNLRIEVK
Ī			MKKQSSNDLFQVNSTSDDEIPRKRPEIWSRSAIVHSRERENIPR
j	İ	1	GSVQFAQEIDQVSSSADETEDERSEAENVAENFSISNPAPQQFQ
1			GIINLAFEDATENECREFSANKKFKRSVLLSVDECRELGSDEGE
			VHTPFQASVDSFSPSDVFDGISHEHHGRTCYSRFSRESEDNILE
			CKONKGNSVCKNESTVLDLSSIDSSRKNKOSVSATEKKNTIDVI.
1		İ	SSRSRQLLREDKKVNNGSNVENDIQQRSKFLDSDVKSQERPCHL
1			DLHQREPNSDIPKNSSTKSLDSFRSQVLPQEGPVKESHSTTTEK
1		1	ANIALSAGDIDDCDTLAQTRMYDHRPSKTLSPIYEMDVIEAFEQ
ł		ĺ	KVESETHVTDMDF*DDQHFAKQDWTLLKQLLSEQDSNLDVTNSV PEDLSLAQYLINQTLLLARDSSKPQGITHIDTLNRWSELTSPLD
ı	İ		SSASITMASFSSEDCSPQGEWTILELETQH
5819	1	5557	AAAGLIGALHLVMTLVVAAARAEKEAFVQSESIIEVLRFDDGGL
			LQTETTLGLSSYQQKSISLYRGNCRPIRFEPPMLDFHEOPVGMP
			KMEKVYLHNPSSE*TITLVSIFATTSHFHASFFONRKILPGGNT
1			SFDVS/VFLARVVGNVENTLFINTSNHGVFTY\OVFGVGVPNPY
	,	i	RLRPFLGARVTVNSSFSPIINIHNPHSEPLQVVEMYSSGGDLHL
ĺ			BLPTGQQGGTRKLWEIPPYETKGVMRASFSSREADNHTAFIRIK
1			TNASDSTEFIILPVEVEVTTAPGIYSSTEMLDFGTLRTQDLPKV LNLHLLNSGTKDVPITSVRPTPQ\NDAITVHFKPITLKAS\ESK
	. 1		YTKVASISFDASKAKKPSQFSGKITVKAKEKSYSKLEIPYQAEV
1	-		LDGYLGFDHAATLFHIRDSPADPVERPIYLTHTFSFAILIHDVL
ł			LPEEAKTMFKVHNFSKPVLILPNESGYIFTLLFMPSTSSMHIDN
			NILLITNASKPHLPVRVYTGFLDYFVLPPKIEERFIDFGVLSAT
			EASNILFAIINSNPIELAIKSWHIIGDG\LSIELVAVDRGNRTT
İ			IISSLPECEKSSSSDQSSVTLASGYF\AVFRVKLTAKKL\EGTH
1	}		DGAIQITTDYELLTIPVK\AVIAVGSLTCSPKHVVLPPSFPGKI
1	}		VHQSLNIMNSFSQKVKIQQIRSLSBDVRFYYKRLRGNKEDLEPG KKSKIANIYFDPGLQCGDHCYVGLPFLSKSEPKVQPGVAMQEDM
	ľ		WDADWDLHQSLFKGWTGIKENSGHRLSAIFEVNTDLQKNIISKI
			TABLSWPSILSSPRHLKFPLTNTNCSS\EEEITLENP/SQDVPV
			YVQFIPLALYSNPSVFVDKLVSRFNLSKVAKIDLRTLEFOVFRN
			SAHPLQSSTGFMEG\LSPHLILNLILKPGEKKSVKVK\FTPVHN
1 1			RTVSSLIIVRNNLTVMDAVMVQGQGTTENLRVAGKLPGPGSSLR
			FKITEALLKDCTDSLKLREPNFTLKRTFKVENTGQLQIHIETIE
			ISGYSCEGYGFKVVNCQEFTLSANASRDIIILFTFDFTASRVIR ELKFITTSGSEFVFILNASLPYHMLATCAEALPRPNWELALYII
1	,	ļ	ISGIMSALFLLVIGTA\YLEAQGIWEP\FRRRLS\FEASNPPFD
1	1	1	VGRPFDLRRIVGISSEGNLNTLSCDPGHSRGFCGAGGSSSRPSA
i i			GSHKQ*GPSGHPHSSHSNRNSADVDDVRAYNSGRTSSMTSAOAA
		,	SSQPANKTRPLVLDSNTGAQGHSAGRKSKGAKOSOHGSOHHAHS
1	ł		PLEQHPQPPLPPPVPQPQEPQPERLSPAPLAHPSHPERASSARH
1 1			SSEDSDITSLIBAMDKDFDHHDSPALBVFTEQPPSPLPKSKGKG
1 1			KPLCRKVKPPKKQBEKEKKGKGKPQEDELKDSLADDDSSSTTTE
1 1			TSNPDTEPLLKEDTEKQKGKQAMPEKHESEMSQVKQKSKKLLNI KKEIPTDVKPSSLELPYTPPLESKQRRNLPSKIPLPTAMTSGSK
1			SRNAQKTKGTSKLVDNRPPALAKFLPNSQELGNTSSSEGEKDSP
<b>!</b>		1	PPEWDSVPVHKPGSSTDSLYKLSLQTLNADIFLKQRQTSPTPAS
] }	j		PSPPAAPCPFVARGSYSSIVNSSSSSDPKIKOPNGSKHKIJKAA
	ĺ	į	SLPGKNGNPTFAAVTAGYDKSPGGNGFAKVSSNKTGPSSSLGIS
			HAPVDSDGSDSSGLWSPVSNPSSPDFTPLNSFSAFGNSFNLTGE
			VFSKLGLSRSCNQASQRSWNEFNSGPSYLWESPATDPSPSWPAS
	ľ	1	SGSPTHTATSVLGNTSGLWSTTPFSSSIWSSNLSSALPFTTPAN
	ļ		TLASIGLMGTENSPAPHAPSTSSPADDLGQTYNPWRIWSPTIGR
5820	310		RSSDPWSNSHFPHEN RVSLSGPVSLGVLLCARSSTMGKRDNRVAYMNPIAMARSRGPIQ
		,0	SSGPTIQ\VI*IDQGLPGKK*KSN*KRKK/DSKALAEFEEKMN
			ENWKKELEKHREKLLSGSESSSKKRQRKKKEKKKSW*\DSSSS\
			SSSSDSSSSSSDSEDEDKKQGKRRKKKNRSHKSSESSMSETES
	· <u>-</u>		7 -

SEQ	Predicted	Predicted end	I bmino acid possess
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	E-Histidine, I-Isoleucine, K-Lysine,
ł	corresponding	to first	L-Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine.
	amino acid	residue of	S=Serine, T=Threonine, V=Valine.
i	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion.
	sequence		\=possible nucleotide insertion)
ŀ	Į.		DSKDSLKKKKKSKDGTEKEKDIKGLSKKRKMYSEDKPLSSESLS
1	1	ļ	ESEYIEEVRAKKKKSSEEREKATEKTKKKKKKKKKKKKKKKKKK
1			SSSPDSP*H*EKSGFPYKESAMSEEISTVKTTTYLLKCMNFLVF
5821	179	915	GIIPGLFSSHSDATV
	•••	913	KWRNQSWRWPKPGTNWMLSCSVCWRRVTWTGSVWMRKLGKHPQT
Ì			PT/IKDCSIAATGKRPSARFPHQRRKKRREMDDGLAEGGPQRSN TYVIKLFDRSVDLAQFSENTPLYPICRAWMRNSPSVRERECSPS
			SPLPPLPEDEEG\SEVTNSKSR*CVQACPPTHTPGGQPKNACR\
1			SRIPSPLAALRMQGTP*RWSPFEPEPSPSTLIYRNMQRWKRIRQ
			RWKEASHRNQLRYSESMKILREMYERQ
5822	464	4379	QTLKEMPIVMARDLEETASSSEDBEVISQEDHPCIMWTGGCRRI
1 1			PVLVFHADAILTKDNNIRVIGERYHLSYKIVRTDSRLVRSILTA
1 1	}		HGFHEVHPSSTDYNLMWTGSHLKPFLLRTLSEAQKVNHPPRSYE
			LTRKDRLYKNIIRMQHTHGFKAFHILPOTFLLPABYAEFCNSYS
1 .			KORGPWIVKPVASSRGRG\VYLINNPNOISLEENTLVSRVINND
1 1			LLIDDFKFDVRLYVLVTSYDPLVIYLYEEGLARFATVRYDOGAK
1 1			NIRNQFMHLTNYSVNKKSGDYVSCDDPEVEDYGNKWSMSAMLRV
1 1			LKQEGRDTTALMAHVEDLIIKTIISAELAIATACKTEVPHRSSC
!	-		FELYGFDVLIDSTLKPWLLEVNLSPSLACDAPLDLKIKASMISD
1			MFTVVGFVCQDPAQRASTRPIYPTFESSRRNPFQKPQRCRPLSA
			SDAEMKNLVGSAREKGPGKLGGSVLGLSMEEIKVLRRVKEENDR
			RGGFIRIFPTSETWEIYGSYLEHKTSMNYMLATRLFQDRMTADG APELKI*SLNSKAKLHAALYERKLLSLEVRKRRRSSRLRAMRP
1 1		•	KYPVITQPAEMNVKTETBSEBEBEEVALDNEDBEQEASQEBSAGF
	ł		LRENQAKYTPSLTALVENTPKENSMKVREWNNKGGHCCKLETQE
1 1	Í		LEPKFNLMQILQDNGNLSKMQARIAFSAYLQHVQI\RLMKDSGG
1 1	•		QTFSASWAAKEDEQMELVVRFLKRASNNLQHSLRMVLPSRRLAL
1 [	1		LERTRILAHQLGDFIIVYNKETEQMAEKKSKKKVEEEEEDGVNM
1 [	ļ		ENFORFIRQASEAELEEVLTFYTOKNKSASVFLGTHSKISKNYN
1			NYSDSGAKGDHPETIMEEVKIKPPKOOOTTEIHSDXLSRETTSA
] [	1		EKEAKLVYSNSSSGPTATLOKIPNTHLSSVTTSDLSPGDCHHSS
1			LSQIPSAIPSMPHQPTILLNTVSASASPCLHPGAONIPSDTCLD
1 1			RCRSGSHTIGPFSSFQSAAHIYSOKLSRPSSAKAGSCYLNKHHS
1			GIAKTQKEGEDASLYSKRYNQSMVTAELQRLAEKQAARQYSPSS
	,		HINLLTQQVTNLNLATGIINRSSASAPPTLRPIISPSGPTWSTQ
1 1			SDPOAPENHSSSPGSRSLQTGGFAWEGEVENNVYSQATGVVPOH KYHPTAGSYQLQFALQQLEQQKLQSRQLLDQSRARHQAIFGSQT
1			LPNSNLWTMNNGAGCRISSATASGQKPTTLPQKVVPPPSSCASL
] ]		j	VPKPPPNHEQVLRRATSQKASKGSAEGQLNGLQSSLNPAAPVP
<del> </del>			ITSSTDPAHTKIMNHKHTEKQPVHHSWVHD
5823	42	2293	LLTALSMEGGGGRDEPSACRAGDVNMDDPKKEDILLLADEKEDE
	ĺ	1	DLSLSSSANEDDEVFFGPFGHKERCTAASLELNNBUDDODDID
		ľ	TSESPFAWSPLAGEKFVEVYKEAHLLALHIESSSRNQAAQAAKP
			EDPRSQGVERFIQESKF\KINLFEKEKEMKKSPTST.KPETVVT.e
1			DSPLLGPPVGEPRLLASSPALPSSGAQARLTRAPGPPHSAHALP
1		}	RESCTAHAASQAATQRKPGTKLLLPRAASVRGRGIPGAAEKPKK
		ĺ	EIPASPSRTKIPABKESHRDVLPDKPAPGAVNVPAAGSHLGQGK RAIPVP\NKLGLKKTLLKAPGSYSN\LQRKSSSGA\VWSGASSA
		.	CTPQPVAKAKSSEFASIPAN*LPGLCPNISKS\GRMGPAMLRPA
			L\PAGPVG\ASSWQAKRVDVSELAAEQLTAPP\SASPTQPQTPE
1	1	i	GGG\QWLNSSCAWSESSQLNKTRSIRRRDSCLNSKTKVMDTDTN
		1	QFKIPKFSIGDS\PDSSTPKLSRAORPOSCTSVGRVTVHSTDVD
			RSSGPAPQSLLSAWRVSALPTPASRRCSGLPPMTPKTMPPAVGS
	1	1	PL\CVPARRRSSEPRKNSAMRTEPTRESNRKTDSR\LVDVSDDR
	1	3	GSPPSRVPQALNFSPEESDSTFSKSTATEVAREEAKPGGDAAPS
	1		EALLVDIKLEPLAVTPDAASOPLIDLPLIDFCDTPEAHVAVGGE
1		i	SRPLIDLMINTPDMNKNVAKPSPVVGQLIDLSSPLIQLSPEADK
5824	42		ENVDSPLLKF
1			LLTALSMEGGGGRDEPSACRAGDVMMDDPKKEDILLLADEKFDF DLSLSSSSANEDDEVFFGPFGHKERCIAASLELNNPVPEQPPLP
			TSESPFAWSPLAGEKFVEVYKEAHLLALHIESSSRNQAAQAAKP

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine
	location	corresponding	H=Histidine, I=Isoloucine, K=Lysine,
	corresponding to first	to first	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			EDPRSQGVERFIQESKF\KINLFEKEKEMKKSPTSLKRETYVLS
			DSPLLGPPVGEPRLLASSPALPSSGAOARLTRAPGPPHSAHAI.b
		•	RESCTAHAASQAATQRKPGTKLLLPRAASVRGRGIPGAAEKPKK
1			EIPASPSRTKIPAEKESHRDVLPDKPAPGAVNVPAAGSHLGQGK
1			RAIPVP\NKLGLKKTLLKAPGSYSN\LQRKSSSGA\VWSGASSA CTPQPVAKAKSSEFASIPAN+LPGLCPNISKS\GRMGPAMLRPA
		İ	L\PAGFYG\ASSWQAKRYDVSELAAEQLTAPP\SASPTQPQTPE
			GGG\QWLNSSCAWSESSQLNKTRSIRRRDSCLNSKTKVMPTPTN
			QFKIPKFSIGDS\PDSSTPKLSRAORPOSCTSVGRVTVHSTPVR
1	}	1	RSSGPAPQSLLSAWRVSALPTPASRRCSGLPPMTPKTMPRAVGS
1			PL\CVPARRRSSEPRKNSAMRTEPTRESNRKTDSR\LVDVSPDR
			GSPPSRVPQALNFSPEESDSTFSKSTATEVAREEAKPGGDAAPS
			EALLVDIKLEPLAVTPDAASQPLIDLPLIDFCDTPEAHVAVGSE SRPLIDLMTNTPDMNKNVAKPSPVVGQLIDLSSPLIQLSPEADK
L	ł		ENVDSPLLKF
5825	2	4210	FLQIESASPAPPSSGFLAAHPHSPGGSLATKGRSRLSAPGMLHL
	•		SAAPPAPPPEVTATARPCLCSVGRRGDGGKMAAAGALERSFVEI.
1			SGAERERPRHFREFTVCSIGTANAVAGAVKYSESAGGFYYVESG
			KLFSVTRNRFIHWKTSGDTLELMEESLDINLLNNAIRLKFONCS
	İ		VLPGGVYVSETQNRVIILMLTNQTVHRLLLPHPSRMYRSELVVD
	•		SQMQSIFTDIGKVDFTDPCNYQLIPAVPGISPNSTASTAWLSSD GEALFALPCASGGIFVLKLPPYDIPGMVSVVELKQSSVMQRLLT
			GWMPTAIRGDQSPSDRPLSLAVHCVEHDAFIFALCQDHKLRMWS
			YKEQMCLMVADMLEYVPVKKDLRLTAGTGHKLRLAYSPTMGLVT.
1		1	GIF\MHAPKRGQFCIFQLVSTESNRYSLDHISSLFTSOETLIDE
		}	ALTSTDIWALWHDAENQTVVKYINFEHNVAGQWNPVFMQPLPEE
[- ]			EIVIRDDQDPREMYLQSLFTPGQFTNEALCKALQIFCRGTERNL
			DLSWSELKKEVTLAVENELQGSVTEYEFSQEEFRNLQQEFWCKF YACCLQYQEALSHPLALHLNPHTNMVCLLKKGYLSFLIPSSLVD
			HLYLLPYENLLTEDETTISDDVDIARDVICLIKCLRLIEESVTV
		İ	DMSVIMEMSCYNLQSPEKAAEQILEDMITIDVENVMEDICSKLQ
ĺ		!	EIRNPIHAIGLLIREMDYETEVEMEKGFNPAOPLNIRMNLTOLV
			GSNTAGYIVCRGVHKIASTRFLICRDLLILOOLLMRLGDAVIWG
1			TGQLFQAQQDLLHRTAPLLLSYYLIKWGSECLATDVPLDTLESN
			LQHLSVLELTDSGALMANRFVSSPQTIVELFFQEVARKHIISHL
.			FSQPKAPLSQTGLNWPEMITAITSYLLQILWPSNPGCLFLECLM GNCQYVQLQDYIQLLHPWCQVNVGSCRFMLGRCYLVTGEGQKAL
1 1	•		ECFCQAASEVGKEEFLDRLIRSEDGEIVSTPRLQYYDKVLRLLD
] ]			VIGLPELVIQLATSAITEASDDW\KSQATL\RTCIFKHHL\DLG
			\HNSQAYGSL*PQIPDSSRQLDCLRQLVVVLCERSOLODLVEFS
:		ţ.	YVNLHNEVVGIIESRARAVDLMTHNYYELLYAFHIYRHNYRKAG
			TVMFBYGMRLGREVRTLRGLEKQGNCYLAALNCLRLIRPEYAWI
ļ	i		VQPVSGAVYDRPGASPKRNHDGECTAAPTNRQIEILELEDLEKE
			CSLARIRLTLAQHD?SAVAVAGSSSAEEMVTLLVQAGLFDTAIS LCQTFKLPLTPVFEGLAFKCIKLQPGGEAAQAEAWAWLAANQLS
1			SVITTKESSATDEAWRLLSTYLERYKVQNNLYHHCVINKLLSHG
			VPLPNWLINSYKKVDAAELLRLYLNYDLLDLTPYOVIRICGC
5826	3	871	KSQLLRDHSAPPPKPCTSVGAMGC*PRO/SPKEOOROLKKOKNR
1			AAAQRSRQKHTDKADALHQQHESLEKDNLALRKEIOSLOAELAW
	· ·		WSRTLHVHERLCPMDCASCSAPGLLGCWDQAEGLLGPGPQGQHG
	1		CREQLELFQTPGSCYPAQPLSPGPQPHDSPSLLQCPLPSLSLGP
1	1		AVVAEPPVQLSPSPLLFASHTGSSLQGSSSKLSALQPSLTAQTA PPQPLELEHPTRGKLGSSPDNPSSALGLARLQSREHKPALSAAT
			WQGLVVDPSPHPLLAFPLLSSAQVHF
5827	194	2287	GMGSENSALKSYTLREPPFTLPSGLAVYPAVLQDGKFASVFVYK
	į	1	RENEDKVNKAAKVP * * HLKTLRHPCLLRFLSCTVEADGIHLVTE
1		ļ.	RVQPLEVALETLSSAEVCAGIYDILLALIFLHDRGHLTHNNVCL
1	İ	1	SSVFVSEDGHWKLGGMETVCKVSQATPEFLRSIQSIRDPASIPP
ļ	i	<u> </u>	EEMSPEFTTLPECHGHARDAFSFGTLVESLLTILNEOVSADVIS
		Ì	SFQQTLHSTLLNPIPKWRPALCTLLSHDFFRNDFLEVVNFLKSL
		<u> </u>	TLKSEERKTEFFKFLLDRVSCLSEELIASRLVPLLLNQLVFAEP

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
}	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
- [	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ŀ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
j	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
i i	residue of	amino acid	W-Tryptophan, Y-Tyrosine, X-Unknown, *-Stop
İ	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	boquomoc	\=possible nucleotide insertion)
	-	+	/-possible indirecting insertion)
	i		VAV\KSFLPYLLGPKKDHAQGETPCLLSPALFQSRVIPVLLQLF
			EVHEEHVRMVLLSHIEAYVGALSLREQLKKV\IL\PQVLLG\LR
1			D\TSDSIVAITLHSLAVLVSLLGPEVVVGGERTKIFKRTAP\SF
1			TK\NTDLSLEGDPFSQPIKFPINGLSDVKNTSEDSENFPSSSKK
1			SEEWPDWSGPE\EPENQTVNI\QIWP\REP\CDDVKSQCTTLDV
İ			BESSWDDCEPSSLDTKVNPGGGITATKPVTSGEQKPIPALLSLT
1		İ	EESMPWKSSLPQKISLVQRGDDADQIEPPKVSSQERPLKVPSEL
1			GLGEEFTIQVKKKPVKDPEMDWFADMIPEIKPSAAFLILPELRT
ľ			EMVPKKDDVSPVMQFSSKFAAAEITEGEAEGWEEEGELNWEDNN
5828	2	257	W
1 3020	*	257	AREGGSLGAVAACGELSYSCDFCPARPHTSW_TRFVKMEPQAVV
	İ		MAVGGGSRMTDLTSSIPKPLLPVGNKPLIWY?LNLLERVGFEEV
į			IVVTTRDVQKALCABFKMKMKPDIVCIPDDADMGTADSLRYIYP
-			KLKTDVLVLSCDLITDVALHEVVDLFRAYDASLAMLMRKGQDSI
1		1	EPVPGQKGKKKAVEQRDFIGVDSTGKRLLFMANEADLDEELVIK
1		1	GSILQKHPRIRFHTGLVDAHLYCLKKYIVDFLMENG\SITSIRS
			BL\IPYLV/RGKQFSSASSQQGTRKEKEGGSKGKRGLKSFRISY
5829	260	1259	SFY*KEANYTGTGAPY\D\ACWI
3025	1	1259	PDGRLIVSCSEDKTIKIWDTTNKQCVNNFSDSVGFANFVDFNPS
	ł	ľ	GTCIASAGSDQTVKVWDVRVNKLLQHYQVHSGGVNCISFHPSGN
			YLITASSDGTLKILDLLKGRLIYTLQGHTGPVFTVSFSKGGELF
	i		ASGGADTQVLLWRTNFDELHCKGLTKRNLKRLHFDSPPHLLDIY
	1		PRTPHPHEBKVETVEDFFLHLLRLIQSLR*SICRSLLPLLWISF
1		ľ	LLILPQQQKPVVGLCQTRVKRPVDIS*TLP*CHQNVCQQPRKRK
1		<b>.</b>	QKT+VTSPVKVK/VSIPLAVTDALEHIMEQLNVLTQTVSILEQR
5830	4496	3139	LTLTEDKLKDCLENQQKLFSAVQQKS
""	34,76	3139	GGKMAAPEERDLTQEQTEKLLQFQDLTGIESMDQCRHTLEQHNW
}			NIEAAVQDRLNEQEGVPSVFNPPPSRPLQVNTADHRIYSYVVSR
1			POPRGLLGWGYYLIMLPFRFTYYTILDIFRFALRFIRPDPRSRV
			TDPVGDIVSFMHSFEEKYGRAHPVFYQGTYSQALNDAKRELRFL
1 .	,	į.	LVYLHGDDHQDSDEFCRNTLCAPEVISLINTRMLFWACSTNKPE
1			GYRVSQALRENTYPFLAMIMLKDRRE*PV\VGRLEGLI\QPDDL
1	İ		INQLTFIMDANQTYLVSERLEREERNQTQVLRQQQDEAYLASLR
		Į	ADQEKERKKREERERKRRKKEEVQQQKLABERRRQNLQEEKERK
			LECLPPEPSPDDPESVKIIFKLPNDSRVERRFHFSQSLTVIHDF
1	[		LFSLKESP\EKFQIEA\NFPRR\VLPCIPSEE\WPNPPTLQE\A
5831	71	2897	GLSHTEVLFVQDLTDE
	'-	2691	FCSKDKCCLYLPDSINRSKSCTAKPGAHSQDRHAVMDSERQVKD
j .	1		TDDIESPKRSIRDSGYIDCWDSBRSDSLSPPRHGRDDSFDSLDS
1			FGSRSRQTPSPDVVLRGSSDGRGSDSESDLPHRKLPDVKKDDMS
			ARRTSHGEPKSAVPFNQYLPNKSNQTAYVPAPLRKKKABREEYR
ł			KSWSTATSPAGLGKKALQDYGPRT\PVS\DDAESTSMFDMRCEE
			EAAVQPHSRARQEQLQLINNQLREEDDKWQDDLARWKSRKRSVS
			QDLIKKEEERKKMEKLLAGEDGTSERRKSIKTYREIVQEKERRE
			RELHEAYKNARSQEEAEGILQQYIERFTISEAVLERLEMPKILE
			RSHSTEPNLSSFLNDPNPMKYLRQQSLPPPKFTATVETTIARAS
i			VLDTSMSAGSGSPSKTVTPKAVPMLTPKPYSQPKNSQDVLKTFK
	·		VDGKVSVNGETVHREEEKERECPTVAPAHSLTKSQMFEGVARVII
			GSPLELKQDNGSIEINIKKPNSVPQELAATTEKTEPNSQEDKND
			GGKSRKGNIELASSEPQHFTTTVTRCSPTVAFVEFPSSPQLKND
	ł		VSEEKDQKKPENEMSGKVELVLSQKVVKPKSPEPEATLTFPFLD
			KMPEANQLHLPNLNSQVDSPSSEKSPVTTPFKFWAWDPEEERRR
		i	QEKWQQEQBRLLQERYQ\KEQDK\LKEE\WEKAQKEVEEEERRY
	,	ł	YEEEP*II\EDPVVPFTVSSSSADQLSTSSSMTEGSGTMNKIDL
			GNCQDEKQDRRWKKSFQGDDSDLLLKTRESDRLEEKGSLTEGAL
	ľ		AHSGNPVSKGVHEDHQLDTEAGAPHCGTNPQLAQDPSQNQQTSN
	ļ	j	PTHSSEDVKPKTLPLDKSINHQIESPSERRKSISGKKLCSSCGL
	1		PLGKGAAMIIETLNLYFHIQCFRCG\ICKGQLGDAVSGTDVRIR
5832	2454	930	NGLLNCNDCYMRSRSAGQPTTL
	2474	829	PGRRFRHGSCAFQKQCYMLHICQYFLQGECKFGTSCKRSHDFSN
	<u> </u>		SENLEKLEKLGMSSDLVSRLPTIYRNAHDIKNKSSAPSRVPPLF

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location ·	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine.
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	residue of	residue of	S=Serine, T=Threonine, V=Valine,
	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	sequence	Codon, /=possible nucleotide deletion,
	2042000	<del> </del>	\=possible nucleotide insertion\ \VPQGTSERKDSSGSVSPNTLSQEEGDQICLYHIRKSCSFQDKCH
			RVHFHLPYRWQFLDRGKWEDLDNMELIEEAYCNPKIERILCSES
1			ASTFHSHCLNFNAMTYGATQARRLSTASSVTKPPHFILTTDWIW
			YWSDEFGSWQEYGRQGTVHPVTTVSSSDVEKAYLAY/WYTGV*R
}	}		PGSHLEVPGRKAQLRVRFQSLRSEKPGLWHN*KGLPQTQIR\AP
1	}		QDVTTMQTCNTKFPGPKSIPDYWDSSALPDPGFQKITLSSSSEE
	1		YQKVWNLFNRTLPFYPVQKIERVQNLALWEVYQWQKGQMQKQNG
]			GKAVDERQLFHGTSAIFVDAICQQNFDWRVCGVHGTSYGKGSYF
1			ARDAAYSHHYSKSDTQTHTMFLARVLVGEFVRGNASFVRPPAKE
ł	i		GWSNAFYDSCVNSVSDPSIFVIFEKHQVYPBYVIQYTTSSKPSV
5833	. 170	2000	TPSILLALGSLFSSRQ
3033	1, 1,0	3289	SILCLLSPCVVQFGKPVVSILSSRSRHSPCTKKGWEGMRKHLHT
į			RQGHK*VHVEISKALWVYRDDYFIRHSISVSAVIVRAWITHKYR
			GROWNVKWEEN:LHAVAKNYTLLQTIPPFERPFKDHQVCLEWNM
			GYIWNLRANRIPQCPLENDVVALLGFPYASSGENTGIVKKFPRF RNRELEATRRORMDYPVFTVSLWLYLLHYCKANLCGILYFVDSN
		•	EMYGTPSVFLTEEGYLHIQMHLVKGEDLAVKTKFIIPLKEWFRL
1			DISFNGGQIVVTTSIGQDLKSYHNQTISFREDFHYNDTAGYFII
			GGSRYVAGIEGFFGPLKYYRLRSLHPAQIFNPLLEKQLAEQIKL
1			YYERCAEVQEIVSVYASAAKHGGERQEACHLHNSYLDLORRYGR
			PSMCRAFPWEKELKDKHPSLFQALLEMDLLTVPRNONESVSEIG
			GKIFEKAVKRLSSIDGLHQISSIVPFLTDSSCCGYHKASYYLAV
			FYETGLNVPRDQLQGMLYSLVGGQGSERLSSMNLGYKHYQGIDN
1			YPLDWELSYAYYSNIATKTPLDQHTLQGDQAYVETIRIKDDEIL
			KVQTKEDGDVFMWLKHEATRGNAAAQQRLAQMLFWGQQGVAKNP EAAIEWYAKGALETEDPALIYDYAIVLFKGQGVKKNRRLALELM
			KKAASKGLHQAVNGLGWYYHKFKKNYA\KAAKYWLKA\EE\MGN
			PDASYNLGVLHLDGIFPGVPGRNQTLAGEYFHKAAQGGHMEGTL
1 1			WCSLYYITGNLETFPRDPEKAVVWAKHVAEKNGYLGHVIRKGLN
]	}		AYLEGSWHEALLYYVLAAETGIEVSQTNLAHICEERPDLARRYL
			GVNCVWRYYNFSVFQIDAPSFAYLKMGDLYYYGHQNQSQDLELS
1 1			VQMYAQAALDGDSQGFFNLALLIEEGTIIPHHILDFLEIDSTLH
1 1			SNNISILQELYERCWSHSNEBSFSPCSLAWLYLHLRLLWGAILH
1 1	}		SALIYFLGTFLLSILIAWTVQYFQSVSASDPPPRPSQASPDTAT STASPAVTPAADASDQDQPTVTNNPEPRG
5834	17	4020	RFRRGGGRVPPGAFPASPSDSLGQGNSQGPPRTPKPPRT/QECG
1 1			SAAPGPIPGQSSS+VPLRLEQIQQKADCPLSLELALKPRMAAQV
]			TLEDALSNVDLLEELPLPDQQPCIEPPPSSLLYQPNFNTNFEDR
1 1			NAFVTGIARYIEQATVHSSMNEMLEEGQEYAVMLYTWRSCSRAI
1 1			POVKCNEOPNRVEIYEKTVEVLEPEVTKLMNFMYFORNAIERFC
1			GEVRRLCHAERRKDFVSEAYLITLGKFINMFAVLDELKNMKCSV
1			KNDHSAYKRAAQFLRKMADPQSIQBSQNLSMFLANHNKITQSLQ
			QQLEVISGYEELLADIVNLCVDYYENRMYLTFSEKHMLLKVMGF
1 1		1	GLYLMDGSVSNIYKLDAKKRINLSKIDKYFKQLQVVPLFGDMQI ELARYIKTSAHYEENKSRWTCTSSGSSPQYNICEQMIQIREDHM
1 1	1	j	RFISELARYSNSEVVTGSGRQEAQKTDAEYRKLFDLALQGLQLL
] ]			SQWSAHVMEVYSWKLVHPTDKYSNKDCPDSAEEYERATRYNYTS
] ]	· .	1	EEKFALVEVIAMIKGLQVLMGRMESVFNHAIRHTVYAALQDFSQ
] [	ì	ļ	VTLMEPLRQAIKKKNVIQSVLQAIRKTVCDWETGHEPFNDPAL
	ļ	i	RGEKDPKSG*DIKVPRRAVGPSSTQLYMVRTMLESLIADKSGSK
	<u> </u>	}	KTLRSSLEGPTILDIEKFHRESFFYTHLINFSETLQQCCDLSQL
	į		WFREFFLELTMGRRIQFPIEMSMPWILTDHILETKEASMMBYVL
			YSLDLYNDSAHYALTRFNKQFLYDEIEAEVNLCFDQFVYKLADQ
[ ]	}		IFAYYKVMAGSLLLDKRLRSECKNQGATIHLPPSNRYETLLKQR
i l			HVQLLGRSIDLNRLITQRVSAAMYKSLELAIGRFESEDLTSIVE LDGLLEINRMTHKLLSRYLTLDGFDAMFREANHNVSAPYGRITL
			HVFWELNYDFLPNYCYNGSTNRFVRTVLPFSQEFQRDKQPNAQP
		ļ	QYLHGSKALNLAYSSIYGSYRNFVGPPHFQVICRLLGYQGIAVV
			MESLLKVVKSLLQGTILQYVKTLMEVMPKICRLPRHEYGSPGIL
	ļ	ĺ	EFFHHQLKDIVEYAELKTVCFQNLREVGNAILFCLLIEOSLSLE
			EVCDLLHAAPFQNILPRVHVKEGERLDAKMKRLESKYAPLHLVP
·			

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ļ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
į	sequence	· -	\=possible nucleotide insertion)
			LIBRIGTPQQIAIAREGDLLTKERLCCGLSMFEVILTRIRSFLD
1		į	DPIWRGPLPSNGVMHVDECVEFHRLWSAMQFVYCIPVGTHEFTV
1	1	1	EQCFGDGLHWAGCMIIVLLGQQRRFAVLDFCYHLLKVQKHDGKD
1			EIIKNVPLKKMVERIRKFQILNDEIITILDKYLKSGDGEGTPVE
	1		HVRCFQPPIHQSLASS
5835	4209	1904	SGNIRMAQGSHQIDFQVLHDLRQKFPEVPEVVVSRCMLQNNNNL
1			DACCAVLSQBSTRYLYGEGDLNFSDDSGISGLRNHMTSLNLDLO
			SQNIYHHGREGSRMNGSRTLTHSISDGQLQGGQSNSELFQQEPQ
1	]		TAPAQVPQGFNVFGMSSSSGASNSAPHLGFHLGSKGTSSLSQQT
	]		PRFNPIMVTLAPNIQTGRNTPTSLHIHGVPPPVLNSPQGNSIYI
1			RPYITTPGGTTRQTQQHSGWVSQFNPMNPQQVYQPSQPGPWTTC
	J		PASNPLSHTSSQQPNQQGHQTSHVYMPISSPTTSQPPTIHSSGS
			SQSSAHSQYNIQNISTGPRKNQIEIKLEPPQRNNSSKLRSSGPR
1			TSSTSSSVNSQTLNRNQPTVYIAASPPNTDRLMSRSQPKVYISA
1			NAATGDEQVMRNQPTLFISTNSGASAASRNMSGQVSMGPAFIHH
1 1			HPPKSRAIGNNSATSPRVVVTQPNT\EYTFKITVSPNKPPAVSP
			GVVSPTFELTNLLNHPDHYVETENIHHLTDPTLAHVDRISETRK
}			LSMGSDDAAYTQDI*RISNSWLGMVAHACNSSALGGQDGRII*A
! !			QEFETSWGNIWRLRLYRRF+NYAGMVAHTCSPSYSVD+ALLVHQ
			KARMERLQRELBIQKKKLDKLKSEVNEMENNLTRRRLKRSNSIS
			QIPSLEEMQQLRSCNRQLQIDIDCLTKEIDLFQARGPHFNPSAI
	•		HNFYDNIGFVGPVPPKPKDQRSIIXTPKTQDTBDDEGAQWNCTA
1			CTFLNHPALIRCEQCEMPRHF
5836	361	2303	FHITMCGICCSVNFSAEHFSQDLKEDLLYNLKQRGPNSSKQLLK
1			SDVNYQCLFSAHVLHLRGVLTTQPVEDERGNVFLWNGEIFSGIK
1 1			VZAEENDTQILPNYLSSCKNESEILSLFSEVQGPWSFIYYQASS
1			HYLWFGRDFFGRRSLLWHFSNLGKSFCLSSVGTQTSGLANQWQE
1			VPAS\DFSELILSLLSFPDALFYNCILGNIFLGRILLKKMLIA*
1 1			VKFQQTYQHLYQR*QMKPNCILKNLLFL*I*CCHKLHWRLIAVI
			FPMCHLQERYFKSFLLMYT*KEVIQQFIDVLSVAVKKRVLCLPR
1	•		DENLTANEVLKTCDRKANVAILFSGGIDSMVIATLADRHIPLDE
1 1			PIDLLNVAFIAEEKTMPTTFNREGNKQKNKCEIPSEEFSKDVAA
1 1			AAADSPNKHVSVPDRITGRAGLKELQAVSPSRIWNFVEINVSME
1 1			ELQKLRRTRICHLIRPLDTVLDDSIGCAVWFASRGIGWLVAQEG
1 1	}		VKSYQSNAKVVLTGIGADEQLAGYSRHRVRFQSHGLEGLNKEIM
1	ļ		MELGRISSRNLGRDDRVIGDHGKEARFPFLDENVVSFLNSLPIW
1			EKANLTLPRGIGEKLLLRLAAVELGLTASALLPKRAMQFGSRIA
1	İ		KMEKINEKASDKCGRLQIMSLENLSIBKETKL
5837	4792	903	NGNAVAQAPVTNCCYLATGSKDQTIRIWSCSRGRGVMILKLPFL
1 1	ł		KRRGGGIDPTVKERLWLTLHWPSNQPTQLVSSCFGGELLQWDLT
1	İ		QSWRRKYTLFSASSEGQNHSRIVFNLCPLQTEDDKQLLLSTSMD
		•	RDVKCWDIATLECSWTLPSLGGFAYSLAFSSVDIGSLAIGVGDG
1 1	ļ		MIRVWNTLSIKNNYDVKNFWQGVKSKVTALCWHPTKEGCLAFGT
1 1	į		DDGKVGLYDTYSNKPPQISSTYHKKTVYTLAWGPPVPPMSLGGE
1 1			GDRPSLALYSCGGEGIVLQHNPWKLSGEAFDINKLIRDTNSIKY
1 1	ł		KLPVHTBISWKADGKIMALGNEDGSIEIFQ\IPNLKLICTIQQH
1 1			HKLVNTISWHHE\HGSPAQKLSYL\MPSGSQQCSPFTCHNLKNC
			P*KAAPESPSDPLQSPYRTPPQGHTAQDYPVWAWEPHIH*WEGL
	1		VFCPPIDGYSPGCWD\AFPGKEAPVAIFRG\HQGRLLCVAWSPL
]		i	DPDCIYSG\ADDFCVHKWLTSMQDHSRPPQGKKSIBLEKKRLSQ
			PKAKPKKKKKPTLRTPVKLESIDGNEESMKENSGPVENGVSDQ
1			EGEEQAREPELPCGLAPAVSREPVICTPVSSGFEKSKVTINNKV
[ [		İ	ILLKKEPPKEKPETLIKKRKARSLLPLSTSLDHRSKEELHODCL
		ŀ	VLATAKHSRBLNEDVSADVEERFHLGLFTDRATLYRMIDIEGKG
<i> </i>	1		HLENGHPELFHQLMLWKGDLKGVLQTAAERGELTDNLVAMAPAA
	1		GYHVWLWAVEAFAKQLCFQDQYVKAASHLLSIHKVYBAVE:LKS
	i		NHFYREAIAIAKARLRPEDPVLKDLYLSWGTVLERDGHYAVAAK
	1		CYLGATCAYDAAKVLAKKGDAASLRTAAELAAIVGEDELSASLA
	ļ	Ì	LRCAQELLLANNWVGAQEALQLHESLQGQRLVFCLLELLSRHLE
1	İ	ļ	EKQLSEGKSSSSYHTWNTGTEGPFVERVTAVWKSIFSLDTPEOY
i		1	QEAFQKLQNIKYPSATNNTPAKQLLLHICHDLTLAVLSQOMASW

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L-Leucine, M-Methionine, N-Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ŀ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
		<u> </u>	DEAVQALLRAVVRSYDSGSFTIMQEVYSAFLPDGCDHLRDKLGD
1	]		HQSPATPAFKSLEAFFLYGRLYEFWWSLSRPCPNSSVWVRAGHR
l .			TLSVEPSQQLDTASTEETDPETSQPEPNRPSELDLRLTEEGERM
1			LSTFKELFSEKHASLQNSQRTVAEVQETLAEMIRQHQKSQLCKS
į.			TANGPDKNBPEVEAEQPLCSSQSQCKEEKNEPLSLPELTKRLTE
1			ANQRMAKFPESIKAWPFPDVLECCLVLLLIRSHFPGCLAQEMQQ
			QAQELLQKYGNTKTYRRHCQTFCM
5838	110	98	KTMPHLLVTFRDVAIDFSQEEWECLDPAQRDLYRDVMLENYSNL
			ISLDLESSCVTKKLSPEKEIYEMES\PSGRIWGNVSTITFQYNG
1			LGDNMECKGNLEGQVSKSEGLYMCVKITCEEKATESHSTSSTFH
i			RII/HYQGKIVKCKECRQGFSYLSCLIQHEENHNI*KCSEVNKH
1			RNTFSKKPSYI*HQ\KFRLGEKPYECMECGKAFGRTSDLIQHQK
-		i	IHTNEKPYQCNACGKAFIRGSQLTEHQRVHTGEKPYDCKKCGKA
			FSYCSQYTLHQRIHSGEKPYECKDCGKAFILGSQLTYHQRIHSG
			EKPYECKECGKAFILGSHLTYHQRVHTGEKPYICKECGKAFLCA
1			SQLNEHQRIHTGEKPYECKECGKTFFRGSQLTYHLRVHSGERPY
			KCKECGKAFISNSNLIQHQRIHTGEKPYKCKECGKAFICGKQLS
			EHQRIHTGEKPFECKECGKAFIRVAYLTQHBKIHGEKHYECKEC
	i i		GKTFVRATQLTYHQRIHTGEKPYKCKECDKAF/HLWLTILSEHQ
1	· ·		RIHRGEKPYECKQCGR/LFIRGSHL/NEHLRTHTGEKPYECKEC
			GRAFSRGSEHTLHQRIHTGEKPYTCVQCGKDFRCPSQLTQHTRL
5839	1	2425	HN*EYSSHKICMHSIALASLDFAHLQEKNPEN
1 3035	*	2425	GRPFPRPPRALPRLPLRGRRQDGRWTVDFEECLKD\SPRFRAAL EEVEGDVAELELKL\DKLVKLCIA\MIDTGKAFCVANKQFMNGI
1			RD\LAQNS\NNDA\VVETKFAPSFLDSLQEMINFHTIL/L*PNS
1	·		EIN*GHSFQNFVKEDLRKFKDAKKQFENSQ*KRKKIALVKNAPV
1			PSRPASLEL*KPPNILTATRKCFRHIALDYVLQINVLQSKRRSE
			ILKSMLSFMYAHLAFFHQGYDLFSBLGPYMKDLGAQLDRLVGDA
i l			AKEKREMEÇKHSTIQQKDFSRDDSKLKYNVDAANGIVMEGYLFK
			RASNAFKTWNRRWFSIQNNQVVYQKKFKDNPTVVVEDLRLCTVK
			HCEDIERRFCFEVVSPTKSCMLQADSEKLRQAWIKAVQTSI\AT
			AYREKDDESEKLDKKSSPSTGSLDSGNESKEKLLKGESALQRVQ
]			CIPGNASCCDCGLADPRWASINLGITLCIECSGIHRSLGVHFSK
1			VRSLTLDTWEPELLKLMCELGNDVINRVYEANVEKMGIKKPQPG
1			QRQEKEAYIRAKYVERKFVDKIFL*SLSPP\EQQKK\FVSKSSE
			EKRLSISKFGP\GDQVRASAQSSVRSNDSGIQQSSDDGRBSLPS
1			TVSANSLYEPEGERQDSSMFLDSKHLNPGLQLYRASYEKNLPKM
	·		AEALAHGADVNWANSEENKATPLIQAVLGGSLVTCEFLLQNGAN
			VNQRDVQGRGPLHHATVLGHTGQVCLFLKRGANQHATDEBGKDP
			LSIAVEAANADIVTLLRLARMNEEMRESEGLYGQPGDETYQDIF
			RDFSQMASNNPEKLNRFQQDSQKF
5840	698	3610	KHLHLPRQHLTTLWQISSPRWRSPQRAFMSALSKTQTQSAPALQ
) J			GLSSLLQSVTGNPVPASEAASQSTSASPANTTVYTIKGRNLPSS
1			AQPFIPKSFNYSPNSSTSEVSSTSASKASIGQSPGLPSTAFKLP
1 1	Ì		SNTKGFTATHNTSPAAPPTEVTICQSSEVSKPKL\ESESTSPSL
			\EMKIHNFLKGNPGFSVA*NLKHPNPAGSLGSSAPSESHPSDFQ
	-		RGPTSTSIDNIDGTPVRDERSGTPTQDEMMDKPTSSSVDTMSLL
}	1		SKIISPGSSTPSSTRSPPPGRDESYPRELSNSVSTYRPFGLGSE
	}		SPYKQPSDGMERPSSLMDSSQEKFYPDTSFQEDEDYRDFEYSGP
1 [	!		PPSAMMNLQKKPAKSILKSSKLSDTTEYQPILSSYSHRAQEFGV
1 . 1	İ		KSAFPPSVRALLDSSENCDRLSSSPGLFGAFSVRGNEPGSDRSP
			SPSKNDSFFTPDSNHNSLSQSTTGHLSLPQKQYPDSPHPVPHRS
[ [	. 1		LFSPONTLAAPTGHPPTSGVEKVLASTISTTSTIEFKNMLKNAS
[ [			RKPSDDKHFGQAPSKGTPSDGVSLSNLTQPSLTATDQQQQBEHY
	ļ		RIETRVSSSCLDLPDSTEEKGAPIETLGYHSASNRRMSGEPIQT
	[		VESIRVPGKGNRGHGREASRVGWFDLSTSGSSFDNGPSSASELA
			SLGGGGSGGLTGFKTAPYKERAPQFQESVGSFRSNSFNSTFEHH
			LPPSPLEHGTPFQRBPVGPSSAPPVPPKDHGGIFSRDAPTHLPS
			VDLSNPFTKEAALAHAAPPPPPGEHSGIPFPTPPPPPPPGEHSS
		l	SGGSGVPFSTPPPPPPPVDHSGVVPFPAPPLAEHGVAGAVAVFP
	<u></u> 1		KDHSSLLQGTLAEHFGVLPGPRDHGGPTQRDLNGPGLSRVRESL

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding		H=Histidine, I=Isoleucine, K=Lysine,
1	to first	to first	1.=Leucine, M=Methionine, N=Asparagine,
]	amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	residue of	residue of	S=Serine, T=Threonine, V=Valine,
Ī		amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion.
	sequence		\=possible nucleotide insertion)
ļ			TLPSHSLEHLGPPHGGGGGGGSNSSSGPPLGPSHRDTISPSGIT
1			LRSPREDFRPREPFLSRDPFHSLKRPRPPFARGPPFFAPKRPFF
<u> </u>	.1	}	PPRY
5841	1908	762	GLRLPLVLTVWPMMKPSWLSRTEFSKRLLCRTLWCQSGWSSRSY
			TRSMLKMTTSINRRSRTSTKSTRTSARPGLTATVSIGLSDSPTW
	İ	i	RHCWMTARSCSGEKGGHWAPRQVGVYLLPGRVGCVSSRVSPSFP
			GDGLDSGLARRGSAVSALASGLVEEPMLGPPFHPTPRFKAVSAK
1			CKEDI UCOCERRENTED PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO PROGRAMMENTO
	İ		SKEDLVSQGFTEFTIEDFHNTFMDLIEQVEKQTSVADLLASFND
1		ł	QSTSDYLVVYLRLLTSGYLQRESKFFEHFIEGGRTVKEFCQ\QE
1	i		\VEPMCKESDHIHIIALAQGLQRVHPGWEYMGPRPRAATTNPHI
	ļ		FP*GLPSPKVYLLYRPG\HYDILYKIGLGSSPLGCPGCPLLARA
5842	307		LGHCYRGFSVVVKWSYFTPFFLSHDPPPMFY
3012	307	1918	QEPTADFKLRSTCGCGREMTCPDKPGQLINWFICSLCVPRVRKL
1	1		WSSRRPRTRRNLLLGTACAIYLGFLVSQVGRASLQHGQAAEKGP
	ŀ		HRSRDTAEPSFPEIPLDGTLAPPESOGNGSTLOPNVVVITURGK
	ĺ		RSKPANIRGTVKPKRRKKHAVASAAPGOEALVGPSLOPORA\EG
i			KLML*HLGTLREQTWLRLESDPGGWCGVRE/WRAGGPDFLOPGS
1	ĺ		RESNIRIYSESAPSWLSKDDIRRMRLLADSAVAGLRPVSSRSGA
			RLLVLEGGAPGAVLRCGPSPCGLLKOPLDMSEVFAFHLDRILGI
1			NRTLPSVSRKAEFIQDGRPCPIILWDASLSSASNDTHSSVKLTW
1			GTYQQLLKQKCWQNGRVPKPESGCTEIHHHBWSKMALFDFLLQI
-			YNRLDTNCCGFRPRKEDACVQNGLRPKCDDQGSAALAHIIQRKH
			DPRHLVFIDNKGFFDRSEDNLNFKLLEGIKEFPASAVYVLKSQH
i			LRQKLLQSLFLDKGYWESQGGRQGIEKLIDVIEHRAKILITYIN
			AHGVKVLPMNR
5843	500	1453	GTARLVTCWVLHGQ+VKKPAWEPGVVWL+Q+RCRPKGWGLGAGM
			RGSRMSQPPQCLRRAQSSCCHFMVKLLDDGTPMIPGEKVAHTSL
			DALVTPHOQKPIEPRRBLLTQPCRQKDPANVDYEDLFLYSNAVA
			EEAACPVSAPEEASPKPVLCHQSKERKPSAEM/RQNNHQGSHFL
1			LPPKIPSWRDPPETLEEPQNAPRERPEGPAAAKKPPRHCELVVT
l l			LCCPRIUCDI DEPUNDICADORE DECIDE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE C
1	j		LGCPEIHGDLRPWDRKRQPRSLRGSHLGGQRLHGSLCGHISQKP
} I	}		LTAPGTKRQKGPHQEGREVGQLH*GDPRGQELAPNGSESPILPG VQARAPGLGRA
5844	202	2471	
		23/1	FDSAVLSSINVMAVLPGPLQLLGVLLTISLSSIRLIQAGAYYGI
1 '		•	KPLPPQIPPQMPPQIPQYQPLGQQVPHMPLAKDGLAMGKEMPHL
1 1			QYGKEYPHLPQYMKEIQPAPRMGKEAVPKKGKEIPLASLRGEQG
1 1			PRGEPGPRGPPGPPGLPGHGIPGIKGKPGPQGYPGVGKPGMPGM
i 1			PGKPGAMGMPGAKGEIGQKGEIGPMGIP+PQGPPGPHGLPGIGK
1 1	i		PGGPGLPGQPGPKGDRGPKGLPGPQGLRGPKGDKGFGMPGAPGV
ļ j			KGPPGMHGPPGPVGLPGVGKPGVTGFPGP\QGPLGK\PGAPGEP
1 1	1	1	GPQGPIGVPGVQGPPGIPGIGKPGQDG\IPGQPGFPGGKGEQGL
!!			PGLPGPPGLPGIGKPGFPGPKGDRGMCGVPGALGPRGEKGPIGA
Î I			PGIGGPPGEPGLPGIPGPMGPPGAIGFPGPKGEGGIVGPQGPPG
1			PKGEPGLQGFPGKPGFLGEVGPPGMRGFPGPIGPKGFHGOKGVP
l i			GLPGVPGLLGPKGEPGIPGDQGLQGPPGIPGIGGPSGPTGPPGT
1 1	ľ		PGPKGEPGLPGPPGFPGIGKPGVAGLHGPPGKPGALGPOGOPGI.
1	1	1	PGPPGPPGPPDAVMPPTPPPQGEYLPDMGLGIDGVKPPHAVC
J		İ	AKKGKNGGPAYEMPAFTAELTAPFPPVGAPVKFNKLLYNGRONY
i			NPQTGIFTCEVPGVYYFAYHVHCKGGNVWVALFKNNEPVMYTYD
' i			EYKKGFLDQASGSAVLLLRPGDRVFLQMPSEQAAGLYAGQYVHS
		<b>}</b>	SFSGYLLYPM
5845	215	2061	HASNKSASLQDKMANPKEKTAMCLVNELARFNRVQPQYKLLNER
ł	1	1	GPAHSKMFSVQLSLGEQTWESEGSSIKKAQQAVGNKALTESTLP
	ļ	ļ	KPI*KPPKSNVNNNPGCITPTVELNGLAMKRG\KPAIHRPLDPK
- 1	}	1	PEPNNRANYNEOUMYNODYUCD TRYCONIA THE PLOPK
1	ì	İ	PFPNNRANYNFQVMYNQRYHCPIPKIFYVQLTVGNNEFFGEGKT
1			RQAARHNAAMKALQALQNEPIPERSPQNGESGKDMDDDKDANKS
- 1		j	EISLVFEIALKRNMPVSFEVIKESGPPHMKSFVTRVSVGEFSAE
1			GEGNSKKLSKKRAATTVLQELKKLPPLPVVEKPK\HFFKKRPKT
}	}		IVKAGPEYGQGMNPISRLAQIQQAKKEKEPDYVLLSERGMPRRR
ſ			EFVMQVKVGNEVATGTGPNKKIAKKNAAEAMLLQLGYKASTNLQ
			DQLEKTGENKGWSGPKPGFPEPTNNTPKGILHLSPDVYQEMEAS

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	1	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
"""	location	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	1	corresponding	H=H1Stidine, I=Isoleucine, K=Lvsine
1	corresponding to first	to first	L=Leucine, M=Methionine, N=Asparagine,
1		amino acid	P=Proline, Q=Glutamine, R=Arginine.
	amino acid	residue of	S=Serine, T=Threonine, V=Valine.
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown *-Ston
ł	amino acid	sequence	Codon, /=possible nucleotide deletion
ļ	sequence	1	\=possible nucleotide insertion)
			RHKVISGTTLGYLSPKDMNQPSSSFFSISPTSNSSATIARELLM
	i		NGTSSTAEAIGLKGSSPTPPCSPVQPSKQLEYLARIQGFQVHYC
1	1		DRQSGKECVTCLTLAPVQMTFHAIGSSIEASHDQV*YATAILLC
j		ł	YGPARKWKAIKMEAMCAHAALLSLIHYLLAPSARLEKSKLFALG
1			N.
5846	1126	456	1 "
		1.50	FSKLIMKTFIIGISGVTNSGKTTLAKNLQKHLPNCSVISQDDFF
i	†		KPESEIETDKNGFLQYDVLEALNMEKMMSAISCWMESARHSVVS
		İ	TDQESAEEIPILIIEGFLLFNYKPLDTIWNRSYFLTIPYEECKR
1	1		RRSTRVYQPPDSPGYFDGHVWPMYLKYRQEMQDITWEVVYLDGT
ł	1		KSEEDLFLQVYEDLIQELAKQKCLQVTA*RRNTTNPS/CK*IRK
5847	2260		LQGVI
1 304,	2769	505	APEMEDLSSPDSTLLQGGHNLLSSASFQESVTFKDVIVDFTQEE
1	1	ľ	WKQLDPGQRDLFRDVTLENYTHLVSIGLOVSKPDVISOLROGTE
1			PWIMEPSIPVGTCADWETRLENSVSAPEPDISEEELSPRVTVFK
			HKRDDSWSSNLLESWEYEGSLERQOANOOTLPKEIKVTEKTIPS
1			WEKGPVNNEFGKSVNVSSNLVTQEPSPEETSTKRSIKONSNDVK
			KEKSCKCNECGKAFSYCSALIRHORTHTGEKPYKCN*/CVEKAR
1			SRSENLINHQRIHTGDXPYKCDQCGKGFIEGPSLTQHQRIHTGE
1			KPYKCDECGKAFSQRTHLVQHQRIHTGEKPYTCNECGKAFSQRG
	•		HFMEHQKIHTGEKPFKCDECDKTFTRSTHLTQHQKIHTGEKTYK
l .	1		CNECGKAFNGPSTFIRHHMIHTGEKPYECNECGKAFSQHSNLTQ
I	1		HOKTHTGEKPYDCAECGKSFSYWSSLAQHLKIHTGEKPYKCNEC
{			GKAFSYCSSLTQHRRIHTREKPFECSECGKAFSYLSNLNQHQKT
			HTQEKAYECKECGKAFIRSSSLAKHERIHTGEKPYQCHECGKTF
1	1		SYGSSLIQHRKIHTGERPYKCNECGRAFNQNIHLTQHKRIHTGA
	l		KPYECAECGKAFRHCSSLAQHQKTHTEEKPYQCNKCEKTFSQSS
	1		HITOHODIUTGERDYRONEGDYN BOD GRUN TOWN TOWN
	į		HLTQHQRIHTGEKPYKCNECDKAFSRSTHLTQHQRIHTGEKPYK
	}		CNECGK\TFSQSTYLIQHQRIHSGEKPFGCNDCGKSFRYRSALN KHORLHPGI
5848	22	2961	
1		2,01	AAPRRLLRGGDGDRTPRFPLPALLRPGPPAEAAPERKMPAVSK
r			
			GDGMRGLAVFISDIRNCKSKEAEIKRINKELANIRSKFKGDKAL
			DGYSKKKYVCKLLFIFLLGHDIDFGHMEAVNLLSSNRYTEKOTG
			DGYSKKKYVCKLLFIFLLGHDIDFGHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCIASV
			DGYSKKKYVCKLLFIFLLGHDIDFGHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCIASV GSREMAEAFAGEIPKVLVAGDTMDSVKOSAALCLIRLYPTSDDL
			DGYSKKKYVCKLLFIFLIGHDIDFGHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCTASV GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMGDWTSRVVHLLNDQHLGYVTAATSLITTLAGKNPEFFKTSV
			DSYSKKKYVCKLLFIFLLGHDIDFGHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCIASV GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEEFKTSV SLAVSRLS\RIVTSASTDLQDYTY*FCPGFLGLSVKLLRLJ
			DGYSKKKYVCKLLFIFLLGHDIDFGHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCIASV GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEEFKTSV SLAVSRLS\RIVTSASTDLQDYTY*FCPGFLGLSVKLLRLLQCY PPPDPAVRGRLTECLETILNKAQEPPKSKKVONSNAKNAVLFFA
			DGYSKKKYVCKLLFIFLLGHDIDFGHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCIASV GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEEFKTSV SLAVSRLS\RIVTSASTDLQDYTY*FCPGFLGLSVKLLRLQCY PPPDPAVRGRLTECLETILNKAQEPPKSKKVQHSNAKNAVLFEA ISLIIHHDSEPNLLVRACNQLGQFLOHRETNLRYLALESNCTLA
			DSYSKKKYVCKLLFIFLLGHDIDFGHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCIASV GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEEFKTSV SLAVSRLS\RIVTSASTDLQDYTY*FCPGFLGLSVKLLRLQCY PPPDPAVRGRLTECLETILNKAQEPPKSKKVQHSNAKNAVLFEA ISLIIHHDSEPNLLVRACNQLGQFLQHRETNLRYLALESMCTLA SSEFSHEAVKTHIETVINALKTERDVSVRQRAVDLLYAMCDRSN
			DSYSKKKYVCKLLFIFILIGHDIDFGHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCTASV GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEEFKTSV SLAVSRLS\RIVTSASTDLQDYTY*FCPGFLGLSVKLLRLLQCY PPPDPAVRGRLTECLETILNKAQEPPKSKKVQHSNAKNAVLFEA ISLIIHHDSEPNLLVRACNQLGQFLQHRETNLRYLALESMCTLA SSEFSHEAVKTHIETVINALKTERDVSVRQRAVDLLYAMCDRSN APQIVAEMLSYLETADYSTREEIVLKVAILAEKYAVDYTWV
			DGYSKKKYVCKLLFIFLLGHDIDFGHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTEMGLALHCTASV GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMGDWTSRVVHLLNDQHLGYVTAATSLITTLAQKNPEEFKTSV SLAVSRLS\RIVTSASTDLQDYTY*FCPGFLGLSVKLLRLLQCY PPPDPAVRGRLTECLETILNKAQEPPKSKKVQHSNAKNAVLFEA ISLIIHHDSEPNLLVRACNQLGQFLQHRETNLRYLALESMCTLA SSEFSHEAVKTHIETVINALKTERDVSVRQRAVDLLYAMCDRSN APQIVAEMLSYLETADYSIREEIVLKVAILAEKYAVDYTW\YVD TILNIRIAGDYVSEEVWYRVIOIVINRDDVCGYAAKTUFFALO
			DSYSKKKYVCKLLFIFLLGHDIDFGHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCIASV GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEEFKTSV SLAVSRLS\RIVTSASTDLQDYTY*FCPGFLGLSVKLLRLLQCY PPPDPAVRGRLTECLETILNKAQEPPKSKKVQHSNAKNAVLIFEA ISLIIHHDSEPNLLVRACNQLGQFLQHRETNLRYLALESMCTLA SSEFSHEAVKTHIETVINALKTERDVSVRQRAVDLLYAMCDRSN APQIVAEMLSYLETADYSIREEIVLKVAILAEKYAVDYTW\YVD TILNLIRIAGDYVSEEVWYRVIQIVINRDDVQGYAAKTVFEALQ APACHENLVKVGGYILGEFGNLIAGDDRSSPLTOWHLBURUN
			DGYSKKKYVCKILFTFLIGHDIDFGHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCIASV GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEEFKTSV SLAVSRLS\RIVTSASTDLQDYTY*FCPGFLGLSVKLLRLLQCY PPPDPAVRGRLTECLETILNKAQEPPKSKKVQHSNAKNAVLFEA ISLIIHHDSEPNLLVRACNQLGQFLQHRETNLRYLALESMCTLA SSEFSKEAVKTHIETVINALKTERDVSVRQRAVDLLYAMCDRSN APQIVAEMLSYLETADYSIREEIVLKVAILAEKYAVDYTW\YVD TILNILRIAGDYVSEEVWYRVIQIVINRDDVQGYAAKTVFEALQ APACHENLVKVGGYILGEFGNLIAGDPRSSPLIQFHLLHSKFHL CSVPTRALLLSTYIKFVNLPPBVKPTIODVLRSDSOLBNADVEL
			DSYSKKKYVCKILFIFLIGHDIDFGHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCIASV GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEEFKTSV SLAVSRLS\RIVTSASTDLQDYTY*FCPGFLGLSVKLLRLLQCY PPPDPAVRGRLTECLETILNKAQEPPKSKKVQHSNAKNAVLFEA ISLIIHHDSEPNLLVRACNQLGQFLQHRETNLRYLALESMCTLA SSEFSHEAVKTHIETVINALKTERDVSVRQRAVDLLYAMCDRSN APQIVAEMLSYLETADYSIREEIVLKVAILAEKYAVDYTW\YVD TILNLIRIAGDYVSEEVWYRVIQIVINRDDVQGYAAKTVFEALQ APACHENLVKVGGYILGEFGNLIAGDPRSSPLIQFHLHSKFHL CSVPTRALLLSTYIKFVNLPPBVKPTIQDVLRSDSQLRNADVEL QQRAVEYLRLSTVASTDILATVLEEMPPFPERESSILAKLKKKK
			DSYSKKKYVCKILFIFLIGHDIDFGHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCIASV GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEEFKTSV SLAVSRLS\RIVTSASTDLQDYTY*FCPGFLGLSVKLLRLLQCY PPPDPAVRGRLTECLETILNKAQEPPKSKKVQHSNAKNAVLFEA ISLIIHHDSEPNLLVRACNQLGQFLQHRETNLRYLALESMCTLA SSEFSHEAVKTHIETVINALKTERDVSVRQRAVDLLYAMCDRSN APQIVAEMLSYLETADYSIREEIVLKVAILAEKYAVDYTW\YVD TILNLIRIAGDYVSEEVWYRVIQIVINRDDVQGYAAKTVFEALQ APACHENLVKVGGYILGEFGNLIAGDPRSSPLIQFHLHSKFHL CSVPTRALLLSTYIKFVNLPPBVKPTIQDVLRSDSQLRNADVEL QQRAVEYLRLSTVASTDILATVLEEMPPFPERESSILAKLKKKK
			DGYSKKKYVCKLLFIFLLGHDIDFGHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCTASV GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMGDWTSRVVHLLNDQHLGYVTAATSLITTLAQKNPEEFKTSV SLAVSRLS\RIVTSASTDLQDYTY*FCPGFLGLSVKLLRLLQCY PPPDPAVRGRLTECLETILNKAQEPPKSKKVQHSNAKNAVLFEA ISLIIHHDSEPNLLVRACNQLGQFLQHRETNLRYLALESMCTLA SSEFSHEAVKTHIETVINALKTERDVSVRQRAVDLLYAMCDRSN APQIVAEMLSYLETADYSIREEIVLKVAILAEKYAVDYTW\YVD TILNLIRIAGDYVSEEVWYRVIQIVINRDDVQGYAAKTVFEALQ APACHENLVKVGGYILGEFGNLIAGDPRSSPLIQFHLLHSKFHL CSVPTRALLLSTYIKFVNLFPBVKFPIQDVLRSDSQLRNADVEL QQRAVEYLRLSTVASTDILATVLEEMPFFPERESSILAKLKKKK GPSTYTDLEDTKRDRSVDVNGGPEPAPASTSAVSTPSSPSDLLG LGAAPPAPAGPPPSSGGGGLLVDVFSDSASVVAPLAPGSEDNFA
			DGYSKKKYVCKLLFIFLLGHDIDFGHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCTASV GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMGDWTSRVVHLLNDQHLGYVTAATSLITTLAQKNPEEFKTSV SLAVSRLS\RIVTSASTDLQDYTY*FCPGFLGLSVKLLRLLQCY PPPDPAVRGRLTECLETILNKAQEPPKSKKVQHSNAKNAVLFEA ISLIIHHDSEPNLLVRACNQLGQFLQHRETNLRYLALESMCTLA SSEFSHEAVKTHIETVINALKTERDVSVRQRAVDLLYAMCDRSN APQIVAEMLSYLETADYSIREEIVLKVAILAEKYAVDYTW\YVD TILNLIRIAGDYVSEEVWYRVIQIVINRDDVQGYAAKTVFEALQ APACHENLVKVGGYILGEFGNLIAGDPRSSPLIQFHLLHSKFHL CSVPTRALLLSTYIKFVNLFPBVKFPIQDVLRSDSQLRNADVEL QQRAVEYLRLSTVASTDILATVLEEMPFFPERESSILAKLKKKK GPSTYTDLEDTKRDRSVDVNGGPEPAPASTSAVSTPSSPSDLLG LGAAPPAPAGPPPSSGGGGLLVDVFSDSASVVAPLAPGSEDNFA
		1	DSYSKKXVCKLLFIFLLGHDIDFGHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCTASV GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMGDWTSRVVHLLNDQHLGYVTAATSLITTLAQKNPEEFKTSV SLAVSRLS\RIVTSASTDLQDYTY*FCPGFLGLSVKLLRLLQCY PPPDPAVRGRLTECLETILNKAQEPPKSKKVQHSNAKNAVLFEA ISLIIHHDSEPNLLVRACNQLGQFLQHRETNLRYLALESMCTLA SSEFSHEAVKTHIETVINALKTERDVSVRQRAVDLLYAMCDRSN APQIVAEMLSYLETADYSIREEIVLKVAILAEKYAVDYTW\YVD TILNIIRIAGDYVSEEVWYRVIQIVINRDDVQGYAAKTVFEALQ APACHENLVKVGGYILGEFGNLIAGDPRSSPLIQFHLLHSKFHL CSVPTRALLLSTYIKFVNLFPEVKPTIQDVLRSDSQLRNADVEL QQRAVEYLRLSTVASTDILATVLEEMPPFPERESSILAKLKKKK GSSTVTDLEDTKRDRSVDVNGGPEPAPASTSAVSTPSFSADLLG LGAAPPAPAGPPPSSGGSGLLVDVFSDSASVVAPLAPGSEDNFA RFVCKNNGVLFENQLLQIGKSEFRONLGRMFIFYGNKTSTOFT.
		1	DSYSKKXVCKILFIFILGHDIDFGHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCTASV GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCLIRLYRTSPDL VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEEFKTSV SLAVSRLS\RIVTSASTDLQDYTY*FCPGFLGLSVKLLRLLQCY PPPDPAVRGRLTECLETILNKAQEPPKSKKVQHSNAKNAVLIFEA ISLIIHHDSEPNLLVRACNQLGQFLQHRETNLRYLALESMCTLA SSEFSHEAVKTHIETVINALKTERDVSVRQRAVDLLYAMCDRSN APQIVAEMLSYLETADYSIREEIVLKVAILAEKYAVDYTW\YVD TILNLIRIAGDYVSEEVWRVIQIVINRDDVQGYAAKTVFEALQ APACHENLVKVGGYILGEFGNLIAGDPRSSPLIQFHLLHSKFHL CSVPTRALLLSTYIKFVNLPPEVKPTIQDVLRSDSQLRNADVEL QQRAVEYLRLSTVASTDILATVLEEMPPFPERESSILAKLKKKK GPSTVTDLEDTKRDRSVDVNGGPEFAPASTSAVSTPSPSADLLG LGAAPPAPAGPPPSSGGSGLVDVFSDSASVVAPLAPGSEDNFA RFVCKNNGVLFENQLLQIGLKSEFRQNLGRMFIFYGNKTSTQPL NFTPTLICSDDLQPNLNIQTKPVDPTVEGGAQVOVOVNTECVSD
			DSYSKKKYVCKILFIFILGHDIDFGHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCIASV GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCLIRLYRTSPDL VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEEFKTSV SLAVSRLS\RIVTSASTDLQDYTY*FCPGFLGLSVKLLRLLQCY PPPDPAVRGRLTECLETILNKAQEPPKSKKVQHSNAKNAVLIFEA ISLIIHHDSEPNLLVRACNQLGQFLQHRETNLRYLALESMCTLA SSEFSHEAVKTHIETVINALKTERDVSVRQRAVDLLYAMCDRSN APQIVAEMLSYLETADYSIREEIVLKVAILAEKYAVDYTW\YVD TILNLIRIAGDYVSEEVWYRVIQIVINRDDVQGYAAKTVFEALQ APACHENLVKVGGYILGEEGNLIAGDPRSSPLIQFHLLHSKFHL CSVPTRALLLSTYIKFVNLFPBVKPTIQDVLRSDSQLRNADVEL QQRAVEYLRLSTVASTDILATVLEEMPPFPERESSILAKLKKKK GPSTVTDLEDTKRDRSVDVNGGPEPAPASTSAVSTPSPSADLLG LGAAPPAPAGPPPSSGGSGLLVDVFSDSASVVAPLAPGSEDNFA RFVCKNNGVLFENQLLQIGLKSEFRQNLGRMFIFYGNKTSTQFL NFTETLICSDDLQPNLNIQTKPVDPTVEGGAQVQQVVNIECVSD FTEAPVLNIQFRYGGTFQNVSVQLPITLNKFFOPTEMASODFFO
			DSYSKKKYVCKLLFIFLLGHDIDFGHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTMGLALHCTASV GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCLIRLYRTSPDL VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEEFKTSV SLAVSRLS\RIVTSASTDLQDYTY*FCPGFLGLSVKLLKLLQCY PPPDPAVRGRLTECLETILNKAQEPPKSKKVQHSNAKNAVLFEA ISLIHHDSEPNLLVRACNQLGQFLQHRETNLRYLALESMCTLA SSEFSHEAVKTHIETVINALKTERDVSVRQRAVDLLYAMCDRSN APQIVAEMLSYLETADYSIREEIVLKVAILAEKYAVDYTW\YVD TILNLIRIAGDYVSEEVWYRVIQIVINRDDVQGYAAKTVFEALQ APACHENLVKVGGYILGEFGNLIAGDPRSSPLIQFHLLHSKFHL CSVPTRALLLSTYIKFVNLFPBVKPTIQDVLRSDSQLRNADVEL QQRAVEYLRLSTVASTDILATVLEEMPFPERESSILAKLKKKK GPSTVTDLEDTKRDRSVDVNGGPEPAPASTSAVSTPSPSADLLG LGAAPPAPAGPPPSSGGSGLLVDVFSDSASVVAPLAPGSEDNFA RFVCKNNGVLFENQLLQIGLKSEFRQNLGRMFIFYGNKTSTQFL NFTPTLICSDDLQPNLNIQTKPVDPTVEGGAQVQOVNIECVSD FTEAPVLNIQFRYGGTFQNVSVQLPITLNKFPQPTEMASQDFFQ RWKQLSNPQQEVQNIFKAKHPMDTEVTKAKIIGFGSALLERVDP
			DSYSKKKYVCKLLFIFLLGHDIDFGHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCTASV GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEEFKTSV SLAVSRLS\RIVTSASTDLQDYTY*FCPGFLGLSVKLLRLLQCY PPPDPAVRGRLTECLETILNKAQEPPKSKKVQHSNAKNAVLFEA ISLIIHHDSEPNLLVRACNQLGQFLQHRETNLRYLALESMCTLA SSEFSHEAVKTHIETVINALKTERDVSVRQRAVDLLYAMCDRSN APQIVAEMLSYLETADYSIREEIVLKVAILAEKYAVDYTW\YVD TILNLIRIAGDYVSEEVWYRVIQIVINRDDVQGYAAKTVFEALQ APACHENLVKVGGYILGEFGNLIAGDPRSSPLIQFHLLHSKFHL CSVPTRALLLSTYIKFVNLPPBVKETIQDVLRSDSQLRNADVEL QQRAVEYLRLSTVASTDILATVLEEMPFPERESSILAKLKKKK GPSTVTDLEDTKRDRSVDVNGGPFBAPASTSAVSTPSPSADLLG LGAAPPAPAGPPPSSGGSGLLVDVFSDSASVVAPLAPGSEDNFA RFVCKNNGVLFENQLLQIGLKSEFRQNLGRMFIFYGNKTSTOPL NFTPTLICSDDLQPNLNIQTKPVDPTVEGGAQVQOVVNIECVSD FTEAPVLNIQFRYGGTFQNVSVQLPITLNKPFQPTEMASQDFFQ RWKQLSNPQQEVQNIFKAKHPMDTEVTKAKIIGFGSALLEEVDP NPANFVGAGIIHTKTTQIGCLLKLEPNLQAQMYRLTIRTSXEAV
5849	3545	·	DSYSKKXYVCKLLFIFLLGHDIDFGHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCIASV GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEEFKTSV SLAVSRLS\RIVTSASTDLQDYTY*FCPGFLGLSVKLLRLLQCY PPPDPAVRGRLTECLETILNKAQEPPKSKKVQHSNAKNAVLFEA ISLIIHHDSEPNLLVRACNQLGQFLQHRETNLRYLALESMCTLA SSEFSHEAVKTHIETVINALKTERDVSVRQRAVDLLYAMCDRSN APQIVAEMLSYLETADYSIREEIVLKVAILAEKYAVDYTW\YVD TILNLIRIAGDYVSEEVWYRVIQIVINRDDVQGYAAKTVFEALQ APACHENLVKVGGYILGEFGNLIAGDPRSSPLIQFHLLHSKFHL CSVPTRALLLSTYIKFVNLPPBVKPPIQDVLRSDSQLRNADVEL QQRAVEYLRLSTVASTDILATVLEEMPPFPERESSILAKLKKKK GPSTYTDLEDTKRDRSVDVNGGPEPAPASTSAVSTPSSADLLG LGAAPPAPAGPPPSSGGSGLLVDVFSDSASVVAPLAPGSEDNFA RFVCKNNGVLFENQLLQIGLKSEFRQNLGRMFIFYGRKTSTQFL NFTPTLICSDDLQPNLNIQTKPVDPTVEGGAQVQQVVNIECVSD FTEAPVLNIQFRYGGTFQNVSVQLPITLNKFFQPTEMASQDFFQ RWKQLSNPQQEVQNIFKAKHPMDTEVTKAKIIGFGSALLEEVDP NPANFYGAGIIHTKTTQIGCLLRLEPNLQAQMYRLTLRTSKEAV SQRLCELLSAQF
5849	3545	1895	DSYSKKKYVCKLLFIFLLGHDIDFGHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCTASV GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMGDWTSRVVHLLNDQHLGYVTAATSLITTLAQKNPEEFKTSV SLAVSRLS\RIVTSASTDLQDYTY*FCPGFLGLSVKLLRLLQCY PPPDPAVRGRLTECLETILNKAQEPPKSKKVQHSNAKNAVLFEA ISLIIHHDSEPNLLVRACNQLGQFLQHRETNLRYLALESMCTLA SSEFSHEAVKTHIETVINALKTERDVSVRQRAVDLLYAMCDRSN APQIVAEMLSYLETADYSIREIVLKVAILAEKYAVDYTW\YVD TILNIIRIAGDYVSEEVWYRVIQIVINRDDVQGYAAKTVFEALQ APACHENLVKVGGYILGEFGNLIAGDPRSSPLIQFHLLHSKFHL CSVPTRALLLSTYIKFVNLFPEVKPTIQDVLRSDSQLRNADVEL QQRAVEYLRLSTVASTDILATVLEEMPPFPEESSILAKLKKKK GPSTVTDLEDTKRDRSVDVNGGPEPAPASTSAVSTPSFSADLLG LGAAPPAPAGPPPSSGGSGLLVDVFSDSASVVAPLAPGSEDNFA RFVCKNNGVLFENQLLQIGLKSEFRQNLGRMFIFYGNKTSTQFL NFTPTLICSDDLQPNLNIQTKPVDPTVEGGAQVQQVVNIECVSD FTEAPVLNIQFRYGGTFQNVSVQLPITLNKFFQPTEMASQDFFQ RWKQLSNPQQEVQNIFKAKHPMDTEVTKAKIIGFGSALLEEVDP NPANFVGAGIIHTKTTQIGCLLRLEPNLQAQMYRLTLRTSKEAV SQRLCELLSAQF KRREIKETVFHHVAQAGLELLSSNPPSSASRSAGTTGMPUOVO
5849	3545	. 1895	DSYSKKXVCKLLFIFLLGHDIDFGHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCTASV GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEEFKTSV SLAVSRLS\RIVTSASTDLQDYTY*FCPGFFLGLSVKLLRLLQCY PPPDPAVRGRLTECLETILNKAQEPPKSKKVQHSNAKNAVLIFEA ISLIIHHDSEPNLLVRACNQLGQFLQHRETNLRYLALESMCTLA SSEFSHEAVKTHIETVINALKTERDVSVRQRAVDLLYAMCDRSN APQIVAEMLSYLETADYSIREEIVLKVAILAEKYAVDYTW\YVD TILNIIRIAGDYVSEEVWXVIQIVINRDDVQGYAAKTVFEALQ APACHENLVKVGGYILGEFGNLIAGDPRSSPLIQFHLLHSKFHL CSVPTRALLLSTYIKFVNLFPEVKPTIQDVLRSDSQLRNADVEL QQRAVEYLRLSTVASTDILATVLEEMPPFPERESSILAKLKKKK GPSTVTDLEDTKRDRSVDVNGGPBPAPASTSAVSTPSPSADLLG LGAAPPAPAGPPPSSGGSGLLVDVFSDSASVVAPLAPGSEDNFA RFVCKNNGVLFFNQLLQIGLKSEFRQNLGRMFIFYGNKTSTQPL NFTPTLICSDDLQPNLNIQTKPVDPTVEGGAQVQOVVNIECVSD FTEAPVLNIQFRYGGTFQNVSVQLPITLNKFFQPTEMASQDFFQ RWKQLSNPQQEVQNIFKAKHPMDTEVTKAKIIGFGSALLEEVDP NPANFVGAGIHTKTTQIGCLLRLEPNLQAQMYRLTLRTSKEAV SQRLCELLSAQF KRRIKETVFHHVAQAGLELLSSNPPSSASRSAGITGMRHQVQ P*DPCMSLSPPCFTEEDRFSLEALOTIHKOMDDDKGGIFVERG
5849	3545	1895	DSYSKKXVCKLLFIFLLGHDIDFGHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCIASV GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEEFKTSV SLAVSRLS\RIVTSASTDLQDYTY*FCPGFFLGLSVKLLRLLQCY PPPDPAVRGRLTECLETILNKAQEPPKSKKVQHSNAKNAVLIFEA ISLIIHHDSEPNLLVRACNQLGQFLQHRETNLRYLALESMCTLA SSEFSHEAVKTHIETVINALKTERDVSVRQRAVDLLYAMCDRSN APQIVAEMLSYLETADYSIREEIVLKVAILAEKYAVDYTW\YVD TILNLIRIAGDYVSEEVWYRVIQIVINRDDVQGYAAKTVFEALQ APACHENLVKVGGYILGEFGNLIAGDPRSSPLIQFHLLHSKFHL CSVPTRALLLSTYIKFVNLPPEVKPTIQDVLRSDSQLRNADVEL QQRAVEYLRLSTVASTDILATVLEEMPPFPERESSILAKLKKKK GPSTVTDLEDTKRDRSVDVNGGPEFAPASTSAVSTPSPSADLLG LGAAPPAPAGPPPSSGGSGLLVDVFSDSASVVAPLAPGSEDNFA RFVCKNNGVLFENQLLQIGLKSEFRQNLGRMFIFYGNKTSTQPL NFTPTLICSDDLQPNLNIQTKPVDPTVEGGAQVQQVVNIECVSD FTEAPVLNIQFRYGGTFQNVSVQLPITLNKFFQPTEMASQDFFQ RWKQLSNPQQEVQNIFKAKHPMDTEVTKAKIIGFGSALLEEVDP NPANFVGAGIIHTKTTQIGCLLRLEPNLQAQMYRLTLRTSKEAV SQRLCELLSAQF KRREIKETVFHHVAQAGLELLSSNPPSSASRSAGITGMRHQVQ P*PPCMSLSPPCFTBEDRFSLEALQTIHKQMDDDKDGGIEVEES DEFIREDMKYKDATNKHSHLHREDKHITIEDLWKRWKTSFVINM
5849	3545	1895	DSYSKKXYCKLLFIFLLGHDIDFGHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCTASV GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCLIRLYRTSPDL VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEEFKTSV SLAVSRLS\RIVTSASTDLQDYTY*FCPGFLGLSVKLLKLLQCY PPPDPAVRGRLTECLETILNKAQEPPKSKKVQHSNAKNAVLFEA ISLIIHHDSEPNLLVRACNQLGQFLQHRETNLRYLALESMCTLA SSEFSHEAVKTHIETVINALKTERDVSVRQRAVDLLYAMCDRSN APQIVAEMLSYLETADYSIREEIVLKVAILAEKYAVDYTW\YVD TILNLIRIAGDYVSEEVWYRVIQIVINRDDVQGYAAKTVFEALQ APACHENLVKVGGYILGEFGNLIAGDPRSSPLIQFHLLHSKFHL CSVPTRALLLSTYIKFVNLPPBVKETIQDVLRSDSQLRNADVEL QQRAVEYLRLSTVASTDILATVLEEMPFPERESSILAKKKK GPSTVTDLEDTKRDRSVDVNGGPFBAPASTSAVSTPSPSADLLG LGAAPPAPAGPPPSSGGSGLLVDVFSDSASVVAPLAPGSEDNFA RFVCKNNGVLFENQLLQIGLKSEFRQNLGRMFIFYGNKTSTOPL NFTPTLICSDDLQPNLNIQTKPVDPTVEGGAQVQOVVNIECVSD FTEAPVLNIQFRYGGTFQNVSVQLPITLNKFFQPTEMASQDFFQ RWKQLSNPQQEVQNIFKAKHPMDTEVTKAKIIGFGSALLEEVDP NPANFVGAGIIHTKTTQIGCLLRLEPNLQAQMYRLTLRTSKEAV SQRLCELLSAQF KRREIKETVFHHVAQAGLELLSSSNPPSSASRSAGITGMRHQVQ P*DPCMSLSPPCFTBEBRFSLEALQTIHKQMDDDKDGGIEVEES DEFIREDMKYKDATNKHSHLHREDKHITIEDLWKRWKTSEVHNW TLEDTLQWIIEFVELPQYEKNFRDNNVKGTTLPRIAVHPPSEMT
5849	3545	1895	DSYSKKXYVCKLLFIFLLGHDIDFGHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCIASV GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEEFKTSV SLAVSRLS\RIVTSASTDLQDYTY*FCPGFLGLSVKLLRLLQCY PPPDPAVRGRLTECLETILNKAQEPPKSKKVQHSNAKNAVLFEA ISLIIHHDSEPNLLVRACNQLGQFLQHRETNLRYLALESMCTLA SSEFSHEAVKTHIETVINALKTERDVSVRQRAVDLLYAMCDRSN APQIVAEMLSYLETADYSIREEIVLKVAILAEKYAVDYTW\YVD TILNLIRIAGDYVSEEWYRVIQIVINRDDVQGYAAKTVFEALQ APACHENLVKVGGYILGEFGNLIAGDPRSSPLIQPHLLHSKFHL CSVPTRALLLSTYIKFVNLPPBVKFTIQDVLRSDSQLRNADVEL QQRAVEYLRLSTVASTDILATVLEEMPFPERESSILAKLKKKK GPSTYDDLEDTRRDRSVDVNGGPEPAPASTSAVSTPSPSADLLG LGAAPPAPAGPPPSSGGSGLLVDVFSDSASVVAPLAPGSEDNFA RFVCKNNGVLFENQLLQIGLKSEFRQNLGRMFIFYGNKTSTQFL NFTPTLICSDDLQPNLNIQTKPVDPTVEGGAQVQQVVNIECVSD FTEAPVLNIQFRYGGTFQNVSVQDPITLNKFFQPTEMASQDFFQ RWKQLSNPQQEVQNIFKAKHPMDTEVTKAKIIGFGSALLEEVUP NPANFVGAGIIHTKTTQIGCLLRLEPNLQAQMYRLTLRTSXEAV SQRLCELLSAQF KRREIKETVFHHVAQAGLELLSSNPPSSASRSAGITGMRHQVQ P*DPCMSLSPPCFTEEDRFSLEALQTIHKQMDDKDGGIEVEES DEFIREDMKYKDATNKHSLHRREDKHITIEDLWKRWKTSEVHNW TLEDTLQWLIEFVELPQYEKNFRDNNVKGTTLPRIAVHEPSFMI SQLKISDRSHRQKLQLKALDVVLFGPLTRPPHNWMKDFILTVST
5849	3545	1895	DSYSKKXYVCKLLFIFLLGHDIDFGHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCIASV GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEEFKTSV SLAVSRLS\RIVTSASTDLQDYTY+FCPGFLGLSVKLLRLLQCY PPPDPAVRGRLTECLETILNKAQEPPKSKKVQHSNAKNAVLFEA ISLIIHHDSEPNLLVRACNQLGQFLQHRETNLRYLALESMCTLA SSEFSHEAVKTHIETVINALKTERDVSVRQRAVDLLYAMCDRSN APQIVAEMLSYLETADYSIREEIVLKVAILAEKYAVDYTW\YVD TILNLIRIAGDYVSEEVWYRVIQIVINRDDVQGYAAKTVFEALQ APACHENLVKVGGYILGEFGNLIAGDPRSSPLIQFHLLHSKFHL CSVPTRALLLSTYIKFVNLFPBVKPFIQDVLRSDSQLRNADVEL QQRAVEYLRLSTVASTDILATVLEEMPFFPERESSILAKLKKKK GPSTVTDLEDTKRDRSVDVNGGPEPAPASTSAVSTPSSADLLG LGAAPPAPAGPPPSSGGSGLLVDVFSDSASVVAPLAPGSEDNFA RFVCKNNGVLFENQLLQIGLKSEFRQNLGRMFIFYGRKTSTOFL NFTPTLICSDDLQPNLNIQTKPVDPTVEGGAQVQQVVNIECVSD FTEAPVLNIQFRYGGTFQNVSVQLPITLNKFFQPTEMASQDFFQ RWKQLSNPQQEVQNIFKAKHPMDTEVTKAKIIGFGSALLEEVDP NPANFVGAGIHTKKTTQIGCLLRLEPNLQAQMYRLTLRTSXEAV SQRLCELLSAQF KRREIKETVFHHVAQAGLELLSSNPPSSASRSAGITGMRHQVQ P*PPCMSLSPPCFTEEDRFSLEALQTIHKQMDDDKDGGIEVEES DEFIREDMKYKDATNKHSHLHRRDKHITIEDLWKRWKTSEVHNW TLEDTLQWLIEFVELPQYEKNFRDMVKGTTLPRIAVHEPSFMI SQLKISDRSHRQKLQLKALDVVLFGPLTRPPHNWKDFILTVSI VIGVGGCWFAYTQNKTSKEHVAKMMKDLESLOTAECSIMDLOER
5849	3545	1895	DSYSKKXYVCKLLFIFLLGHDIDFGHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCTASV GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMGDWTSRVVHLLNDQHLGYVTAATSLITTLAQKNPEEFKTSV SLAVSRLS\RIVTSASTDLQDYTY*FCPGFLGLSVKLLRLLQCY PPPDPAVRGRLTECLETILNKAQEPPKSKKVQHSNAKNAVLFEA ISLIIHHDSEPNLLVRACNQLGQFLQHRETNLRYLALESMCTLA SSEFSHEAVKTHIETVINALKTERDVSVRQRAVDLLYAMCDRSN APQIVAEMLSYLETADYSIREEIVLKVAILAEKYAVDYTW\YVD TILNIIRIAGDYVSEEVWYRVIQIVINRDDVQGYAAKTVFEALQ APACHENLVKVGGYILGEFGNLIAGDPRSSPLIQFHLLHSKFHL CSVPTRALLLSTYIKFVNLPPEVKPTIQDVLRSDSQLRNADVEL QQRAVEYLRLSTVASTDILATVLEEMPPFPEESSILAKLKKKK GPSTVTDLEDTKRDRSVDVNGGPEPAPASTSAVSTPSFSADLLG LGAAPPAPAGPPPSSGGSGLLVDVFSDSASVVAPLAPGSEDNPA RFVCKNNGVLFENQLLQIGLKSEFRQNLGRMFIFYGNKTSTQFL NFTPTLICSDDLQPNLNIQTKPVDPTVEGGAQVQQVVNIECVSD FTEAPVLNIQPRYGGTFQNVSVQLPITLNKFFQPTEMASQDFFQ RWKQLSNPQQEVQNIFKAKHPMDTEVTKAKIIGFGSALLEEVDP NPANFVGAGIIHTKTTQIGCLLRLEPNLQAQMYRLTLRTSKEAV SQRLCELLSAQF KRREIKETVFHHVAQAGLELLSSNPPSSASRSAGITGMRHQVQ P*DPCMSLSPPCFTEEDRFSLEALQTIHKQMDDDKDGGIEVEES DEFIREDMKYKDATNKHSHLHREDKHITIEDLWKRWKTSEVHNW TLEDTLQWLIEFVELPQYEKNFRDNNVKGTTLPRIAVHEPSFMI SQLKISDRSHRQKLQLKALDVVLFGPLTRPPHNWMCDFILTVSI VIOVGGCWFAYTQNKTSKEHVAKMMKDLESLQTAEQSLMDLQER LBKAQEENRNVAVEKQNL*RKMMEINYAKEEACRLRELREGAE
5849	3545	1895	DSYSKKXYVCKLLFIFLLGHDIDFGHMEAVNLLSSNRYTEKQIG YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCIASV GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEEFKTSV SLAVSRLS\RIVTSASTDLQDYTY+FCPGFLGLSVKLLRLLQCY PPPDPAVRGRLTECLETILNKAQEPPKSKKVQHSNAKNAVLFEA ISLIIHHDSEPNLLVRACNQLGQFLQHRETNLRYLALESMCTLA SSEFSHEAVKTHIETVINALKTERDVSVRQRAVDLLYAMCDRSN APQIVAEMLSYLETADYSIREEIVLKVAILAEKYAVDYTW\YVD TILNLIRIAGDYVSEEVWYRVIQIVINRDDVQGYAAKTVFEALQ APACHENLVKVGGYILGEFGNLIAGDPRSSPLIQFHLLHSKFHL CSVPTRALLLSTYIKFVNLFPBVKPFIQDVLRSDSQLRNADVEL QQRAVEYLRLSTVASTDILATVLEEMPFFPERESSILAKLKKKK GPSTVTDLEDTKRDRSVDVNGGPEPAPASTSAVSTPSSADLLG LGAAPPAPAGPPPSSGGSGLLVDVFSDSASVVAPLAPGSEDNFA RFVCKNNGVLFENQLLQIGLKSEFRQNLGRMFIFYGRKTSTOFL NFTPTLICSDDLQPNLNIQTKPVDPTVEGGAQVQQVVNIECVSD FTEAPVLNIQFRYGGTFQNVSVQLPITLNKFFQPTEMASQDFFQ RWKQLSNPQQEVQNIFKAKHPMDTEVTKAKIIGFGSALLEEVDP NPANFVGAGIHTKKTTQIGCLLRLEPNLQAQMYRLTLRTSXEAV SQRLCELLSAQF KRREIKETVFHHVAQAGLELLSSNPPSSASRSAGITGMRHQVQ P*PPCMSLSPPCFTEEDRFSLEALQTIHKQMDDDKDGGIEVEES DEFIREDMKYKDATNKHSHLHRRDKHITIEDLWKRWKTSEVHNW TLEDTLQWLIEFVELPQYEKNFRDMVKGTTLPRIAVHEPSFMI SQLKISDRSHRQKLQLKALDVVLFGPLTRPPHNWKDFILTVSI VIGVGGCWFAYTQNKTSKEHVAKMMKDLESLOTAECSIMDLOER

SEQ	Predicted	Predicted end	I hmino cold comment
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ļ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /-possible nucleotide deletion,
1	sequence	1	\=possible nucleotide insertion)
			AHSSSLDEVDHKILEAKKALSELTTCLRERLFRWQQIEKICGFQ
ŀ		[	IAHNSGLPSLTSSLYSDHSWVVMPRVSIPPYPIAGGVDDLDEDT
į.			PPIVSQFPGTMAKPPGSLARSSSLCRSRRSIVPSSPQPQRAQLA
	1		PHAPHPSHPRHPHHPQHTPHSLPSPDPDILSVSSCPALYRNBEE
i		ŀ	EEAIYFSABKQWEVPDTASECDSLNSSIGRKQSPP/SKPRDIPN
ĺ	· ·	i	IIS/DERYQEMRCP*RIPSGGIL
5850	3	1895	KAVLNFSASGSVISLTGSNPMHDASMWHLKKNGIIVYLDVPLLN
			LICRLKLMKTDRIVGQNSGTSMKDLLKFRRQYYKKWYDARVFCE
			SGASPEEVADKVLNAIKRYQDVDSETFISTRHVWPEDCEQKVSA
1	<b>i</b> !		EFFIEAVIEGLASDGGLFVPAKEFPKLSCGEWKSLVGATYVERA
	1		QILLERCIHPADIPAARLGEMIETAYGENFACSKIAPVRHLSGN
1			QFILELFHGPTGSFKDLSLQLMPHIFAQCIPPSCNYMILVATSG
			DTGSAVLNGFSRLNKNDKQRIAVVAFFPENGVSDFQKAQIIGSQ
			RENGWAVGVESDFDFCQTAIKRIFNDSDFTGFLTVEYGTILSSA
1	j	•	NSINWGRLLPQVVYHASAYLDLVSQGFISFGSPVDVCIPTGNFG
1			NILAAVYAKMMGIPIRKFICASNQNHVWTDFIKTG\HYDLRGKE
1			N*AQTFFTVQ*IFLPNLSNLERHLHLMANKDGQLMTELFNRLES
			QHHFQIEKALVEKLQQDFVADWCSEGECLAAINSTYNTSGYILD
1			PHTAVAKVVADRVQDKTCPVIISSTAHYSKFAPAIMQALKIKEI
}			NETSSSQLYLLGSYNALPPLHEALLERTKQQEXMEYQVCAADMN
			VLKSHVEQLVQNOFI
5851	3120	1802	RCYLQFLALLLTSTSARAAAIAAAEEPAGSPSVMTRAGDHNRQ
			RGCCGSLADYLTSAKFLLYLGHSLSTWGDRMWHFAVSVFLVELY
<u> </u>			GNSLLLTAVYGLVVAGSVLVLGAIIGDWVDKNARLKVAQTSLVV
1			QNVSVILCGIILMMVFLHKHELLTMYHGWVLTSCYILIITIANI
ł			ANLASTATAITIQRDWIVVVAGEDRSKLANMNATIRRIDQLTNI
1			LAPMAVGQIMTFGSPVIGCGFISGWNLVSMCVEYVLLWKVYQKT
			PALAVKAGLKEEETELKQLNLHKDTEPKPLEGTHLMGVKDSNIH
1 1			ELEHEQEPTCASQMAEPFRTFRDGWVSYYNQPVF/LGWHGSCFP
1 1			LYDCPGL*LHHHRVRLHSGTEWFHPQYFDGSISYNWNNGNCSFY
			LATSKMWFGSDRSDLRIGTAFLFDLVCDLCIHAWKPPGLVRFSF
5852	1	422	KTTFPSSLCPLRQLPEVRGYSGQPLTDPLISLCRSHKCRGKGWG
1 1	1		SSSYPSLPALLRARSAPGHCTHRSCGPEWRIDSISRLEMQGARR
			SGWAQAQPTILLLVPRLRKSLPSIWG/SLMGFFITSGPG/WFRO
			YYFFISGRH*VLFTESDFYYVAMDFGGHGL9SHYSPGVPYYLOT
			FVSBIRRVVAGKKQSVYFRRCGGCSRAPPLITGGGVGSRKQRWP
1			ESGAWALAPGLPAIHGRSWES
5853	223	1346	RLLGLSRVKGLHGPAASAWISDPETRGDPGGPWGMWRGSDLRPR
1 1			PVSLTGLTLVCK*AAQGPQV\HSVKLCFGLGG\PCLL\FPIFRP
1 ]		•	LLLHPRRPRLHPGTRGVAVEPHALRVVHVAHGEEAGIRAAGPGH
1 1			GGVEIPQG/VGSLGARRGLRPSRPSSRHRNRVPAPPPGRPLATP
			HRRRFPPDPALTCPGLGODOGPREOOKOGSGRHDTTLGDWGESE
		i	SRWVRGNFRTGTAATLIGFSRNPTLNGSENWGSLVSIOEEGPDT
			GWEREKRNPAEMGNPQRWASPIHTPPLGPEILRAMPEALRAMPE
[	į		ALGLRPDPATSVPSALS/QTF/PESWPRSCLRNQGETLGMGPVP
			LSSLCITESPSQNWTPCLLLLTCPRGLF
5854	86	938	KGRNTAPEKKGAALNNRENASS*NGY/SRWKQDIRRIENHIIQE
.			LKHLCAMIKRVLLERLENTRKLRELTEGRTLDWPONRITEVSAK
	1		RQIVTEYREKGKRN*EEKKRDLEGRSRRYNLCIIGIPETEDRAS
į į	1	ł	GAETIKOLLE/ENFPELKNELDLQMEKAHRIPLKFNEKKAASRH
		j	IRVTFL/KFQRRNILQASSQRKQVTYKGAKVRLTSDFSPAILNA
	}		RRQW/N/PISRVLRENNFEPRIIYSAKLSFLYKGNWKTFLDIQG
5055		·	LGKYINQELSLKILLKDLLQLTENLN
5855	536	2391	LRSYGCKAPSRISHLHK\FLFLLLPSLLMGYSESPPPITDSWAP
!			FISLTHHVLSQSQSPLSSNCWICLSTHTQ*FTALPADLLTWTOS
İ	ļ	i	NVSLHISYLAIPFLADSFLKPV/L*PGNSAKHLSFKLSSLSMVS
		1	GRAVALLHLIASGLTSIQTNTASSKPPIWGY\LSTOTSFISPPP
İ	[	1	LCLSRTYPNPAHATMVGQVPQSLCGLIFTL/RTPCRPSILHPNY
ļ <b>J</b>	ļ	ļ	KIISTSAWQKVLCFSGSPTIHTSLHLTTGSSFLSFHPIPGFPAA
			NSALYVSSLKGPPGKNVTIPSPVTGT*QPPHRGSN/RLTVDKDN
		-	

SEC	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ł	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
J	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
}	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
•	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	}	\=possible nucleotide insertion)
			FFLSPKPNSLHQLPSQ\TPYQALTGAALAGSYPIWENENTLSWL
1			PTFTYNFCLSTPSLFFLCDTN+YLCLPANWSGTCTLVFQAPTIN
1	•	ŀ	ILPPNQTILISVEASISSSPIRNKWALHLITLLTGLGITAALGT
			GIAGITTSITSYQTLFTTLSNTVEDMHTSITSLQRQLDFLVGVI
	1	ł	LQNWRVLDLLTTEKGGTCIYLQEECCFCVNESGIVHIAVRRLHD
}	ŀ		RAAEL+HQVADSWWQGSSLLRWIPWVAPFLGPLIFLFLLLMIGP
ł			CIFNLVSRFISQRLNCFIQASNQXHIDNIFHLCHV+YQSLRGNH
İ			SEAPEPRP
5856	173	1137	PWLHGLGLSAVFLFYL*/YVTFHLYGGIILLLLIFISIAGILYK
	Ì	·	FQDVLLYFPEQPSSSRLYVPMPTGIPHENIFIRTKDGIRLNLIL
1	1		IRYTGDNSPYSPTIIYFHGNAGNIGHRLPNALLMLVNLKVNLLL
1	1		VDYRGYGKSEGEASERGLYLDSEAVLDYVMTSPDLDKTKIYLSG
1			RSLG\GAAAIHLASDNSHRISAIMVENTFLSIPHMASTLFSFFP
			MRYLPLWCYKNKFLSYRKISQCRMPSLFISGLSDQLIPPVMMKQ
1			LYELSPSRTKRLAIFPDGTHNDTWQCQGYFTALEQFIKEVVKSH
1	i I		SPEEMAKTSSNVTII
5857	1597	563	KLIGKVLVLSVVADAMAAFAVEPQGPALGSEPMMLGSPTSPKPG
l I	1		VNAQFLPGFLMGDLPAPVTPQPRSISGPSVGVMEMRSPLLAGGS
1			PPQPVVPAHKDKSGAPPVRSIYDDISSPGLGSTPLTSRRQPNIS
1			VMQSPLVGVTSTPGTGQSMFSPASIGQPRKTTLSPAQLDPFYTQ
			GDSLTSEDH\LDDSWGDCIWGFLKASA\SYILL\QFAQYGGIS*
			NMWMSNTGNWMHIRYQSKLQARKALSKDGRIFGESIMIGVKPCI
i			DKSVMESSDRCALSSPSLAFTPPIKTLGTPTQPGSTPRISTMRP
			LATAYKASTSDYQVISDRQTPKKDESLVSKAMEYMFGW
5858	355	1419	PPHQPAAASTSXHQQQQPPPPPQDSSKPVVAQGPGPAPGVGSAP
1 1	[		PASSSAPPATPPTSGAPPGSGPGPTPTPPPAVTSAPPGAPPPTP
1 1			PSSGVPTTPPQAGGPPPPPPAAVPGPGPGPKQGPGPGGPKGGKMP
1 1			GGPKPGGGPGLSTPGGHPKPPHRGGGEPRGGROHHPPYHOOHHO
1			GPPPGGPGGRSEEKISGPRRGFKANLSLLRRPGEKTYTORCRFC
1 1	}		LLGIYLLISRRMNSRRLFAKIWENQEKFLSTKAKDSEFIKLESR
1			ALA*NCPKFELG*YTP*GGROLPSSLFPTHACLPLSCSVIFSPF
1	ĺ		MFPQ*NCWGRKPFRPNLGPHLKGAVCNRWDDPWEGPTGKGHCLN
		•	FAS ·
5859	307	1503	GGSSARPRASSRRMLSRKKTKNEVSKPAEVQGKYVKKETSPLLR
1 1			NLMPSFIRHGPTIPRRTDICLPDSSPNAFSTSGDGVVSRNOSFI.
i 1			RTPIQRTPHEIMRRESNRLSAPSYLARSLADVPREYGSSQSFVT
			EVSFAVENGDSGSRYYYSDNFFDGQRKRPLGDRAHEDYRYYEYN
1 1			HDLFQRMPQNQGRHASGIGRVAATSLGNLTNHGSEDLPLPPGWS
1 1		i	VDWTMRGRKYYIDHNTNTTHWSHPLEREGLPPGWERVESSEFGT
		ļ	YYVDHTNKKAQY\RHPCAPTCTSV*STTSCHI/AS/RQQTERNQ
			SLLVPANPYHTAEIPDWLQVYARAPVKYDHILKWELFQLADLDT
l í			YQGMLKLLFMKELEQIVKMYEAYRQALLTELENRKQRQQWYAQQ
5860	2956	1000	HGKNP
	6930	1270	TIRVEBFPLCPGGGKAQLSSASLLGAGLLLQPPTPPPLLLLLFP
	İ		LLLFSRLCGALAGPIIVEPHVTAVWGKNVSLKCLIEVNETITQI
			SWEKIHGKSSQTVAVHHPQYGFSVQGBYQGRVLFKNYSLNDATI
[	ſ	1	TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKG
		ľ	PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFP
	ļ		NETATIISQYKLFPTRFARGRRITCVVKHPALEKDIRYSFILDI
			QYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLDG
		[	QWPDGLLASDNTLHFVHPLTFNYSGVYICKVT\NSPGSKEVTQK
		l	VHPTFQDPSLPTYPPLPALQFQWASPSTA*TSRD\LATEP*KIA
		İ	PSPLSTL\ATIKGWTQLPTIIA*CSGVGALFIV\LVKCFGLGIF
		į	CYRRRRTFRGDYFAKNYIPPSDMQKESQIDVLQQDELDPYPDSV
ļ	1		KKENKNPVNNLIRKDYLEEPEKTQWNNVENLNRFERPMDYYEDL
5861	2051	1305	KMGMKFVSDEHYDENEDDLVSHVDGSVISRRENYV
1	=	2303	EVCACVQAFNLVASSGDDSQGGDKCGCEVGSWVGSMRVVMARLL
J	İ		SEGEOGIPTACAAFAQQPAG/BPRRGLAGVGEGGPQCSWVNYRC
[		ľ	TLEFLVSLLGTDLARGRGNSASGPTAPADSKQL/ML*DVHRRVI
		<u></u>	LE*RMNSGSPARDNAPSQRFCTNLSEGLRFGISPSWREALYGCH

SEQ	Predicted	Predicted end	I bring agid agency
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	United Acid, Fernenylalanine, GeGlycine,
ı	corresponding	to first	H-Histidine, I-Isolcucine, K-Lysine,
ı	to first		L=Leucine, M=Methionine, N=Asparagine,
1		amino acid	P-Proline, Q-Glutamine, R-Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion.
	sequence		\=possible nucleotide insertion)
			Α .
5862	1556	483	PPFQLIMGEIKVSPDYNWFRGTVPLKKIIVDDDDSKIWSLYDAG
Į.	1	ĺ	PRSIRCPLIFLPPVSGTADVFFRQILALTGWGYRVIALQYPVYW
	l .		DHLEFCDGFRKLLDHLQLDKVHLFGASLGGFLAQKFAEYTHKSP
			RVHSLILCNSFSDTSIFNQTWTANSFWLMPAFMLKKIVLGNFSS
1		ĺ	CDVDDMMADA TO ENGINEE POR COCKET TO THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND THE COLUMN AND
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	1		RDIPVTIMDVFDQSALSTEAKEEMYKLYPNARRAHLKTGGNFPY
1	1		LCRSAEVNLYVQIHL/R/RNSMEPNTRPLTHQWSVPRSLRCRKA
			ALASARRSSSVSLAVNDELTRCVLV+SVASAPVSRPFPSGSSGS
Ĺ			PVLTVSGK
5863	2714	249	PFPSRGSLPLAAPREDTMGPLMVLFCLLFLYPGLADSAPSCPQN
J	<b>(</b>		VNISGGTFTLSHGWAPGSLLTYSCPQGLYPSPASRLCKSSGQWQ
1	[	1	TPGATRSLSKAVCKPVRCPAPVSFENGIYTPRLGSYPVGGNVSF
!			ECEDGFI\LRGSPVRQCRPNGMWDGETAVCDNGAGHCPNPGISL
1			CD/VETCEDEGUCDATEUD COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOOGET TO COOKY VI MOO
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	1		DGK\SHMGGSPKTAVDHIREILNINQKRNDYLDIYAIGVGKLDV
i			DWRELNELGSKKDGERHAFILQDTKALHQVFRHMLDVSKLTDTI
	i .		CGVGNMSANASDQERTPWHVTIKPKSQET\C\RGALISDQWVLT
	i		AAHCFRDGNDHSLWRVNVGDPKSQWGKEFLIEKAVISPGFDVFA
	!		KCNQGIL\EFYGD\DIALL\KLAQKVKM\STHCQGPSCLP\CTM
	l		CONGRETATION DIALITY (KLAQKVKM\STHCQGPSCLP\CTM
			\EANLGFLRETFKGSTCR\DHENEL/VWNKQSV\PAHF\VAL\N
	1		GSKLEHLTLRMGVEWTSCCRGLSPKKKTM\FFNLT\DVRB\VVT
1 1			D\QFL\CS\GPQEDESP\CK*E\SGGA\VFLERRFRLSAGGVWC
			SWGL\YNP\CLGSA\DKNSPKKGPSVAKVPPFTR/DFHIN\LFP
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			EWATLRTL
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1	!		KLPPSIPPSSPLACVLKNLKPLQLTPDLKPKCLIFFCNTAWPQY
			KLDNDSK*PENGTFEFSILQVLDNSCHKMGKWSEVPDVQAFF\S
1			HWSLPSLCSQC/GLIPNLSSFSPFCSFG/PPPQVPSP/TESFFS
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			MDSSDLPPSPQAAPRQAEPGPNSHLASAPPPYNPFITSPPHTWS
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1 1	ĺ	ļ	LSVCVCVQVGSWICV/CVSMCACVSLCTC\ICRCISMYTREHAC
[	. 1		ACTRV*VYMCMS/VCTCVSTCIDVRVCAHVCVYMCLCLGYA*AC
			TCV*MCVCMHEHVCMC/VCACSCVLL/CRGHICM/MCMSAYICI
1			/CVYVCVLCVWACMRMSTCVWLVYG*ACTCVWMHM/CSCTCP/c
1		ļ	VHVCCMSMHACECLCVYLHICGCAGTRRWWAGSARGSRSCSRLP
1			CWAPGPGLSLPGPSCPSVEQGLGGGPGQLQGRSGEARLGEHRGW
			GSPAAVCSRNCTVSPRRGADCFEAPDVPKQPPGWGRASFEERGC
ļ į	1		GGRGWVCAPPLMGPQCCCFSIKPELKAKKKK
5866	98	3197	ADDEUDADDAM GOOGLANDELKAKKK
		3131	ARPEVPAPPAWLSRRGAAKMGDKKDDKDSPKKNKGKERRDLDDL
		ł	KKEVAMTEHKMSVEEVCRKYNTDCVQGLTHSKAQEILARDGPNA
		1	LTPPPTTPEWVKFCRQLFGGFSILLWIGAILCPLAYGIQAGTED
1	}	• 1	DPSGDNLYLGIVLAAVVIITGCFSYYQEAKSSKIMESFKNMVPO
i i	1		QALVIREGEKMQVNAEEVVVGDLVEIKGGDRVPADLRIISAHGC
<b> </b>			KVDNSSLTGESEPQTRSPDCTHE\NPLKTRNITFFSNNFVEGTA
	1	ļ	RGVVVATGDRTVMGRIATLASGLEVGKTPIAIEIEHFIQLITGV
		ļ	WELCACE THE CAME AND THE TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL
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1	1		CLTLTAKRMARKNCLVKNLEAVETLGS'ISTICSDKTGTLTQNRM
j	}	j	TVAHMWFDNQIHEADTTEDQSGTSFDKSSHTWVALF+H/LLGFC
J			NRPVFKGGQDNIPVLKRDVAGDASESALLKCIELSSGSVKLMRE
- 1		1	RNKKVAEIPFNSTNKYQLSIHETEDPNDNRYLLVMKGAPERILD
			RCSTILLQGKEQPLDEEMKEAFQNAYLELGGLGERVLGFCHYYL
ļ			PEEQFPKGFAPDCDDVNFTTDNLCFVGLMSMIGPPRAAVPDAVG
<u></u>			KCRSAGIKVIMVTGDHPITAKAIAKGVGIIFEGNETVEDIAARL
			The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	1	Glutamic Acid, F=Phenylalanine, G=Glycine,
	4	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ļ	corresponding to first	to first	L=Leucine, M=Methionine, N=Asparagine,
1		amino acid	P=Proline, Q=Glutamine, R=Arginine,
ľ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
· J	amino acid	sequence	Codon, /=possible nucleptide deletion
	sequence		\=possible nucleotide insertion)
			NIPVSQVNPRDAKACVIHGTDLKDFTSEQIDEILQNHTEIVFAR
Į.			TSPQQKLIIVEGCQRQGAIVAVTGDGVNDSPALKKADIGVAMGI
1	1		AGSDVSKQAADMILLDDNFASIVTGVBEGRLIFDNLKKSIAYTL
1	1		TOURDETTOOL PENANTED BY COMPANY CORP.
ľ	1	•	TSNIPEITPFLLPIMANIPLPLGTITILCIDLGTDMVPAISLAY
1	1	i .	EAAESDIMKRQPRNPRTDKLVNERLISMAYGQIGMIQALGGFFS
1	1	ľ	YFVILAENGFLPGNLVGIRLNWDDRTVNDLEDSYGQQWTYEQRK
		1	VVEFTCHTAFFVSIVVVQWADLIICKTRRNSVFQQGMKNKILIF
	1		GLFEETALAAFLSYCPGMDVALRMYPLKPSWWFCAFPYSFLIFV
F065	ļ <u></u>		YDEIRKLILRRNPGGWVEKETYY
5867	3	1485	LPGRRARGGRGLGWPPAQALDGSRMGKAKVPASKRAPSSPVAKP
1		1	GPVKTLTRKKNKKKKRFWKSKAREVSKKPASGPGAVVRP2KAPE
1			DFSQNWKALQEWLLKQKSQAPEKPLVISOMGSKKKPKIIOONKK
1	,		ETSPQVKGEEMPAGKDQEASRGSVPSGSKMDRRAPVPRTKASGT
1			EHNKKGTKERTNGDIVPERGDIEHKKRKAK\GQPQPHPPR/IDI
1			WFDDVDPADIEAAIGPEAAKIARKQLGQSEGSVSLSLVKEQAFG
ļ	1		GLTRALALDCEMVGVGPKGEESMAARVSIVNQYGKCVYDKYVKP
1	1		TEPVTDYRTAVSGIRPENLKQGEELEVVQKEVAEMLKGRILVGH
			AL HNDLKIN EI DUDKKKIBDEGKKKEBKGREVOKEVAEMLKGRILVGH
1 .			ALHNDLKVLFLDHPKKKIRDTQKYKPFKSQVKSGRPSLRLLSEK
	1		ILGLQVQQAEHCSIQDAQAAMRLYVMVKKEWESMARDRRPLLTA
ł			PDHCSDDA+QSCPAAAAAPLQRQCDQSQGQITSPQSGNSGETFS
5868	2122		ESWQRGVAWCY
3000	2122	833	LTAGASHTQDASQSTSAKYPAAAQNL/CVTNAMREDLADIWYIR
ĺ	1		AVTVYDKPASFFKETPLDLQHRLFMKLGSMHSPFRARSEPEDPU
i	!		TERSAFTERDAGSGLVTRLRERPALLVSSTSWTEDEDPSTLLAA
	! !		LESRV*T\MTLDGHNLPSLVCVITGKGPLREYYSRLIHOKHFOH
1	i i		IQVCTPWLEAEDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMPG
j	]	•	CCLPVCAVNFKCLHELVKHEENGLVFEDSBELAAQLQMLFSNFP
L			DPAGKLNQFRKNLRESQQLRWDESWVQTVLPLVMDT
5869	2122	833	LTAGASHTQDASQSTSAKYPAAAQNL/CVTNAMREDLADIWYIR
l .			AVTVYDKPASFFKETPLDLQHRLFMKLGSMHSPFRARSEPEDPV
1			TERSAFTERDAGSGLVTRLRERPALLVSSTSWTEDEDFSILLAA
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			CCLPVCAVNFKCLHELVKHEENGLVFEDSEELAAQLQMLFSNFP
5870	2122		DPAGKLNQFRKNLRESQQLRWDESWVQTVLPLVMDT
50,0	2122	833	LTAGASHTQDASQSTSAKYPAAAQNL/CVTNAMREDLADIWYIR
			AVTVYDKPASPFKETPLDLQHRLFMKLGSMHSPFRARSEPEDPV
į l	1		TERSAFTERDAGSGLVTRLRERPALLVSSTSWTEDEDFSILLAA
<u> </u>	İ		LESRV*T\MTLDGHNLPSLVCVITGKGPLREYYSRLIHOKHFOH
			IQVCTPWLEAEDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFG
	• [		CCLPVCAVNFKCLHELVKHEENGLVFEDSEELAAQLQMLFSNFP
1			DPAGKLNQFRKNLRESOOLRWDESWVOTVI.PIAMDT
5871	. 3	3465	FFFCRPLRLYSKTTGDRSAMAGAAGLTAEVSWKVLERRARTKRS
[			VLKLL*LSLRRL*LEPTI*NGLLT*CSRLSVFRFLKV\GSVYEP
	1	1	LKSINLPRPDNETLWDKLDHYYRIVKSTLLLYQSPTTGLFPTKT
		ļ	CCCCOCKAKTODGI VCAACAMATATATATATATATATATATATATATATATATAT
1	1		CGGDQKAKIQDSLYCAAGAWALALAYRRIDDDKGRTHELEHSAI
	· •		KCMRGILYCYMRQADKVQQFKQDPRPTTCLHSVFNVHTGDELLS
ĺ	1	j	YEEYGHLQINAVSLYLLYLVEMISSGLQIIYNTDEVSFIQNLVF
	1		CV\ERVYRVP\DFG\VWGKREGKYY*/SGSTELHSSSVGLGKRQ
	- 1	ļ	L+KQFNGFNLFGNQGCSWSVIFVDLDAHNRNRQTLCSLLPRESR
· .	<b>!</b>		SHNTDAALLPCISYPAFALDDEVLFSOTLDKVVRKLKGKYGFKR
1	1	1	FLRDGYRTSLEDPNRCYYKPAEIKLFDGIECEFPIFFLYMMIDG
l	1	i	VFRGNPKQVQEYQDLLTPVLHHTTEGYPVVPKYYYVPADFVEYE
!		[	KNNPGSQKRFPSNCGRDGKLFLWGQALYIIAKLLADELISPKDI
,	ļ	•	DPVQRYVPLKDQRNVSMRFSNQGPLENDLVVHVALIAESQRLQV
1		. 1	FLNTYGIQTQTPQQVEPIQIWPQQELVKAYLQLGINEKLGLSGR
ł		ĺ	PDRPIGCLGTSKIYRILGKTVVCYPIIFDLSDFYMSQDVFLLID
J		ļ	DIKNALQFIKQYWKMHGRPLFLVLIREDNIRGSRFNPILDMLAA
ı	j	ŀ	LKKGI ICGUMANDI OTI TOOMETOI DEL
J			LKKGIIGGVKVHVDRLQTLISGAVVEQLDFLRISDTEELPEFKS
ì			PEELEPPKHSKVKRQSSTPSAPELGQQPDVNISEWKDKPTHBIL
			QKLNDCSCLASQAILLGILLKREGPNFITKEGTVSDHIERVYRR

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, R=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
j	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	i -	\=possible nucleotide insertion)
			AGSQKLWSVVRRAASLLSKVVDSLAPSITNVLVQGKQVTLGAFG
ı		•	HEEEVISNPLSPRVIQNIIYYKCNTHDEREAVIQQELVIHIGWI
			ISMNPELFSGTLKIRIGWIIHAMEYELQIRGGDKPALDLYQLSP
1			SEVKQLLLDILQPQQNGRCWLNRRQIDGSLNRTPTGFYDRVWQI
			LERTPNGIIVAGKHLPQQPTLSDMTMYEMNFSLLVEDTLGNIDQ
			PQYRQIVVELLMVVSIVLERNPELEFQDKVDLDRLVKEAFNEFQ
1	1	ļ	KDQSRLKEIEKQDDMTSFYNTPPLGKRGTCSYLTKAVMNLLLEG
1	<b>!</b>		EVKPNNDDPCLIS
5872	68	665	VQGYMYRFVIKINSCYSEKTSICRHRCCPELPATQPWPTPTVFF
1			NIAIDSESLGCI\SFKLFADKV/PKRWKKNFVLLNTGEKVLGDK
ł	ļ [.]		GPCFYRIIPG\LCQGGDFTHHNGTGGKSLYSKEFDDENFI/LKH
}			TAPGVLSTANAGPTINGSQFFICTAKTEDG*QHVVFGKVKDGMS
	1	1	IVEALERSGSRNGKTSKKITAANCGOL
5873	2240	506	RRPPEGGSGGGRRTRARMPLPWSLALPLLLSWVAGGFGNAASAR
			HHGLLASARQPGVCHYGTKLACCYGWRRNSKGVCEATCEPGCKF
			GECVGPNKCRCFPGYTGKTCSQDVNECGMKPRPCQHRCVNTHGS
			YKCFCLSGHMLMPDATCVNSRTCAMINCQYSCEDTEEGPQCLCP
			SSGLRLAPNGRDCLDIDECASGKVICPYNRRCVNTFGSYYCKCH
}			IGFELQYISGRYDCIDINECTMDSHTCSHHANCFNTOGSFKCKC
1			KQGYKGNGLRCSAIPENSVKEVLRAPGTIKDRIKKLLAHKNSMK
1			KKAKIKNVTPEPTRTPTPKVNLQPFNYEEIVSRGGNSHGG\KKG
	•		NEEKMKEGLEDEKREEKALKD*HRRERPFRG\DVFFPKVNEAGE
1			FGLIL\VQRKALTSKLEHKADLNISVDCSFNHG\ICDW\KQDR\
1 ' 1			EDDFDW\NPADR\DNAI\GFY\MAVPGLWQGHK\KDIGRLKLLL
			PDLQPQSNFCLLFDYRLAGDKVGKLRVFVKNSNNALAWEKTTSE
			DEKWKTGKIQLYQGTDATKSIIFEAERGKGKTGEIAVDGVLLVS
5874			GLCPDSLLSVDD
38/3	2	3387	ACPRLARRRRVRSLRRRRGWLRARWSRGQNNMAARRITQETFD
	·		AVLQEKAKRYHMDASGEAVSETLQFKAQDLLRAVPRSRABMYDD
			VHSDGRYSLSGSVAHSRDAGRESLRSDVFSGPSFRSSNPSISDD
		•	SYFRKECGROLEFSHSNSRDQVIGHRKLGHFRSQDWKFALRGSW
j			EQDFGHPVSQESSWSQEYSFGPSAVLGDFGSSRLIEKECLEKE\ SRDYDVDHSG\EA\DSVLRGS\SQVQA\RGRALNIVDQEGSLLG
			KGETQGLLTAKGGVGKLVTLRNVSTKKIPTVNRITPKTQGTNQI
			QKNTPSPDVTLGTNPGTEDIQFPIQKIPLGLDLKNLRLPRRKMS
			FDIIDKSDVFSRFGIEIIKWAGFHTIKDDIKFSQLFQTLFELET
1			ETCAKMLASFKCSLKPEHRDFCFFTIKFLKHSALKTPRVDNEFL
			NMLLDKGAVKTKNCFFEIIKPFDKYIMRLQDRLLKSVTPLLMAC
			NAYELSVKMKTLSNPLDLALALETTNSLCRKSLALLGQTFSLAS
			SFRQEKIL*AVGLQDIAPSPAAFPNFEDSTLFGREYIDHLKAWL
[			VSSGCPLQVKKAEPEPMREBEKMIPPTKPEIQAKAPSSLSDAVP
1 1			QRADHRVVGTIDQLVKRVIEGSLSPKERTLLKEDPAYWFLSDEN
į l	j		SLEYKYYKLKLAEMORMSENLRGADOKPTSADCAVRAMLYSRAV
			RNLKKKLLP\WQRRGLLRAQG\LRG\WKARRA\TTGTQTLLFLR
	1		APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP
			QDPSLEASGPSPKPAGVDISEAPQTSSPCPSADIDMKDNGRTAE
	1		KLARFVAQVG\PEIEQF\SI\ENSTDNPDLWFL\HDQNSS\AFK
]	ļ	•	FY\RKKVFELCPSICFTSSPHNL\HTGGGDTT\GSOESPVDLME
		ł	GEARFEDEPPPREAELESPEVMPEREDEDDEDGGERAPA\PGRG
		ļ	GPSLEGSTPADGLPGEA\AEDDL/ALGAPALFTGLLQVTCFPFG
	ļ		RGFSSKSLKVGMIPAPKRVCLIQEPKVHEPVRIAYDRPRGRPMS
	].		KKKKPKDLDFAQQKL\TDK\NLGFQ\MLQKMGWKEGHGLGSLGK
			GIR\SRSACTQQAAWGGSGWGLSPSTCSLPLGSFTAKMAYSWQL
			IFVF
5875	296	1849	LAALGGLPLWRLSRRGFREYLLGLSAPSALGGAMRSVSYVQRVA
			LEFSGSLFPHAICLGDVDNDTLNELVVGDTSGKVSVYKNDDSRP
			WLTCSCQGMLTCVGVGDVCNKGKNLLVAVSAEGWFHLFDLTPAK
		1	VLDASGHHETLIGEEQRPVFKQHIPANTKVMLISDIDGDGCREL
			VVGYTDRVVRAFRWEELGEGPEHLTGQLVSLKKWMLEGQVDSLS
			VTLGPLGLPELMVSQPGCAYAILLCTWKKDTGSPPASEGPTDGS
			/SGDPSCPRRGAAPDIWPYPQQECLHSPNWQHQT\SHGTESSGS

Deginning nucleotide location corresponding to first amino acid residue of amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid acquence	SEQ	Predicted	Predicted end	I hmino paid
Coction   Corresponding	ID			
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bo first mino acid residue of anino acid anino acid sequence    Serine, T-Threonine, V-Valine,   Serine, T-Threonine, V-Valine,   Serine, T-Threonine, V-Valine,   Serine, T-Threonine, V-Valine,   Serine, T-Threonine, V-Valine,   Serine, T-Threonine, V-Valine,   Serine, T-Threonine, V-Valine,   Serine, T-Threonine, V-Valine,   Serine, T-Threonine, V-Valine,   Serine, T-Threonine, V-Valine,   Serine, T-Threonine, V-Valine,   Serine, T-Threonine, V-Valine,   Serine, T-Threonine, V-Valine,   Serine, T-Threonine, V-Valine,   Serine, T-Threonine, V-Valine,   Serine, T-Threonine, V-Valine,   Serine, T-Threonine, V-Valine,   Serine, T-Threonine, V-Valine,   Serine, T-Threonine, V-Valine,   Serine, T-Threonine, V-Valine,   Serine, T-Threonine, V-Valine,   Serine, T-Threonine, V-Valine,   Serine, T-Threonine, V-Valine,   Serine, T-Threonine, V-Valine,   Serine, T-Threonine, V-Valine,   Serine, T-Threonine, V-Valine,   Serine, T-Threonine, V-Valine,   Serine, T-Threonine, V-Valine,   Serine, T-Threonine, V-Valine,   Serine, T-Threonine, V-Valine,   Serine, T-Threonine, V-Valine,   Serine, T-Threonine, V-Valine,   Serine, T-Threonine, V-Valine,   Serine, T-Threonine, V-Valine,   Serine, T-Threonine, V-Valine,   Serine, T-Threonine, V-Valine, V-Valine, V-Valine,   Serine, T-Threonine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine	İ	location		Halistidine Valcolougine, V.
amino acid residue of anino acid anino acid residue of anino acid id anino acid anino acid anino acid anino acid anino acid acquence acid acid acid acid acid acid acid acid	1	corresponding		L=Leucine V-Methiorine N Acres
Sequence    Sequence	ı	to first	amino acid	P=Proline, O=Glutamine, N=Asparagine,
### Artyptophan, Y=Tyrosine, X=Unknown, *=Stop amino acid sequence  ### Sequence    Codon, /-possible nuclectide deletion   -possible nuclectide deletion   -possible nuclectide deletion   -possible nuclectide deletion   -possible nuclectide deletion   -possible nuclectide deletion   -possible nuclectide deletion   -possible nuclectide deletion   -possible nuclectide deletion   -possible nuclectide deletion   -possible nuclectide deletion   -possible nuclectide deletion   -possible nuclectide deletion   -possible nuclectide deletion   -possible nuclectide deletion   -possible nuclectide deletion   -possible nuclectide deletion   -possible nuclectide deletion   -possible nuclectide deletion   -possible nuclectide deletion   -possible nuclectide deletion   -possible nuclectide deletion   -possible nuclectide deletion   -possible nuclectide deletion   -possible nuclectide deletion   -possible nuclectide deletion   -possible nuclectide deletion   -possible nuclectide deletion   -possible nuclectide deletion   -possible nuclectide deletion   -possible nuclectide deletion   -possible nuclectide deletion   -possible nuclectide deletion   -possible nuclectide deletion   -possible nuclectide deletion   -possible nuclectide deletion   -possible nuclectide deletion   -possible nuclectide deletion   -possible deletion   -possible nuclectide deletion   -possible nuclectide deletion   -possible deletion   -possible nuclectide deletion   -possible deletion   -possible deletion   -possible deletion   -possible deletion   -possible deletion   -possible deletion   -possible deletion   -possible deletion   -possible deletion   -possible deletion   -possible deletion   -possible deletion   -possible deletion   -possible deletion   -possible deletion   -possible deletion   -possible deletion   -possible deletion   -possible deletion   -possible deletion   -possible deletion   -possible deletion   -possible	ı		residue of	S=Serine, T=Threonine, V=Valine
sequence	1		amino acid	W=Trvptophan V=Tvrogine Y-Unb
Impossible nucleotide insertion	i		sequence	Codon, /-possible nucleotide deletion
GLPALCTLOGTLAKIMERMEEADKILKSVOYDIGLFALEKIDVYG NCHEREVACANDOGTY I DOMRYTVYEVOUERMESTRIJVKILETXPLST TACKESRAMILITEL INVESTRISTIOTSHINSULPOSIT PER TACKESRAMILITEL INVESTRISTIOTSHINSULPOSIT PER WTCLIAGSOF*IPTLPPKGVYGSHCAAGSITTO HEPLOTYSTIAGHT PER WTCLIAGSOF*IPTLPPKGVYGSHCAAGSITTO HEPLOTYSTIAGHT PER WTCLIAGSOF*IPTLPPKGVYGSHCAAGSITTO DLIMESVSFSPANLSSTGSRVALARUDSANLEKTVGDHPIOVESV REPRITELIHALISERNAME POERETOVAMIKKITGHPIOVESV REPRITELIHALISERNAME POERETOVAMIKKITGHPIOVESV REPRITELIHALISERNAME POERETOVAMIKKITGHPIOVESV REPRITELIHALISERNAME POERETOVAMIKKITULEKALOPUN KARLILISTERNAMEN POERETOVAMIKKOTTULEKALOPUN KARLILISTERNAMEN POERETOVAMIKATULEKALOPUN SARGOLDAFSVIGSUVALIERNAMEN POERETOVAMIKKITULEKALOPUN KARLILISTERNAMEN LANGEN PER LIVAH SERPET PER LOAMIOUL SARGOLDAFSVIGSUVALIERNAMEN PURKUKOTTULKA VALESSUL LIVAHVESIGKK*ITERNAMEN LANGESTERNIKALOH LENGEN PURKUKALOH LIVAHVESIGKK*ITERNAMEN LANGESKAMEN PURKUKALOH LANGEN PURKUKALOH LIVAHVESIGKK*ITERNAMEN LANGESKAMEN PURKUKALOH LINGKKHERSUN KENEREN PURKUKALOH LANGEN VALESSUL LINGKKHERSUN KENEREN PURKUKALOH LANGEN VALESSUL LINGKKHERSUN KENEREN PURKUKALOH LANGEN VALESSUL LINGKKHERSUN KENEREN PURKUKALOH LANGEN VALESSUL LINGKKHERSUN KENEREN PURKUKALOH LANGEN VALESSUL LINGKKHERSUN KENEREN PURKUKALOH LANGEN VALESSUL LINGKKHERSUN KENEREN PURKUKALOH LANGEN VALESSUL LINGKKHERSUN KENEREN PURKUKALOH LANGEN VALESSUL LINGKKHERSUN KENEREN PURKUKALOH LANGEN VALESSUL LINGKKHERSUN KENEREN PURKUKALOH LANGEN VALESSUL LINGKKHERSUN KENEREN PURKUKALOH LANGEN VALESSUL LINGKKHERSUN KENEREN PURKUKALOH LANGEN VALESSUL LINGKKHERSUN KENEREN PURKUKALOH LANGEN VALESSUL LINGKKHERSUN KENEREN PURKUKALOH LANGEN VALESSUL LINGKKHERSUN KENEREN PURKUKALOH LANGEN VALESSUL LINGKKHERSUN KENEREN PURKUKALOH LANGEN VALESSUL LINGKKHERSUN KENEREN PURKUKALOH LANGEN VALESSUL LINGKKHERSUN KENEREN PURKUKAN LANGEN VALESSUL LINGKKHERSUN KENEREN PURKUKAN LANGEN VALESSUL LINGKKHERSUN KENEREN PURKUKAN LANGEN PURKUKAN LANGEN VALESSUL LINGKKHERSUN KANGEN PURKUKAN LANGEN VALESSUL LINGKKHERSUN KANGEN PURKUKAN LANGEN PURKUKAN LANGEN PURKUKA		sequence		\=possible nucleotide insertion)
S876 1122 224 HEPUGUSERS TRIVELE LETYS NOT TACCESSAMILITIS. ILVPCT TRESTINGUELETYS NOT TACCESSAMILITIS. ILVPCT TRESTIGITSHIS VILOSES PER STELLAL LETYS NOT TACCESSAMILITIS. ILVPCT TRESTIGITSHIS VILOSES PER STELLAL LEGIS PER STELLAL LEGIS PER STELLAL LEGIS PER STELLAL LEGIS PER STELLAL LEGIS PER STELLAL LEGIS PER STELLAL LEGIS PER STELLAL STELLA LEGIS PER STELLAL STELLAL LEGIS PER STELLAL LEGIS PER STELLAL LEGIS PER STELLAL LEGIS PER STELLAL LEGIS PER STELLAL LEGIS PER STELLAL LEGIS PER STELLAL LEGIS PER STELLAL LEGIS PER STELLAL LEGIS PER STELLAL LEGIS PER STELLAL LEGIS PER STELLAL LEGIS PER STELLAL LEGIS PER STELLAL LEGIS PER STELLA LEGIS PER STELLA LEGIS PER STELLA LEGIS PER STELLA LEGIS PER STELLA LEGIS PER STELLA LEGIS PER STELLA LEGIS PER STELLA LEGIS PER STELLA LEGIS PER STELLA LEGIS PER STELLA LEGIS PER STELLA LEGIS PER STELLA LEGIS PER STELLA LEGIS PER STELLA LEGIS PER STELLA LEGIS PER STELLA LEGIS PER STELLA LEGIS PER STELLA LEGIS PER STELLA LEGIS PER STELLA LEGIS PER STELLA LEGIS PER STELLA LEGIS PER STELLA LEGIS PER STELLA LEGIS PER STELLA LEGIS PER STELLA LEGIS PER STELLA LEGIS PER STELLA LEGIS PER STELLA LEGIS PER STELLA LEGIS PER STELLA LEGIS PER STELLA LEGIS PER STELLA LEGIS PER STELLA LEGIS PER STELLA LEGIS PER STELLA LEGIS PER STELLA LEGIS PER STELLA LEGIS PER STELLA LEGIS PER STELLA LEGIS PER STELLA LEGIS PER STELLA LEGIS PER STELLA LEGIS PER STELLA LEGIS PER STELLA LEGIS PER STELLA LEGIS PER STELLA LEGIS PER STELLA LEGIS PER STELLA PER STELLA PER STELLA PER STELLA PER STELLA PER STELLA PER STELLA PER STELLA PER STELLA PER STELLA PER STELLA PER STELLA PER STELLA PER STELLA PER STELLA PER STELLA PER STELLA PER STELLA PER STELLA PER STELLA PER STELLA PER STELLA PER STELLA PER STELLA PER STELLA PER STELLA PER STELLA PER STELLA PER STELLA PER STELLA PER STELLA PER STELLA PER STELLA PER STELLA PER STELLA PER STELLA PER STELLA PER STELLA PER STELLA PER STELLA PER STELLA PER STELLA PER STELLA PER STELLA PER STELLA PER STELLA PER STELLA PER STELLA PER STELLA PER STELLA PER STELLA PER STELLA PER STELLA				GLFALCTLDGTLKLMEEMERADKIJ WSVOVDUOL PAT PUT DUTC
S876  1122  224  HEPLGYPSYNGKITYYWEYOLEMBISTNLYKLLETRYP, SYCLIAGESPF*TPTLPPKGYGSHCAARGITKO  PHENGYPSYNGAAMMEGGEERETYOAAMLKTIGGHFJOYEV NERTTEILHHILSERRRVEDDVYLVIEDLKGKASFYEERACH DLAMESVNFSPARAMEGGEERETVOAAMLKTIGGHFJOYEV NERTTEILHHILSERRRVEDDVYLVIEDLKGKASFYEERACH NEWSVNFSPARAMLESTGSRYLANLUSKAALETSLSPIP AWNDLTSDLFRTKSKSEEKIELEKLEKHITATLVLEKCIGDEN KAAELHISTER, AKVDERRGNN, DYELAKSEEREFOLGAGGOU SARGOUDAFSVFIGSLVALLERNMPRIKGOTIELK KILESVID INP, WPSHICKSY REERAK, RELLA, STEARLTREVSY MMEL LERELIELALISROKYLLAGAGEROVIELL HERDEN MELL LINGKIHHEMOVLEKEVEKROSDTOOLOKOLKAAOOTLAATAVO AKERLKSIEKAKGA ISSEELI KVAHERISABAVA VANA AKERLKSIEKAKGA ISSEELI KVAHERISABAVA VANA RERKILSTEKAKGA ISSEELI KVAHERISABAVA VANA PREVETDLEMBGGLLGOMMESTINGUNGLE POEMKLA LINGKIHHEMOVLEKEVEKROSDTOOLOKOLKAAOOTLAATAVO AKERLKSIEKAKGA ISSEELI KVAHERISABAVA VAHERISABAVA AKERLKSIEKAKGA ISSEELI KVAHERISABAVA VAHERISABAVA PRAVETDLEMBGGLLGOMMESTINGUNGLE POEMKLA LINGKIHHEMOVLEKEVEKROSDTOOLOKOLKAAOOTLAATAVO AKERLKSIEKAKGA ISSEELI KVAHERISABAVA VAHERISABA PREVETDLEMBGGLLGOMMESTINGUNGLE POEMKLA LINGKIHHEMOVLEKEVEKROSDTOOLOKOLKAAOOTLAATAVO AKERLKSIEKAKGA ISSEELI KVAHERISABAVA VAHERISAB PREVETDLEMBGGLLGOMMESTINGUNGLE POEMKLA LINGKIHHEMOVLEKEVEKROSDTOOLOKOLKAAOOTLAATAVO AKERLKSIEKAKGA ISSEELI KVAHERISABAVA AKERDISABAVA PREVETDLEMBGGLLGOMMESTINGUNGLE POEMPALIA PREVETDLEMBGGLAVIA SANGA SEELIKAA PREVETDLEMBGGLAVIA SANGA SEELIKAA PREVETDLEMBGGA SEACHAS SEELIKAA PREVETDLEMBGGA SEACHAS SEELIKAA PREVETDLEMBGGA SEACHAS SEELIKAA PREVETDLEMBGGA SEACHAS SEELIKAA PREVETDLEMBGGA SEACHAS SEELIKAA PREVETDLEMBGGA SEACHAS SEELIKAA PREVETDLEMBGGA SEACHAS SEELIKAA PREVETDLEMBGGA SEACHAS SEELIKAA PREVETDLEMBGGA SEACHAS SEELIKAA PREVETDLEMBGGA SEACHAS SEELIKAA PREVETDLEMBGGA SEACHAS SEELIKAA PREVETDLEMBGGA SEACHAS SEELIKAA PREVETDLEMBGGA SEACHAS SEELIKAA PREVETDLEMBGGA SEACHAS SEELIKAAA PREVETDLEMBGGA SEACHAS SEELIKAA PREVETDLEMBGGA SEACHAS SEELIKAAA PREVETDLEMBGGA SEACHAS SEELIKAA PREVETDLEMBGGA SEACHAS SEELIKAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	1			NGHEEVVACAWDGOTYIIDHNRTVVRFOVDFNTDAFCACI VACV
S876 1122 224 HEPLGOVERNAMSTITES.*LIPOFFTKRSTIOTSHRSULFOASSIPPS WCCLIAGROFF *PTILPPKGVYGSKCAAAGIKTGGHFIYOKA PRITTEILHILISERNVDDROVLIVIBLIKKOKASYESEAKYIQ DLIMESVIPSPANLSSTISSYLMALUDSAVALETKOTSLASPJY ANNULTSULFRIKSSEKIKELKEKRILTATILVEKCLGEDV KKAZELHLSTER\AKVDRIRGON\DPLKAKSEFTERKYIQ SARGO\DAFSVIJGSLVALIERNIPPKIKGOTILSHYILVEKCLGEDV KKAZELHLSTER\AKVDRIRGON\DPLKAKSEFTERKYIQ SARGO\DAFSVIJGSLVALIERNIPPKIKGOTILSHYILVEKCLGEDV KKAZELHLSTER\AKVDRIRGON\DPLKAKSEFTERKILGEDLEV KKAZELHLSTER\AKVDRIRGON\DPLKAKSEFTERCILGAGGGFTERLICAGUPD KKAZELKSTEKARKILGALSTERALTREVS\MMEL LIMOKAKHEMOVLEKEVEKROBDOYQLGKARAGILATAVEN LIMOKAKHEMOVLEKEVEKROBDOYQLGKARAGILATAVEN PERPYTTILEMRSGLIGONAMBSTINGVIKALHGODALA/RKKAR CCCTVS\NGSQMTCR:INITILIGSSVCEL PREPYTTILEMRSGLIGONAMBSTINGVIKALHGODALA/RKKAR CCCTVS\NGSQMTCR:INITILIGSSVCEL GLIKKARSSGLIGONAMBSTINGVIKALHGODALA/RKKAR CCCTVS\NGSQMTCR:INITILIGSSVCEL GLIKKARSGGTIKATAVILEGELDIANDFER PLAGGISTAVASULTATIOLISSYCEL AKRAGILAGOVSPOMTVTILOSYTEEMDVVALAGERGIGHTY ISIATAVGHTKASLTATFILIPSEAKRAVULEEDLDIANDFER PLAGGISTHALEDDELYCISANINDOYEHTAPPATAGIGGIGHTY ISIATAVGHTKASLTATFILIPSEAKRAVULEEDLDIANDFER PLAGGISTHALEDDELYCISANINDOYEHTAPPATAMSGLIGGIGHTY MEKDODSTITVICLUMNOYFHEAYTKAMATUFEDLDIANDFER PLAGGISTHALEDDELYCISANINDOYEHTAPPATAMSSDED GTINGGASSAGEDERAPGKRRIGJFSLATAMITFYDIAMTAGMIAU, ALAMVEYMEKSTHALISSARVULETULANTTY TAAAHANGGISTAMASSDED GTINGGASSAGEDERAPGKRRIGJFSLATAMITFYDIAMTAGMIAU, ALAMVEYMEKSTHALIPSTILIPSTYPTICHULGIGI PTSVIVTIGUOVSSITIMVALKI GTINGGASSAGEDERAPGKRRIGJFSLATAMITFYDIAMTAGMIAU ALAMPIYKKIMPSITHAPVANGPATILIPSTYPTICHULGIGI PTSVIVTIGUOVSSITIMVALKI GTINGGASSAGEDRAPGKRRIGJFSLATAMITFYDIAMTAGMIAU ALAMPIYKKIMPSITHAPVANGPTILIPSTYPTICHULGIGI PTSVIVTIGUOVSSITIMVALKI GTINGGASSAGEDRAPGKRRIGJFSLATATACSA SVITKIKISSSGMWBSAASINGSPVIPTPEPHOOLOGNINGGENG KKRRIGGSS\MINGGASSAGEDRAPGKRRIGGTSAMTASANORIN ARBEVYNGLINGGASSAGEDRAPGKRRIGGTSAMTARANORIN ARBEVYNGLINGGASSAGEDRAPGKRRIGGTSAMTARANORIN ARBEVYNGLINGGASSAGEDRAPGKRRIGGTSAMTARANORING ARACKAGASSANISSAGNOPHER PERPAGGIHAGKGGGAACAGAGGGGAACAGAGAGAGAGAGAGAGAGAGA	1			EGRNSPCLVYVTFNOKIYVYWEVOLERMESTNIJVKI LPTYD\ CT
S876  1122  224  HEPLGYPSKVAGSARAMEPGGERETGVAARUKATIKGGHFISYEV NERTTELIHHLISERREVEDDVYLVIEDLKGKASEYEESEKYLG DELMESVNFSFARAMEPGGERETGVAARUKATIKGGHFISYEV NERTTELIHHLISERREVEDDVYLVIEDLKGKASEYEESEKYLG DELMESVNFSFARAMUSSAGSEKUKTUSLASPIP AVNDLTSDLFRTKSKSEEKKIELEKLEKHLTATLVLEKCLGOD KARALHLISTER, VAKVORRORNON DFLEAKSEERFERFOLGAAGDU SARGOLDAFSVPIQSLVALLERNMPRIKGOTIPLK KKLESYLD LINP NPSSICKEY REIERAK NELLAS TEABLITRASY NMELI LINP NPSSICKEY REIERAK NELLAS TEABLITRASY NMELI LINP NPSSICKEY REIERAK NELLAS TEABLITRASY NMELI LINGKIEHBROVLEKEVEKKEDDIO QUGKQUKASAGILATAVYO AKERLISHERAKGAISSEEIKKYARISASAAVCAPLTHVOR PRAPPYTTIDLMSGGLOOKOMPSTOWOKHLEPDDAL/REKTA LINGKIEHBROVLEKEVEKKEDDIO QUGKQUKASAGILATAVYO AKERLISHERAKGAISSEEIKKYARISASAAVCAPLTHVOR PRAPPYTTIDLMSGGLOOKOMPSTOWOKHLEPDDAL/REKTA LINGKIEHBROVLEKEVEKKEDDIO QUGKQUKASAGILATAVYO AKERLISHERAKGAISSEEIKKYARISASAAVCAPLTHVOR PRAPPYTTIDLMSGGLOOKOMPSTOWOKHLEPDDAL/REKTA LINGKKIEHRAKGAISSEEIKKYARISASAAVACAPLTHVOR PRAPPYTTIDLMSGGLOOKOMPSTOWOKHLEPDDAL/REKTA LINGKKIEHRAKGAISSEEIKKYARISASAAVACAPLTHVOR LOOKIEHRAGOVIEROOPON VAVAVATAVATAVA AKERLISHERAKEAISSEEIKKYARISASAAVACAPLTHVOR LOOKIEHRAGOVIEROOPON VAVAVATAVATAVA REKKENDILEROOPON VALTAMATAVA AKERLISHERAKATATINI PERKAPAVULEBEDLIAVOPFS FLOSIHILLEEDDILVCISANNOOGVEHTAADPALLYRVETHALI LINKKRSIVERELEERPKPTPEKKINDOMMAMINPORREGREGUI DOVSRSYHEGIVOLIANNOOFVEHTAADPALLYRVETHALI KKRAVEVEVURLISHESAAVLDIISKNOPCEDSI-PLOTEGITYVAPIR MEKODDFTYTTOLIAKGLHI VALLAVATAVATE MEKODDFTYTTOLIAKGLHI VALLAVATAVATA MEKODDFTYTTOLIAKGLHI VALLAVATAVATA MEKODDFTYTTOLIAKGLHI VALLAVATAVATA MEKODDFTYTTOLIAKGAIN PEREGROADABET ALAMPEYWEKGTHRILYKSIOKTLAFFOYTALLEI THALITOPI ANTAGHULU ALAMPEYWEKGTHRILYKSIOKTLAFFOYTALLEI THALITOPI ANTAGHULU ALAMPEYWEKGTHRILYKSIOKTLAFFOYTALLEI THALITOPI ANTAGHULU ALAMPEYWEKGTHRILYKSIOKTLAFFOYTALLEI THALITOPI ANTAGHULU ALAMPEYWEKGTHRILYKSIOKTLAFFOYTALISHI THALITOPI ANTAGHULU ALAMPEYWEKGTHRILYKSIOKTLAFFOYTALISHI THALITOPI ANTAGHULU ALAMPEYWEKGTHRILYKSIOKTLAFFOYTALISHI THALITOPI ANTAGHULU ALAMPEYWEKGTHRILYKSIOKTANAVATAVAGAAAVATACAAA ALELELIKATAAAAAAAAAAAAA	1	İ	Į.	TACCRSWAWILTTSL*LVPCFTKRSTIOTSHHSWIDOASDIDDS
### HPLGUPSKVAGAAMEPGERETQVAAMIKKTEGHETGVETS ####################################				WTCLIAGEGFF*TPTLPPKGVFGSHCAAAGSITKO
DLIMESVINES PRAILSTEINKHLEUKALUSAVALDKASTYSERKYLQ DLIMESVINES PRAILSTESTEN KIRALUSAVALDKASTISTALASTYS AVNINLTSILEPKIPTSILASTYS AVNINLTSILAPKIPTSILASTYS AVNINLTSILAPKIPTSILASTYS AVNINLTSILAPKIPTSILASTYS AVNINLTSILAPKIPTSILASTYS AVNINLTSILAPKIPTSILASTYS AKOOLOGASTYTOLAKKULESVID IMPUPSICSK RIEBAN KERLA (SIEBALTENSVINDA SAROOLOGASTYSERLISALEDLEV SAROOLOGASTYTOLOGANOTA (SIEBALTAN KERLA) SIEBALTINSVINDA MERILISARI SAROKILOGASTERRILSALEDLEV LINGKKHHEMOVLEKSYEKOSDIQUOKOKASTERRILSALEDLEV LINGKKHHEMOVLEKSYEKOSDIQUOKOKASTERRILSALEDLEV REKELKSIS KARKIGA ISSERI KYAHRI RASKIAVCAPLINWEGD PRRYYTDLEMEGOLOGMONN PSTROVNGHIDAAL/RKKAR PREPATYDLEMEGOLOGMONN PSTROVNGHIDAAL/RKKAR CPCSTVS/NGSMOTTC*INITILILOKSYCEL GLIKKOKQUOGHTHENOGS*PTPROQOFO/VPVAVIAGARRYNYLY RMURSLLSAGOVSPOMITVFIDGYTEEPMOVALFGIRGIOHTP ISIKNARVGHYKASLIATENTPERAKFAVUESDLDIAVPFST FLOGISHLEEDDSILVCISAMUNOGYSHTAEDPALLYKVETHOG LIGWURRSILVKELESPKUPTPERKLEDDMANGERGREECII SUNGRASHEGIVOLIAMUNYSHEAYSKKIRENTVOOLOLIAVOSL KKRAVEVEURLISSARVUHENSPECESSPLOETHIVAVETHOF DDVSRSYHFGIVOLIAMUNYSHEAYSKKIRENTVOOLOLIAVOSL KKRAVEVEURLISSARVUHENSPECESSPLOETHIVAVETHOF USASSYHFGIVOLIAMUNYSHEAYSKKIRENTVOOLOLIAVOSL KKRAVEVEURLISSARVUHENSPECESSPLOETHIVAVETHOF USASSYHFGIVOLIAMUNYSHEAYSKKIRENTVOOLOLIAVOSL KKRAVEVEURLISSARVUHENSPECESSPLOETHIVAVETHOOLOLIAVOSL KKRAVEVEURLISSARVUHENSPECESSPLOETHIVAVETHOOLOLIAVOSL KKRAVEVEURLISSARVUHENSPERKISPERLISPERTATANTOILARUNGULARUNGATATOILARUNGATATOILARUNGATATOILARUNGATATOILARUNGATATOILARUNGATATOILARUNGATATOILARUNGATATOILARUNGATATOILARUNGATATOILARUNGATATOILARUNGATATOILARUNGATATOILARUNGATATOILARUNGATATOILARUNGATATOILARUNGATATOILARUNGATATOILARUNGATATOILARUNGATATOILARUNGATATOILARUNGATATOILARUNGATATOILARUNGATATOILARUNGATATOILARUNGATATOILARUNGATATOILARUNGATATOILARUNGATATOILARUNGATATOILARUNGATATOILARUNGATATOILARUNGATATOILARUNGATATOILARUNGATATOILARUNGATATOILARUNGATATOILARUNGATATOILARUNGATATOILARUNGATATOILARUNGATATOILARUNGATATOILARUNGATATOILARUNGATATOILARUNGATATOILARUNGATATOILARUNGATATOILARUNGATATOILARUNGATATOILARUNGATATOILARUNGATATOILARUNGATATOILARUNGATATOILARUNGATATOILARUNG	5876	1122	224	HLPLGVPSKVAGAAMEPOEERETOVAAWLKKTEGDHPT 20VPV
DILMESVINSPANLSTGSMINALUDSAVALETKOTSLASFIP ANNOLTSILPKIKSKESEI KIELEKLEKUNILVEKCIO, EUN KARALILSTER\AKUNDRROMM\DFILKAKSEEPRGIJAGEOL SARGO\DAFSVIGSUALILEKEWIPILKOOTPILK\KKESSID KARALILSTER\AKUNDRROMM\DFILKAKSEEPRGIJAGEOL SARGO\DAFSVIGSUALILEKEWIPILKOOTPILK\KKESSID LIMP\WPSHCSK*RITERAK\RELA\SITERWIPILKOOTPILK\KKESSID LIMP\WPSHCSK*RITERAK\RELA\SITERWIPILKOOTPILK\KKESSID LIMP\WPSHCSK*RITERAK\RELA\SITERWIPILKOOTPILK\KKESSID LIMP\WPSHCSK*RITERAK\RELA\SITERWIPILKOOTPILK\KKESSID LIMP\WPSHCSK*RITERAK\RELA\SITERWIPILKOOTPILK\KKESSID LIMP\WPSHCSK*RITERWIKLOOLOGUSTARTAVYO AKEKLISERGILGOMENPSTIGIVORGILLISTOOTPILK\KITATAYO AKEKLISERGOMETC**INILTLICKSVCGII PRIPTYTILEMRGGILGOMENPSTIGIVORGILLISTOOTPILTAYOO AKEKLISERGOMETC**INILTLICKSVCGII PRIPTYTILEMRGGILGOMENPSTIGIVORGILLISTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOTPILTOOT	1		ŀ	NPRTTEILHHLSERNRVRDRDVYLVIEDLKOKASEYESEAKYLO
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SARGQ\DAFSVP\GSLVALIRENMPRIKQQTIPIKK\KKLESYLD  SARG\DAFSVP\GSLVALIRENMPRIKQQTIPIKK\KKLESYLDEV  LIMP\NPSHCSK*RIEBAK\RELA\SIRBALIRENMPRIVS\MBIL  SRSLIEMALSTROKULQAGEROVULHIRDGEFQLIKKLA  LINGGKHHHRMOYLEKSVEKROSDIQQLOKQLKDAEQILATAVYO  AKKELKSIEKARKGAISSEIIKYAHISASNAVCABLIWVEGO  PRRYYPTDLEMRSGLIGGMNNPSTNGYNGHLPGDALA\RRITAR  CPCSTVS\NOSQMTCR*INIILIIQKSVCEL  SARG  SON  2113  SUMKCRUCQGHTHRVOP*PTPRQGGGVVVPAVIAGNRPNYLY  RMLRSLLSAQOVSPQNITYFIDGYTEEMDVVALFGIRGIGHTF  ISIKNARVSQNYKASLITAFILIFERAKFUEDLDIAVDFFS  FLOSSIHLLEEDDSLYCISANNDGYEHTAEDDALL\RVETHPO  LGWVLRSIYKRELEFKUPTPEKUNDUNMREDORRGICII  PDVSRSYHGGIVGINNNGYPHEAYFKHHPYTVPOVQLRNVDSL  KKRAYSVEWHLISERBPLUBISKNPCEDSPLDPIEGHTVVAFIK  MEKDDDFTTWOLAKCHINDLOVRONHEGUMELFRKNHPLVV  GVPASSYSVEKKPPSVTPIFLEPPKRGAGAPAPEOT  ALMWYEFWEKSTHRULGERLYKINGTYLLFYGTATATAGHLVL  ALAMYEFWEKSTHRULGKSRPVLTABETSFRKAATHASSDED  GTMGGASSAGEDEERAFGKRRIGFLATAWITFYDIAMTAGHLVL  ALAMYEFWEKSTHRULKSCOMTLAFFGTAATHASSDEDL  GTMGGASSAGEDEERAFGKRRIGFLATAWITFYDIAMTAGHLVL  ALAMYEFWEKSTHRULKSCOMTLAFFGTAATHASSDEDL  GTMGGASSAGEDEERAFGKRRIGFLATAWITFYDIAMTAGHLVL  ALAMYEFWEKSTHRULKSCOMTLAFFGTAATHASSDEDL  GTMGGASSAGEDEERAFGKRRIGFLATAWITFYDIAMTAGHLVL  ALAMYEFWEKSTHRULKSCOMTLAFFGTAATHASSDEDL  GTMGGASSAGEDEERAFGKRRIGFLATAWITFYDIAMTAGHLVL  ALAMYEFWEKSTHRULKSCOMTLAFFGTAATHASSTEDL  GTMGGASSAGEDEERAFGKRRIGFLATAWITFYDIAMTAGHLVL  ALAMYEFWEKSTHRULKSCOMTLAFFGTAATHASSTEDL  TETRYSFYTESLLDHLPYTKARNTNFTILIFVAGATHASSTEDL  TETRYSFYTESLLDHLPYTKARNTNFTILIFVAGATHASSTEDL  SERVENGHSSSGWWFSAASDRDSSVVLRPGPGVQLDSGTGWVLSD  *KKRGRCSS\MISGYDYSCYVLLBESMAGERRAASDVL  CREALANTHGURHATHATAMCQHAACCO  ASYOGELARSTROHARCHAACCO  ASYOGELARSTROHARCHAACCO  ASYOGELARSTROHARCHAACCO  ASYOGELARSTROHARCHAACCO  ASYOGELARSTROHARCHAACCO  ASYOGELARSTROHARCHAACCO  CCCCSSBOGGELLRHVAGCCO  CCCCSSBOGGELLRHVAGCCO  ASYOGELARSTROHARCHAACCO  ASYOGELARSTROHARCHAACCO  ASYOGELARSTROHARCHAACCO  CCCCSSBOGGELLRHVAGCCO  CCCCSSBORMSCAVSCVVSGVTILKLSKRMVVQAPGGGLE-MGPFD  LQDVETIYROKYGCONSMTERTSTTTO/AYLELSSLRSBTIAV  HICATOTV  HICATOTV  HICATOTV  SEVERGOSSOWSCVVSGVTILKLSKRMVVQAPGGGLE-MGPFD  LDV	1			KKAELHLSTER\AKVDNRRONM\DFLKAKSEEFREGIOAGEOL
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LSRELIEMLATSRNQKILGAGERGVUELLIHRGGEGELMKLA LNOGKIHHRMQUEKBYEKROSIDQGUGKEAGOILATAYYO AKEKIKSISKARKGAISSEIIKYAHRISASNAVCAPLTWUPGG PRRYYTDILEMRSGLIGGOMNESTNGWIGHLGGGAIARAKTAR FREYRYTDILEMRSGLIGGOMNESTNGWIGHLGGAIARAKTAR CPCSTVS/NGSQMTCN*INILILIQKSVCEL  S878  950  2113  GLWKCWCLQGPHTHRVQF*PTPRQGGGQVVVVAVLAGNRNYLYX GLWKCWCLGGPHTHRVQF*PTPRQGGGQVVVVAVLAGNRNYLYX FRAMENSLISAGOVSPQNITTYLGGYYEERDDVALAFGLRGIGHTP ISIKNARVSQHYKASITATFALIPFEAKFAVVLEEDLIJAVDFFS FLSGSIHLLEEDDSLYCISANNDQG*EHFDVALAFGLRGIGHTP ISIKNARVSQHYKASITATFALIPFEAKFAVVLEEDLIJAVDFFS FLSGSIHLLEEDDSLYCISANNDGG*EHFDVALAFGLRGIGHTP ISIKNARVSQHYKASITATFALIPFEAKFAVVLEEDLIJAVDFFS FLSGSIHLLEEDDSLYCISANNDGG*EHFDVALAFGLRGICHTY LGWURSKIYHETUTOLAKCLHIWDLOWANHREMBEQRGRCCII PDVSRSYHFGIVOLANNUNGHENPTYDEVQLRWYDSL KKERYEVEWHRLISEREVULDISKNPCEDSPLPDTEGHTYVAFIR MEKDDDFTTWTOLAKCLHIWDLOKONHRGIMAIPFRKNHFLVV GVPASPYSVKKPPSVTPITLEPPPREGAGAPEGOT GTGGGASSAGAGGSSPALOKAGSSPTLOLFSTSPKCAATNASSEDE GTGGGASSAGEDBEAPGKRRLGFLATAMITYD INMTAGKUV. ALMWFYMEKGTHRGIVKSIQKTIKAFGYTBALLITUCLIGIV PTSVLYTUGVUSSRIFMWLITHSI KPLOTESVULFILUARTVT EITRYSFYTSSLIDHLPYFIKMARWFPTILLYPVGVAGELLTIY AALPHVKKTUMFSIRLDHINFTIKITSIRLYDGVULPGGTGWULSD THALPHVKKTUMFSIRLDHINFTIKITSIRLYDGVULPGGTGWULSD *KKKRGRGCSS'MSQOPGHERKEKVULLERSVULPFULMATVIP POPA YFHMLRQRRKVLHGGGI-N-KRMIK*SLGTRFFQNNQDYLSPSF NNNNKOLCEISMIVWFLKI SHCLVAGGGGGFSSONFLQRRGIILAFRERAGFTSALTACSA SVISKGSSSGWBPSAASDRDSFVYIRFPGFVULPSGTGWULSD *KKKRGRGCSS'MSQOPGHERKEKVULLERBRGRAFAASDUL CRSLANDTHOLRTITATAMICCHLAKCLDERGHAQRNVGGRSP DQSHTTGSHTSVQSVIEKLDGERKSVULLERBRGRAFAASDUL CRSLANDTHOLRTITATAMICCHLAKCLDERGHAQRNVGGRSP DQSHTTGSHTSVQSVIEKLDGERKSVULLERBRGRAFAASDUL CRSLANDTHOLRTITATAMICCHLAKCLDERGHAQRNGGGDLQCPH CLOCFSDEGGERLRHVAGCCO  SSRIGLELEKVVULERBRAGGTGAANGGEGDLQCPH CLOCFSDEGGERLRHVAGCCO  SSRIGLENVYGGGRPGTGSQQPPPPBEGGHPGAAQRGGGDLQCPH CLOCFSDEGGERLRHVAGCCO  SSRIGLENVYGGGRPGTGSQQPPPPBEGGHPGAAQRGGGDLQCPH CLOCFSDEGGERLRHVAGCCO  HRCATGTV HRCATGTV HRCATGTV HRCATGTV HRCATGTV HRCATGTV HRCATGTV HRCATGTV HRCATGTV HRCATGTV HRCATGTV HRCATGTV HRCATGTV HRCATGTV HRCATGTV HRCATGTV HRCATGTV H	5877	2030	1907	GTLGKMAASSSGEKEKERLGGGLGVAGGNSTRERLLSALEDLEV
LINGKHHHMOVLEKEVEKBESIQQLQKQLKEREGILATAVYQ AKELKISIKARKGRI SEEI IKYARSANAVCAPITWYGD PRRYYTDLEMRIGLLQOMNNPSTNOVACHLBQDALA/RRKIAR CPCSTUS /MGSQMCTG* INILILIQKSVCUE SHAWAYONAVAGNIKASITATINIPEREKRAVVLEDLDIAA/RRKIAR CPCSTUS /MGSQMCTG* INILILIQKSVCUE GLWKCMQLQGFHTHRVQF*PTRQQGFQ\VPVAVIAGNRPNYLY RMLRSLLSAQGVSPQMITVFIDGYEEPMDVAULFGLRGIGHTF ISIKNARVSQHYKASITATINIPEREKRAVVLEDLDIAVDFFS FLSGSIHLLEEDBILYCISAMNDGYEHTADPALLYRVETMPG LGWVLRRSILYKELEEPKMPTPEKLUDMMRMPEGRGRECII PDVSRSYHEGIVGLIMMGYFHEAYYKKHKPNTVPGVQLRNVDSL KXEAYEVEWHILLSEAEVLUHSKNPCEDSILPDTSHTYVAFIR MEKDDDFTTWTQLAKCHHIWDLDVRGHRGLMELFRKUHFLUV GVPASPYSVKRPSVTFIPLEPPKESAPGAPEOT  S879  3 981 RIFEARAMSGSRAAGMAGSFPTLLPFSFTSPKCAATMASSDED GTMGGASEAGEDREAPGKRRLGFLATAWITFYDIAMTACHLUL ALMWRFYMEKGTHRGLYKSIQKTLYRDFYPLLRIVHCLIGIV PTSVIVTGYQVSSRIFMVWLITHSIKPIQNESVULPILVAWTUT EITRYSFYTFSLLDHLPYFIKARYNNFFILLYPUAGGELLTIY AALPHVKKTGMFSIRLPMKTNVSDYYYFLLTMASYIPJFPQL YFHMLQQRRKULRG\G*-L*KRWIK*SLQTRCFFQNNQDYLSPSP NNNNKOLCEISWIVWFLKY SLUCZUSGUGLGSSONPLORAGILARPREARGTFSALTACSA SVITSKASSSGMPSAASDRDSPVPLRPPGGFQLJESTGMVILSD *KKKRGRCSS/MLSQPQHERKEWULLRSMMEGGRARAASDUL CRSLANETHQLRRTTTATAHHCQHLAKCLDERQHAQRNVCERSP DGSENTOGHTSVQSVIEKLQEENDLLAYRDFMSERAASDUL CRSLANETHQLRRTTTATAHHCQHLAKCLDERQHAQRNVCERSP AGSRIQELEEKVASLHQVSWRQDSREPDAGGHAGAGRAGIDAGPH CLQCFSDEQGEELLEHVABCCQ  SGCVEMIYSHALBARTARDALBERYQMLEGOLTAYDDFMSERAARRR AQSRIQELEEKVASLHQVSWRQDSREPDAGGHAGAGGGDLQCPH CLQCFSDEQGEELLEHVABCCQ  GGIHBSFTERPARQHILTMDCTMRILFILVAAATGTHAQVGLLOSG SVKKEQGASMWSCVVSGYTITKLSHWWQAQPGKGLEMGPD LQDUETIYPQKFQGRVSMTEETSTETTQ/AYLELSSLRSEDTAV HICATDTY HICATDTY HICATDTY HICATDTY SSUKKPGGASMWSCVVSGYTTIKLSHWWQAQPGKGLEMGPD LQDUETIYPQKFQGRVSMTEETSTETTQ/AYLELSSLRSEDTAV HICATDTY HICATDTY SYKLGELARQUIERGKIRPYIQEGSILIKNINGITACDAULER MEQALGAFQSDLSSISSISTICLQCSGAMIRIRINGAVGRUE ELUDGLVVSGAVATAVELSBRIFTIPGCSGAMIRIRINGAVGRUE ELUDGLVSGAVYGEVABELDQLINGETSTAKEIRDEVTSTLKKITLSYTY SYLGRIMKVQCEVABELDQLINGETSTAKEIRDEVTSTLKKITLSKYTLGYYR SYLGRIMKVQCEVABELDQLINGUETSAKEIRDEVTSTLKKITLSKYTLGYYR SYLGRIMKVQCEVABELDGLANGTSAKEIRDEVTSTLKKITLSKYLLSYY SYLGRIMKV	1			LSRELIEMLAISRNOKLLOAGEENOVLELLIHROGREGELMKIA
AKELKSISKARKGAISEEI IKYAHRISASNAVCAPLIWUFGG PRRYYTDLEMRSGLLOGMMNPSTHOKEH,PGDALA/RRKIAR CPCSTVS/MGSGMTCR*INIILILQKSVCEL GAMKCMQLGPHTHRVQF*PTPRQGFQVVAVIAGNRPNYLY RMLRSLLSAQGVSPQMITVFIDGYTEPMDVALFGLBGICHTF ISIKNARVSQHYKASLTATFNIPPEAKFAVLLEGDLIAVDFYS FLOGSIHLDEDDLICISANMDQGYEHTAEDPALLIYRYTMPG LGMWLRSLYKEELEPKMPTPEKLMDMMMRMPEQRRGRECII PDVSRSYHFGIVGIMMGYHEAVFKKHKPTVPGVQLRNVDSL KKRAYEVEVHRLLSEAEVLDHSKHPCEDSPLPDTSCHTYVAFIR MEKDDDFTTMTQLAKCLHINDLDVAGHRGLMRFKKINHFLVV CVPASPYSCHKPPSVTFI PLEPPFRESAGFGAPEOT  SETTS 3 981 RLTEAAAAGSSRAAGMAGSPPTLIPLSFTSPRCAATMASSDED GTMGGASGREDRERPGARRRIGFLATAWLTFYDIAMTAGWLU ALAMVEFYMEKGTHRGLYKSIQKTLKFGTPALLEIVHCLIGIV PTSVIVTGVQVSSRIFMVWLITHSIKFIQHESVUFLVAWTUT EITRYSFYTTSLLDHLPYFIKMARVFFILLPYDVGVAGELLTIY AALPHVKKTGMFSIRLPNKYNVSPDYYYFLLTMASYPLPFQL YFMMLRGRKVLKG\GPSQNPYFILLRSHAGFGFFSALTACSA SVISKGKSSSGMPSAASDRDSPVLRPPQFVQLPSGTGWTLSD *KKKRGRCSS/MLSQPQHEREKEVVLLRRSMAEGERARAASDVL CRSLANETHGULRETLTATHMCQHLACDEQNAQRKVCRGPP DGSEHTDGHTSVGSVIEKLQEENRLLKQKVTHVEDLNAKWQRYN ASRDEYVRGLAAGRTARDAALERVQMLEGQILAYKDPMSERADER AOSRIQELEEKVASLLHQVSWRQDSREPDAGRIHAGSKTAKVLA AADALELWYPGGNPGTGSGQDEPPAGRGRGRGGDLQCPH CLOCFSDEGGELLHRVABCCO GGHFSPFTEAPFAQHLTMDCTWRILFLVAAATGTHAQVQLLOGG SSVKKPGASVMYSCVYSGYTLTKLSMWVRQAPGKGGLE*MQFFD LQDVETIYPQKFQGRPGTGSGQDFPAGRGRGRGGDLQCPH CLOCFSDEGGELLHRVABCCO GGHFSPFTEAPFAQHLTMDCTWRILFLVAAATGTHAQVQLLOGG SSVKKPGASVMYSCVYSGYTLTKLSMWVRQAPGKGLE*MQFFD LQDVETIYPQKFQGRPGTGSGQDFPAGRGRGRGDLQCPH CHCATDTY HCXDTDY HCXDTDY HCXDTDY SGVKKPGASVMYSCVYSGYTLTKLSMWVRQAPGKGLE*MQFFD LQDVETIYPQKFQGRPGTGSGQDFPAGRGRGRDLFLHSGE RTRRD*QLPEAGGPGLQEFLQLIEGLDITSDFFILDEVDG\VDLFR MEGMLGAFGSSLSSEIRTLQCGLDAAAAAVRGQE ARGTAACADVGGVLADRLRVKAVYKIREFILQKIYSFRKPMTNYQ IPGTALLKYRFFYQFLLGNERATAKEIRDEVTSTLKKYLLYSY SYLGRLMKVQYEEVAERDDLMGVETAKEIFBCFKKSKFSLKTLLFSY SYLGRLMKVQYEEVAERDDLMGVETATAKEIRDEVTSTLKKYLLFSY SYLGRLMKVQYEEVAERDDLMGVETAKKGFFKKPSLSKRNTIF TLGTRGSVISPTELEEAPILVPHTAGRGGRGRYPFEALPRSQHYAL LDDSCREVIFICEPFVYGGRAADLEFNTSOMFTLSNTKLHLDSY LDDSCREVIFICEPFVYGGRAADLEFNTSOMFTLSNTKLHLDSY	1			LNQGKIHHEMQVLEKEVEKRDSDIQQLQKOLKEAEQTLATAVVQ
5878  950  2113  GLWKCMGLGGPHTHRVQG*PFTRQGGPQ\VPVAVIAGNRPNYLY RMLSGLKSAGWSPMCT*NITLILIQKSVCEL  GLWKCMGLGGPHTHRVQG*PFTRQGGPQ\VPVAVIAGNRPNYLY RMLSGLKSAGWSPMCT*NITLIGKSKOEL  ISIKNARVSQHYKASLTATFNLFFERKAFVVLEEDLITAUPFFE FLSGSHHLEEDDILYCISAWNDG\CYBETAEDPALLYRVETMPG LGWVLRRSLYKELEEPKWPTPEKLUDHMMMRMFEQRRGECII PDVSRSYHEGIVGLNMGGYFHEAYFKKHKNTHVPGQLRNVDSL KKRAYEVEWHLLSEABVLDHSKNPCSHJPTESHTYVAFIR MEKDDFTTWTOLAKCLHIWDLDVRGNHRGLWRLFRKIGNHFLVV GVDASPYSVKXPPSVTPIFLEPPFREGAGAGAPEOT  5879  3  981  RLTERARAGSGSRAGMGSSPTLLPSFTSPRCAATMASSDED GTMGGASEAGBDRAFGKRRIGFLATAWLTFYDIAMTAGMLVL ALMWRFYMEGTHRGLYKSLGKTLKPFTALLITVUCLIGIV PTSVIVTGYGVSSRIFMVWLTTHSIKPIQMESSVULFLVAWTVT ETTRYSFTYPSLLDHLPYSIKMARYNNFSILITVGVAGELLTIY AALPHVKKTGMFSIRLDHKYNVSDYYYFLLITMASYULFPQL YFHMLQGRRKVLMG\G^*L*KRMIK*SLQTTCFFGNNDDYLSPSF NNNNKLGELSWIVWBLASSAGNDSPVLRPPGPVQLPSGTGWVLSD *KKKRGCSS/MLSGDASDROSPVLRPPGPVQLPSGTGWVLSD *KKKRGCSS/MLSQPCHEREKEVVLLRSMAEGERRARASDVL CRSLANETHGLRTTLTATAHHCGNLAKCLDERQHAQRNVCERSP DQSENTOGHTSVQSVIEKLGSENLLKGVENDELDKAKORYN ASRDSYVGLHAQLGGLQIPHEPELMRKSISRLNRGLERKINDC ASVKGELAASRTARDAALERVOMLEGGILAYDDFMSERADER AQSRIGELEEKVASLLHQVSWRGDSREPDAGRIHAGSKTAKYLA AADALELMYPGGRRPGTGSQQPEPPAEGGHPQAQRGGGILQCPH CLOCFSDEQGEBLLRHVAECCQ  GGHBSFTERPRAGHLTMDCTWRILFLVAAATGTHAQVQLLGSG SVKKPGASAMWSCYVSGYTITKLSHWWVQAPEGKGLGCPH LGDUVETIYPQKFQGRVSMTEETSTETTQ/AYLELSSLRSEDTAV HKCATDTY HKCATDTY HKCATDTY SYLKPEGASAWSCYVSGYTITKLSHWWYQAPEGKGLDFWOPLE RICHDLVWSGANWSCYVSGAVAPAQLALNSDGDL*LHSGE RIRHD"QLPSAGGRGLQCEDLITSDEFILDEVDG\VDLR RICHDLVSGASJSISSEISTLQEGGAMNITLRINGQAVGKKLG ELVDGLWVSGALVYSTLEAPVTPRPSGGGAMNITLRINGQAVGKKLG ELVDGLWVSGALVATUREAPVTPRPSGGGAMNITLRINGQAVGKKLG ELVDGLWSFALVYALLEAPVTPRPSGGGAMNITLRINGQAVGKKLG ELVDGLWSFALVYALLEAPVTPRPSGGGAMNITLRINGQAVGKLG ELVDGLWSFALVYALLEAPVTPRPSGGGAMNITLRINGQAVGKLG ELVDGLWSFALVYALLEAPVTPRPSGCGAMNITLRINGAVGKKLG ELVDGLWSFALVYALLEAPVTPRSGCGAMNTTLRINGAVGKKLG ELVDGLWSFALVYALLEAPVTPRSGCGAMNTTLRINGAVGRKLG ELVDGLWSFALVYALLEAPVTPRSGCAMNTTLRINGAVGRKLG ELVDGLWSFALVYALLEAPVTPRSGCGAMNTTLRINGAVGRKLG LLDGLGKSFALTHARVYGGARAGCTSKTLINGTTTCATHTSYTY SYL	i	i i		AKEKLKSIEKARKGAISSEEIIKYAHRISASNAVCADITUUDGD
5878  950  2113  GLWKCMQCQPTHIRVOP PTPROGGBOLYPVAVIGGREPHYLY RMLRSLLSAQGUSPQMITUTIDGYYEEPMDVVALFGLRGIQHTP LISIKNARVSQHYKASLITATENLFFEAKFAVVLEEDLDIAUDFES FLSGSIHLLEEDBELYCISANNOG PHTAEDPALLTAVETIMPG LGWURRSLIYKEELEPKWPTTEKLWDWDWMMMPEORGRECII PDUSRSYHGIUGINMONYPHEAFWHALDPALLTAVETIMPG LGWURRSLIYKEELEPKWPTTEKLWDWDWMMMPEORGRECII PDUSRSYHGIUGINMONYPHEAFWHALDPOTGRECII RKKRAYEVEWHRLLSEABVLDHISKNPCEDSFLPDTEGHTYVAFIR MEKDDDFTTWTQLAKCLHIWDLDVRONHRGLWRIPFRKINHFLVV GVPASPYSVKKPPSVTFIFLEPPFKEGAPGAPEGT GTGGGASEAGEDRERAPGKRRICHFTWAHTSTYDHTAGMULU, ALAMVEFYMEKGTHRGLYKSIGNTLLFFSTSPCAATMASSDED GTGGGASEAGEDRERAPGKRRICHFTWAHTSTYDHTAGMULU, ALAMVEFYMEKGTHRGLYKSIGNTLLFFSTSPCAATMASSDED GTGGGASEAGEDRERAPGKRRICHFTWAHTSTYDHTAGMULU, ALAMVEFYMEKGTHRGLYKSIGNTLLFFSTSPCAATMASSDED TRYSFYTFSLLDHLPYFIKMARTWHTPTILTPGUVAGELLTIY AALPHYKKTGMFSIRLDHKVINVSFDYYYFLLITMASYIPLFPGL YFMLRGRRKVLHG\G-1-KRMIK-WOLFTCHTONDELSPF NNNNKQLCSISWIWFIKI SLRCLVAGGLGIGFSSONPLQRAGILARPREARGTFSALTACSA SVISKGKSSGMMPSAASDRDSPVPLRPEAPCHGTFSALTACSA SVISKGKSSGMMPSAASDRDSPVPLRPEAPCHGTFSALTACSA SVISKGKSSGMMPSAASDRDSPVPLRPEAPCHGVLJSBF CRELANFTHQLRRITLATHAHMCQHAKCLDERGHLAGRWGERSP DGSEHTDCHTSVQSVIEKLQEENRLLKGKVTHVEDLNAKWGRYN ASREYVRGLHAGLGQIFFAGGATHAGSKTAKYLA AABLELMYPGGRAPGTGSQOPEPPAEGHPGAAGAGGGGDLQCPH CLOCTSDEQGEELLRIVASCCO GGHESPYCAGRUSTESTSTTTQ/AYLELSSLRSEDTAV HCATUTY  5881  26  441  GGGHESPYEAPRAGHTMDCTWRILFLVAAATGTHAQVQLLQSG SEVKKPGASVMVSCYVSGYTITKLSMHWVRQABGKGLB*MGPFD LQDVETIYPQKPGGRVSMTEETSTETTQ/AYLELSSLRSEDTAV HCATUTY HCATUTY  SGCVEMLYSISLEYNPEWISVOSAVAPAGLALNSDGL*LHSGE RTRRD*QLPPAGGPGLQEDLARAAVEQE RTRRD*QLPPAGGPGLQEDLARAAVEQE RTRRD*QLPPAGGPGLQEDLARAAVEQE RTRRD*QLPPAGGPGLQEDLARAAAVEQE RTRRD*QLPPAGGPGLQEDLARAAAVEQE ARGTAACADVRGVLPPALTERTURGRCRYTYPTLISKITNIVQ IPOTALLKYRFFYGFLLGNERATAKEIRDSVTLISKITISYTYR SYLGRIMKVQVEBULABEKDULMGVARTAKKEFFSKPLISKRNTIF TLGTGGSVISPTELBAPILLVHTLARAGREGRYPTLISKITLSTYNA SYLGRIMKVQVEBULABEKDULMGVARTAKKEFFSKPLISKRNTIF LUMSCWELFFILEFYFFERATAKEIRRDFALFFERSHYTIF LLDNSCRYVIPPAGFPAGRACHARAETLSMTLKHLDSV LDNSCRYVIPPAGFPAGRACHALARATAKERDSVYCTISKITHLEND		l		PRRPYPTDLEMRSGLLGQMNNPSTNGVNGHLPGDALA/PRKTAD
SUNKENDLESTRINGOGO PTO PROGOGO VPAVIAGREPNITY  RMERSLESAGOGO POMITYFIDGY PERMENVALEGEGIOHTY  IS INNARVSQHYKASLTATE PALPPEAKFAVULEEDLDIAVDFFS  FLOSSI HLLEEDDSLYCI SAWNDOGY SHEADPALLYNVETIMGE  LGWVLRRSLYKEELE PKWPTPEKLWDWDDWMMMPEGREGECII  PDWSRSYHEGI VGLMMNGY PHENY FKKHKRINTYPGVULRYNDSL  KKRAYSEVEWHRLLSEABRULDHISK PEDSFYLDFSLFTVAFITE  MEKDDDFTTWTQLAKCHI HDLDV RONHRGLWRLFRKKNHFLVV  GVPASPYSVKKP PSVTP I FLEPP PKEEGAFQAFEGT  STERGASEAGEBRERAGKRRIGFILTISTSTRCKATMASSDED  GTMGGASEAGEBRERAGKRRIGFILTISTSTRCKATMASSDED  GTMGGASEAGEBRERAGKRRIGFILTISTSTRCKATMASSDED  GTMGGASEAGEBRERAGKRRIGFILTIST SHEADHALLIVULIGIV  PTSVIVTGYQUSSRIFMVWLITHS I KPIQNEESVULFILVAWTUT  EITRYSFYTFSLIDHLEYFI KWARVIFFI ILTYPGVVAGELLTIY  AALPHVKKTGMFSI FLDNKINVSPDYYFLLITMASVIDLFPQL  YFHMLRQRRKVLHG\G-1-KMRMK*SLQTRCFFQNNODYLSPSF  NNINKOLCEISWI UMPIKLI  5880  1138  1324  SLWCLVAGGIGGFSSONFLQRAGILARPREARGTFSALTACSA  SVISKOKSSSOMWPSAASDRDSFVILRPEGFULPSGTGWUSD  *KKKRGCSS/MLSGOPHREKEKVVLLRRSMAGERRAASDUL  CRSLANFTHOLRRTLTATAHMCQHLAKCLDERQHAQRNVGERSP  DOSENTDCHTSVOSVIEKLQEENRILKGKVTHVBDLNAKWGRYN  ASRDEYVRGHAQLRGLQI PHEPELMREISRININGLERKINDC  ASVKQELAASRTARDAALERVOMLEGQI LAXKDFMSERADRER  AQSRIGELEEKVASLLHOVSMKOGSREPDAGRIHAGSKTAKYLA  ADALELMY PGGWRPGTGSQQPEPPAEGGHPAAGAGGGDLQCPH  CLOCFSDEGGEELIRHVARCCCO  5881  5881  26  441  GGIHPSPTEAPRAGNITHMOCTWR ILFLUANATGTHAGVOLLOSG  SEVKKPGGSUMVSCYVSGYTLTKLSMHWVRQAPGKGLE*MOPFD  LODVETTY POKFQGRVENTETSTETTQ/AYLELSSLRSEDTAV  HICATDTV  SCCWMLYSHSLEYNPEWISVOSAVAPAGLANNSODL-LHSGE  RTRID*GLPSAGGELGRINGLITSDEFILDEVDG\VDLR  HYSKQVSLELQQIEQKSIRDYIQESENIASLINQLTACDAVLER  MEQULGAFGSDUSSISSEIRTUGSGGAMMIRLRNGAVGKKLG  ELVDGLVVPSALVTALLEPAPTTEPFLOQUEDLAKAANAVEQE  ARGTAACADVRGVLDREVKAVTKIRFFLLOKLYSFRKPMTNYQ  I POTALLKYRFFYGPLLGNERATAKETRDEVTLISKTYTSYN  SYLGRIMKVQYEEVLARKODLMGVESTLIKKUTLSTYN  SYLGRIMKVQYEEVLARKODLMGVESTLIKKUTLSTYNY  SYLGRIMKVQYEEVLARKODLMGVESTLAKGFFSKYBLIKRNITIF  TLGTGGSVISPTELBAPTLVEHTARGREGRYPFELFSCHYAL  LDNSCREYVFGCFFVYGGPAHDLFHAMGFTLMTLKHLDGY	5070			CPCSTVS/NGSQMTCR*INIILILOKSVCEL
RMMRSLLSAQGYSPQMITVFIDGYYEEPMDVVALEGLEGIGHTP ISINNANSQHYKASLIATFRALPSKPAVULEEDLDIAVDFFS FLSOSIHLLEEDDSLYCISAWNDOGYEHTAEDPALLYRVETMPG LGWVLRRSLYKEELEPKWPTPEKLWDDMDWMMPEQRGRECII PDVSRSYHEGIVGINMOSYPHEAYFKKHKRNTVPGVOLRNYDEL KKRAYEVEVHRILSEARVLDHSKNPCEDSFLDDTEGHTYVAFIR MEKDDDFTTWTOLAKCLHIWDLDVRGHMRGLWRLFRKKNHFLVV GVPASPYSVKKPPSVTFIFLEPPFKEEGAPGAPEOT GVPASPYSVKKPPSVTFIFLEPPFKEEGAPGAPEOT GUNGASSAGGDERSAPGKRRICHFTWATHTYDIAWTAGWLVL ALAMVEFYMEKGTHRGLYKSIQKTLKFFQTFALLEIVHCLIGIV PTSVIVTGVUGVSSRIFNVWLITHSIKPIQNEESVULFUAWTUT EITRYSFYTFSLLDHLYFIKWANFDYYYFLLITMASYIPLFPQL YFHMLAGRRKVLHG\G*L*KMIK*SLQTTEFGNNDQTUSPSF NNNNKQLCEISWIVWFLKI SLMCLVAGGLGGFSSONPLORAGILARPREARGTFFSAUTACSA SVTKKKSSSGMWPSAASDRDSPVPLRPPGPVQLPSGTGWULSD *KKKRGRCSS/WLSQPQHEREKEVVLLRRSMAGGERARASDVL CRSLANETHOLRRTLTATAHMCQHLAKCLDGRHAQRNVGERSP DOSENTOHTSVGSVIEKUQEENRILKKGKVTHVBLINAKKORYN ASRDEYVRGLHAGJRGLQIPHEPELMRKEISRLNRQLEEKINDC AZVKOBLAASRTARDAALERVQMLEQQILAYKDDFNSERADRER AQSRIQELEEKVASLLHQVSWRQDSREPDAGRHAGKSTRAKLA ADALELWYFGGWAPGTGSQOPEPPAEGHPGAAGRGGGDLQCPH CLOCFSDGGEELLRWASCCO CLOCFSDGGGELLRWASCCO CLOCFSDGGGELLRWASCCO SEVKKPGASWWSCYVSGYTLTKLSMHWVRQAPGKGLE*MOPFD LQDVETTYPQKFGGRVSMTEETSTETTQ/AYLELSSLRSEDTAV HKCATDTY  SGCVEMLYSHSLEYNPEWISVGSAVAPAGLALNNQITACDAVLER MEQMLGAPGSDLSSISSEIRTLGEGSGAMMILRNRQAVROKLG ELVDGLVVPSALVTAILEAPVTEERFLEQUGELDKTSDCL*LHSGE RTRRD*QLPSAGGPGLQRPLLQGGLDLTSDEFTLDEVG\VDLYDLF RTRRD*QLPSAGGPGLQRPLLQGELDLTSDEFTLDEVG\VDLYDLF RTRRD*QLPSAGGPGLQRPLLQGELDLTSDEFTLDEVGLVDLYDLYDLY PATALLKYRFYGVELLGNBRATAKEIRGVCLYSFRRMTITY ILDGTGSVISPTELBAPILLBRATAKEITGREVETLSKIYLSYYR SYLGRIMKVQYEEVAEKDDLMGVEDTAKKIFFSKPSLESKINTIF TLGTGGSVISPTELBAPILLORHATAKEITSRCAVETLSKIYLSYYR SYLGRIMKVQYEEVAEKDDLMGVEDTAKKIFFSKPSLESKINTIF TLGTGGSVISPTELBAPILLORHATAKEFTLORGTFRACHTISKTIYLKHLDGY SYLFFLEGLEPTLORGTBATAKEITGREVETLSKIYLSHYR SYLGRIMKVQYEEVAEKDDLMGVEDTAKKIFFSKPSLESKINTIF TLGTGGSVISPTELBAPILLORHATAKEITGRGCRYPPEALPRSCHYML	3075	950	2113	GLWKCMQLQGPHTHRVQP*PTPRQQGPQ\VPVAVIAGNRPNYLY
151KMARVSCHYKASLTATFNIFPERKRAVILEEDLDIADFFS FLSOSI HILLEEDDSLYCISAMDOGYEHTAEDPALLYRVETMPO LGWVLRRSLYKEELEFKUPTPEKLWDWDMMMRMPEORGRECII PDVSRSYHFGIVOLMMINGYFHEAYFKKHKPMTVPGVQLRNVDSL KKERYEVEVHRILISEAEVLDHSKNPCEDSFLPDTEGHTYMFIR MEKDDDFTTWTQLAKCHHWDLDVRGMRRGLWRLFRKKNHFLVV GVPASPYSVKKPPSVTP IF LEPPERGAPGAPEOT  5879 3 981 RLTEAAAAGSGSRAAGMAGSPFTLLPLSPFTSPRCAATMASSDED GTMGGASEAGEDREAPGKRRRLGFLATAWLFYNIAMTAGWLVL ALAMWFYMEKOTHRGLYKSIQKKFPOTFALLEIVHCLIGIV PTSVIVTGVOVSSRIFMWLTHSIKPIONEESVVLFLVAWTVT EITRYSFYTFSLUDHLPYFIKWARYNFFIILLYVGVAGELLTIY AALPHVKKTGMFSIRLENKYNVSPDYYYFLLITMASVIPLFPQL YFHMLRQRRKVLHGG-V-KMMIK*SLQTRCFFQNNQDYLSPSF NNNKKQLCEISWIWFLKI  5880 1138 1324 SLMCLVAGGIGLGPSSONPLQRAGILARPREARGTFSALTACSA SVISKOKSSSGMWBSAAGDRDSFVPLRPPGPVQLPSGTGWVLSD KKKRGRCSJ/MLSQCPHERREKULRGWATHVEDLNAKWGRYN ASRDEYVRGLHAQLRGLQIPHEPELMRKEISRLNRQLEBKINDC CRSLANETHQLRRTLTATAMCCHLAKCLDERGHAQRNVGERSP DOSENTDCHTSVQSVIEKLQEENRLLKQKVTHVEDLNAKWGRYN ASRDEYVRGLHAQLRGLQIPHEPELMRKEISRLNRQLEBKINDC ASVKQELAASRTARDAALERVQMLEQQILAYKDDFWSERADRER AQSRIGELEEKVASLLHQVSWRODSREPDAGRIHAGSKTAKYLA ADALELMPGGWRPGTGSQOPEPPAEGGHPGAQRGGGDLQCPH CLQCFSDEQGEELLRHVABCCO GGHPSPTEADRAQHLTMDCTMSILFIVAAATGTHAQVOLLOGG SEVKKPGASVWVSCYVSGYTLTKLSHMWRQAPGKGLE*MOPFD LQDVETIYPQKFQGRVSMTEETSTETTQATLEDSLESEBDTAV HCATDTV  2216 SGCVEMYSISLEYNPEWISVQSAVAPAQIALNSDGDL*LHSGE RTRRD*GLPSRGGGGLQEPLQLGELDITSDBFILDEVDG\VDLR HYSKQVSLELQQIEQKSIRDYIQESENIASLHNQITACDAVLER MEQMLGAPQSDLSSISSEIRTLQEOSGAMIRLKNRQAVRGKLG BLVDGLVPSALVTALLEAPVETEPRLEQLGELDAKAAAVREQE ARGTAACADVRGVLDRLRVKAVTKIREFILQKIYSPRKPMTNYQ IPQTALLKYRFFYGPLLGVRRATKREFILQKIYSPRKPMTNYQ IPQTALLKYRFFYGPLLGVRRATKREFILQKIYSPRKPMTNYQ IPQTALLKYRFFYGPLLGVRRATKREFILDGVTFTLKKIYLGYYR SYLGRLMKVQYEEVAEKDDLMOVEDTAKKGFFSKPSLRSNNTIIF TLGTRGSVISPTELEAPILLVPHTAGRGGRYFPERLFRSQHYAL LDNSCRFFYFICEFFYUSGAAAHDAWGRATLARDGVL	1	ľ		RMLRSLLSAQGVSPQMITVFIDGYYEEFMDVVALFGLRGIOHTD
FLSOS HALBEDDSLYCISAMDQGYETRADPALLYRYETMED LGWYLRRSLYKELEFKWFTPEKLADWDMWARPEQREGECII PDVSRSYHEGIVGLMMNGYFHEAYFKKHKPNTVEGVQLRRVOSL KKEAYEVEVHRILSEABULDHSKNPCEDSFLPDTEGHTYVAFIR MEKDDPFTTWTGLAKCHHWDLDVGNHRGLWELFRKNNFLVV GVPASPYSVKKPPSVPJ FJEBPPKEGAPGAPBOT  RLTEAAAAGSGSRAAGWAGSPPTLLDLSPFTSPRCAATMASSDED GTMGGASEAGEDREAPGKRRRLGFLATAWLTFYDIAMTAGWLVL ALAMVEFYMEKGTHRGLYKSIQKTLKFPOTPALLEIVHCLIGIV PTSVIVTGQVOSSRIFMWALTHSIKPIQNESVVLFLVAWTVT AALPHYKKTGMFSIRLDHLPYFIKMARYNFFIILYPVGVAGELLTIY AALPHYKKTGMFSIRLDHLFYFIKMARYNFFIILYPVGVAGELLTIY AALPHYKKTGMFSIRLDHLFYFIKMARYNFFIILYPVGVAGELLTIY AALPHYKKTGMFSIRLDHLFYFIKMARYNFFIILYPVGVAGELLTIY AALPHYKKTGMFSIRLDHLFYFIKMARYNFFIILYPVGVAGELLTIY AALPHYKKTGMFSIRLDHLFYFIKMARYNFFIILYPVGVAGELLTIY AALPHYKKTGMFSIRLDHLFYFIKMARYNFFIILYPVGVAGELLTIY AALPHYKKTGMFSIRLDHLFYFIKMARYNFFIILYPVGVAGELLTIY AALPHYKKTGMFSIRLDHLFYFIKMARYNFFIILYPVGVAGELLTIY AALPHYKKTGMFSIRLDHLFYFIKMARYNFFIILYPVGVAGELLTIY AALPHYKKTGMFSIRLDHLFYFIKMARYNFFIILYPVGVAGELLTIY AALPHYKKTGMFSIRLDHLFYFIKMARYNFFIILYPVGVAGELLTIY AALPHYLGGRRVLHAGG-TLANGHLAKCLDERGHAAGRAUGERSP NNKNKGLCEISWIWFLKI SVISKOKSSSGMWFSAASDRDSPVPLRPPGGVDLPSGTGWVLSD *KKKRGRCSS/WLSQPQHEREKEVVLLRRSMAEGERARAASDVL CRSLAMPTHQLRFTLTATAHMCQHLAKCLDERQHAAGRAUGERSP ASRDEYVRGHAQURGUGILPHREPELMKETSRLNRQLBEKINDC CRSLAMPTHQLRFTLATAHMCQHLAKCLDERQHAAGRAUGERSP AQSRIQELEEKVASLLHQVSWRQDSREPPDAGRIHAGSKTAKYLA ADALELMYPGGWRPGTSGQPEPPAEGGHPGAQRGGGDLQCPH AQSRIQELEEKVASLLHQVSWRQDSREPPDAGRIHAGSKTAKYLA ADALELMYPGGWRPGTSGQPEPPAEGGHPGAQRGGGDLQCPH CLCCCPSDEQGEELLHAWBCCO CCCCPSDEQGEELLHAWBCCO SEVKKPGASVWSCYVSGSYTLTKLSHMWVQAPGKGLE*MGPFD LQDVETTYPQKFQQRVSWTEETSTETTQ/AYLELSSLRSEDTAV HHCATDTV SGCVEMLYSHSLEYNPEWISVQSAVAPAQLALNSDGLL*LHGGE RTRRD*QLPSAGGGGCQEPLQLGELDITSDEFILDEVDG\DDLR HYSKQVSLELQQIEQKSIRDYIQESSNIASLHNQITACDAVLER MEQMLGAPGSDLSSISSEIRTLQEGSGAMNIRRNRRQAYGKLG ARGTAACADVGGVLDRLRVKATKIREFILDEVGLDAAAAVREQE ARGTAACADVGGVLDRLRVKATKIREFILDEVGLDAAAAVREQE ARGTAACADVGFLLGRERTATKERTETVETTLSYTY SYLGRIMKVQYEEVAEKDDLMGVETAKKGFFSKPSLESNNTIF TLGTRGSVISPTILEAPILVPHTAGRGEGRYFFALFRSGNYAL LDNSCREPFVSGCAAHDLFFAGMTSHLLPGY				ISIKNARVSQHYKASLTATFNLFPEAKFAVVI.REDI.DIAVDERS
DWSRSYHGIUGURMORY HEBYY KKKKPNTVPGVQLRNVDSI KKRAYSVEVIRLLSEAEVLDHSKNPCEDSILPDTEGHTYVAFIR MEKDDDTTTTTQLAKCLHIWDLDVRGMRRGLWRIFRKKNFLVV GVPASPYSVKKPPSVTF IF LEPKEGAPGAPEOT  8 1 981 RITEAAAAGGSRAAGWAGSPPTLLPLSPTSPKCAATMASSDED GTNGGASEAGEDREAFGKRRKGFLATAWLFYDIAMTAGWLVL ALAMVRFYMEKSTHRGLYKSTQKFLATAWLFYDIAMTAGWLVL ALAMVRFYMEKSTHRGLYKSTQKKFPOTFALLEIVHCLIGIV PTSVIVTGVQVSSRIFMWWLTTHSIKPIQDRESVVLFLVAWTVT EITRYSFYTFSLLDHLPYFIKWARYNFFILIYPVGVAGELLTTY AALPHVKKTGMFSIRLDNKYNVSPPYYYFLLITMASYTPLFPQL YFHMLRQRKVLHGGS*L*KRMIK*SLQTRCFFQNNQDYLSPSF NNNKKQLCEISWIVWFLKI  5880 1138 1324 SLWCLVAGGLGGFSSONPLQRAGILARPREARGTFSALTACSA SVTSKOKSSSGWWPSAASDRDSPVPLRPAGRVQNDYLSPSF NNNKKQLCEISWIVWFLKI CRSLANETHQLRRTLTATAHCQHLAKCLDERQHAQRNVGERSP DQSEHTDGHTSVQSVIEKLQEENRLLKQKVTHVEDLNAKWQRYN ASRDEVVRGLHAQURGLQIPHEPPELMKEISRLNRQLEEKINDC ASVKQELAASRTARDAALERVQMLEQQILAYKDDFWSERADRER AQSRIQELEEKVASLLHQVSWRQDSREPPDAGRIHAGSKTAKYLA ADALELMYPGGWRPGTGSQOPEPPAGGHPQAQRGQGDLQCPH CLQCFSDEQGEELLRHVABCCQ GGHPSPTEABRAQHITMDCTWSILFILVAATGTHAQVOLLQSG SEVKKPGASWWSCYVSGYVILKSMHWVRQAPGKGLE*MOPFD LQDVETIYPQKFQGRVSMTEETSTETTO/AYLELSSLESEDTAV HHCATDTV HCATDTV HYSKQVSLELQQIEQKSIRDYIQESENIASLINQITACDAVLER MEGMLGAFQSDLSSISSETRIQESGAMNIRLRNRQAVRGKLG ELVDGLVVPSALVTAILEAPVTEPRFLEQLOGELDAKAAAVREQE ARGTAACADVRGVLDRLKVKAVTKKREFILLGKTYSPRKPTNTYQ IPOTALLKYRFYGPLLGWERTKERIDEYVETLSKIYLSYYR SYLGRLMKVQYEEVAEKDDLMGVEDTAKKGFFSKYSLESNNTIIF TLGRGSVISPTLEEAPILLVPHTAGRGEGRYPFBALFRSGNYAL LDNSCREYLFICEFFVSGDAAAHDLFHAWMGRTARMTLKHLDGY LDNSCREYLFICEFFVSGDAAAHDLFHAWMGRTARMTLKHLDGY LDNSCREYLFICEFFVSGDAAAHDLFHAWMGRTARMTLKHLDGY LDNSCREYLFICEFFVSGDAAAHDLFHAWMGRTARMTLKHLDGY LDNSCREYLFICEFFVSGDAAAHDLFHAWMGRTARMTLKHLDGY LDNSCREYLFICEFFVSGDAAAHDLFHAWMGRTARMTLKHLDGY LDNSCREYLFICEFFVSGDAAAHDLFHAWMGRTARMTLKHLDGY LDNSCREYLFICEFFVSGDAAAHDLFHAWMGRTARMTLKHLDGY LDNSCREYLFICEFFVSGDAAAHDLFHAWMGRTARMTLKHLDGY LDNSCREYLFICEFFVSGDAAAHDLFHAWMGRTARMTLKHLDGY LDNSCREYLFICEFFVSGDAAAHDLFHAWMGRTARMTLKHLDGY				FLSQSIHLLEEDDSLYCISAWNDOGYEHTAEDPALL.VPVFTMDC
KKRYEVEVERILISEREVLDHSKNPCEDSFLIPDTEGHTYVAFIR MEKDDPSTTMYDLAKCHINDLOVRGNRRGLWRLFRKKNHFLOV GVPASPYSVKKPPSVTPIFLEPPPKEGGAPGAPEQT RLTEAAAAGGSRAAGWAGSPPTLLFLSPTSPECAATMASSDED GTMGGASEAGEDREAPGKRRLGFLATAWLTFYDIAWTAGWLUL ALAMVRFYMEKGTHRGLYKSIGKTLKFFQTPALLETVHCLIGIV PTSVIVTGVQVSSRIFMVWLITHSIKPIQNESSVULFLUAWTVT EITRYSFYTSLIDHLPYPIKARYNFFILLYPVGVAGELLTIY AALPHVKKTGMPSIRLDHLPYPIKARYNFFILLYPVGVAGELLTIY AALPHVKKTGMPSIRLDHLPYPIKARYNVSFDYYYFLLTTMASYTLFFQL YFHMLEQRRKVLHG\G'*L*KRMIK*SLQTRCFFQNNODYLSPSF NNNKKQLCEISHIVWFLKI SLWCLVAGGLGIGFSSQNPLQRAGILARFREARGTFSALTACSA SVTSKOKSSSGWMPSAASDRDSFVEIRPGFWQLPSGTGWVLSD *KKKRGRCSS', MLSQOPHEREEKEVVLLRRSMABAGBRARAASDVL CRSLAMETHQLRRTLTATAHMCQHLAKCLDERQHAQRNVGERSP DQSEHTDCHTSVQSVIEKLQEENRLLKKOKVTHVEDLNAKWQRYN ASRDEFYVRGLHAQURGLQIPHEPELMKREISRLNRQLEEKINDC AZVKQELAASRTARDAALERVQMLEQQILAYKDDFMSERADRER AQSRIQELEEKVASLLHQVSWRQDSREPDAGRIHAGSKTAKYLA ADALELMYPGGWRPGTGSQOPP PPAEGGHPGAQRGGGDLQCPH CLQCTSDEQGEELLHVAECCQ  5881 26 441 GGIHFSPTEAPRAGHLTMDCTWRILFLVAAATGTHAQVQLLQSG SEVKKPGASVMVSCYVSGYTLTKLSMHWVRQAPGKGLE*MOPFD LQDVETIYPQKFQGRVSMTEETSTETTQ/AYLELSSLRSEDTAV HHCATDTU HHCATDTU HHCATDTU HYSKQVSLELQQIBQKSIRDYJQESENIASLHNQITACDAVLER RTRRD*QLPSAGGPGLQEPLQLGLDITSDEFILDEVDG\VDLR HYSKQVSLELQQIBQKSISSSEIRTJLGSGSGAMIRLRNQQAVGKLG ELVDGLVVPSALVTAILEAPVTEPRFLEQLGCEDAKAAAVREQE ARGTAACADVRGVLDRLRVARVTKIRRFLQKYYSPKKPMTNYQ IPQTALKKYRFTYGFLLGKNSATTAKERTDREVTLSKIYLSYYR SYLGRLMKVQYEEVARKODLMGVEDTAKKGFFSKPSLRSRNTIF TLGTRGSVISPTELEAPILUPHYHTAQRGGRYPFELSKIYLISYYR SYLGRLMKVQYEEVARKODLMGVEDTAKKGFFSKPSLRSRNTIF TLGTRGSVISPTELEAPILLPHYHTAQRGGRYPFELSKIYLLDAY	1	· ·		LGWVLRRSLYKEELEPKWPTPEKLWDWDMWMRMPEORRGRECTI
S879  3 981  RLTEAAAAGSGRAAGWAGSPTLIPLSPTSPERCAATMASSDED GTMGGASEAGEDREAPGKRRIGFILATAWLTPYDIAMTAGWLVL ALAWNRFYMEKGTHRGLYKSLOKTLKFPQTPALLEIVHCLIGIV PTSVIVTGVVSSRIFMVWLITHSIKPIQNESSVULFLUWATVT ETTRYSFYTFSLLDHLPYFIKMARYNFFIILYPWGVAGELLTIY AALPHVKKTGMFSIRLFMKYVSFDYYYFLLITMASYTPLFPGL YFHMLEQRRKVLHG\G*L*KRMIK*SLQTRCFFQNNQDYLSPSF NNNNKGLCEISWIVWFLKI  5880  1138  1324  SLWCLVAGGLGLGFSSONPLQRAGILARPREARGTFSALTACSA SVTSKGKSSSGWMPSAADSDRSPVPLRPPGPVQLPSGTGWVLSD *KKKKRGCSS/MLSQPQHEREKEVVLLRRSMAEGERARASDVL CRSLANETHQLRRTLTATAHMCQHLAKCLDERQHAQRNVGERSP DQSEHTDGHTSVQSVIEKLQEENRLLKGKVTHVEDLANAKWGRYN ASRDEYVRGLHAQLRGLQI PHEPELMRKEISRLNRQLEEKINDC AEVKQELAASRTRARDALERVQMLEQQILAYKDDFMSERADRER AQSRIQELEEKVASLLHQVSWRQDSREPDAGRHAGSKTAKYLA ADALELMVPGGWRPGTGSQQPEPPAEGGHPGAAQRGGDLQCPH CLQCFSDEQGEELLHAVABCCQ  5881  26  441  GGHPSPTEPBPAQHLTMDCTWRILLVAAATGTHAQVQLLQGG SEVKKPGASVMVSCYVSGYTLTKLSMHWVRQAFGKGLE*MGPFD LQDVETIYPQKFQGRVSMTEETSTETTQ/AYLELSSLRSEDTAV HCATDTV HCATDTV  SGCVEMLYSHSLEYNPEWISVQSAVAFAQLAINSDGDL*LHSGE RTRRD*GLPEAGGGPLQEPLQLGELDITSDEFILDEVDG\VDLR HYSKQVELELQQIEQKSIRDYIQESENIASLINQITACDAVLER MEQMLGAFQSILSSISSEIRTLQEGSGANNILRINRQAVRGKLG ELVDGLVVPSALVTAILEAPVTEPRFLEQLQELDAKAAAVREQE ARGTAACADVRGVLDERRYKAVTKIRFFILQKIYSFRKEMTINYQ IPQTALKXRFFYGFLLGNERATAKEIRDEVYETLSKIYLISYYR SYLGRIMKVQYEEVABKDDLMGVEDTAKKGFFSKPSLFRSNTIF TLGTRGSVISPTELEAPILVPHTAGREGRYFFFSLFRSNTYIF TLGTRGSVISPTELEAPILVPHTAGREGRYFFFSLFRSNTIF TLGTRGSVISPTELEAPILVPHTAGREGRYFFFSLFRSNTYIF TLGTRGSVISPTELEAPILVPHTAGREGRYFFFSLFRSNTYIF TLGTRGSVISPTELEAPILVPHTAGREGRYFFFRLFRSGNYAL LDNSCREYLFICEFFVVSGPAAHDLFHAWGRTLSMTLHLDQV				PDVSRSYHFGIVGLNMNGYFHEAYFKKHKFNTVPGVQLRNVDSL
5879  3 981 RLTRAAAAGSSRAAGMAGSPTLIPLSPTSPRCAATMASSDED GTMGASEAGEDREAPGKRRIGFLATAWLTFYDIAMTAGWLUL ALMWAFYMEKGTHRGLYKSIQKTLKAFFOTPALLEIUHCLIGIV PTSVIVTGVQUSSRIFMUWLITHSIKPIQNEESVULFLUWATUT EITRYSFYTFSLLDHLBYFIKMARYNFFILLYPUCVAGELLTIY AALPHVKKTGMFSIRLPNKYNVSFDYYYFLLITMASYTPLPPQL YFHMLRQRRKUHG\G-L+KRMIK*SLQRTCFFFONNQDYLSPSF NNKNKQLCEISWIUWFLKI  5880  1138  1324  SLWCLVAGGIGLGPSSONPLQRAGILARPREARGTFSALTACSA SVTSKGKSSSGMWPSAASDRDSPVPLRPPGFPQULPSGTGWULSD *KKKRGRCSS/MLSQPQHEREKEVULLRSMAEGERARAASDVL CRSLANETHQLRRTLTATAHMCCHLAKCLDERQHAQRNVGERSP DQSHTDGHTSVQSVIEKLQEENRLLKQKVTTWEDLNAKWGYN ASRDEYVRGLHAQLRGLQI PHEPELMRKEISRLINRQLEEKINDC ASVKGELAASRTARDAALERVQMLEQQILAYKDDFMSERADRER AQSRIQELEEKVASLLHQVSWRQDSREPDAGRIHAGSKTAKYLA ADALELMYPGGWRPGTGSQOPEPPAEGGHPGAAQRGGGDLQCPH CLQCFSDEGGEELLRVASCCQ CLQCFSDEGGEELLRVASCCQ SEVKKPGASVWSCTVSGTYLTKLSMHWVRQAPCKGLE*MOPFD LQDUSTIYPQKFQGRVSMTEETSTETTQ/AYLELSSLRSEDTAV HCATDTV  5882  2407  2216  SGCVEMLYSHSLEYNPEWISVQSAVAPAQLAINSDGDL*LHSGE RTRRD*QLPEAGGPGLQEPLQLGELDITSDEFILDEVDG\VDLR HYSKQVELELQQIEQKSIRDYIQESGRIASLHNQITACDAVLER MEQMLGAPGSDLSSISSEIRTLQESGANNILRINRQAYGKLG BLVGLVVPSALVTAILEAPVTEPRIEQLGELDIAKAAVREQE ARGTAACADVRGVLDRIRRVKAVTKIRFFILQKIYSPRKEMTNYQ IPQTALLKYRFYYGFLLGNERATAKEIRDEYVETLSKYILSYYR SYLGRLMKVQYEEVABKDDLMGVEDTAKKGFFSKPSLRSRNTIF TLGTRGSVISPTELEAPILLVPHTAQRGCGYFFFELFRSGNYAL LDNSCREYLFICEFFVVSGFRUFFTARGETSRSHYILHDQY			,	KKEAYEVEVHRLLSEAEVLDHSKNPCEDSFLPDTEGHTYVAFIR
RITEAAAAGGGSRAAGWAGSPPTLLPLSPTSPRCAATMASSDED GTMGGASEAGEDREAPGKRRRIGFLATAWLTFYDIAMTAGWULU ALAMVRFYMEKGTHRGLYKSIQKTLKFPQTPALLEIUVLLIGIU PTSVIVTGVQVSSRIFMVWLITHSIKDIQNEESVULFLVAWTVT EITRYSFYTFSLLDHLPYFIKWARYNFFIILYPVGVAGELLTIY AALPHVKKTGMFSIRLPMKYNVSPDYYYFLLITMASYTLFPQL YFHMLRQRRKVLHG\G-L+KRMIK*SLQTRCFFQNNQDYLSPSF NNKNKQLCEISWIVFLKI  SUMCLVAGGIGLGPSSONPLQRAGILAXPREARGTFSALTACSA SVTSKGKSSSGMWPSAASDRDSPVPLRPPGFVQLPSGTGWVLSD *KKKRGRCSS/WLSQPQHEREKEVVLLRRSMAEGERARAASDVL CRSLANDETBQLRRTITATAMCQHLAKCLDERQHAQRNVGERSP DQSEHTDGHTSVQSVIEKLQEENRLLKGKVTHVBDLINAKWQRYN ASRDEYVRGLHAQLKRGLQIPHEPELMRKEISRLNRQLEEKINDC AZVKGBLAASAFTARDAALERVQMLEQQILAYKDDFMSERADRER AQSRIQELEEKVASLLHQVSWRQDSREPDAGRIHAGSKTAKYLA ADALELMVPGGRRPGTGSQQPEPPAEGGHPGAAQRGQGDLQCPH CLQCFSDEGGEELLRHVAECCQ CGGIHSSPTBAPRAQHLTMDCTWRILFILVAAATGTHAQVQLLQSG SEVKKPGASVWVSCYVSGYTLTKLSMHWVRQAPGKGLE*MOPFD LQDVETIYPQKPQGRVSMTEETSTETTQ/AYLELSSLRSEDTAV HHCATDTV HHCATDTV  SGCVEMLYSHSLEYNPEWISVQSAVAFAQLAINSDGDL*LHSGE RTRRD*GLPEAGGGPLQEPLQGELDITSDEFILDEVDG\VDLR MEQNLGAFQSDLSSISSEIRTLQEGSGANNIRLRNRQAVRGKLG MEQNLGAFQSDLSSISSEIRTLQEGSGANNIRLRNRQAVRGKLG ELVDGLVVPSALVTAILEAPVTEPRPLEQLQELDAKAAAVREQE ARGTAACADVRGVLDRLRVKAVTEPTLQKIYSPRKEMTNYQ IPQTALKXRFFYGFLLGNERATAKEIRDEVVETLSKIYLSYYR SYLGRIMKVQYEEVABKDDLMGVEDTAKKGFFSKPSLRSRNTIF TLGTRGSVISPTELEAPILVPHTAGRGCGYYFFELIFRSQHYAL LDNSCREYLFICEPFVVSGPAAHDLFHAVMGTISMTLHLDQV				MEKDDDFT-TWTQLAKCLHIWDLDVRGNHRGLWRLFRKKNHFLVV
GTINGGASEAGEDREAPGKRRRLGFLATAMLTFYDIAMTAGMLVL ALAMVRFYMEKGTHRGLYKSIQKTLKFFQTFALLEIUHCLIGIV PTSVIVTGUQVSSIPHWWLITHSIKPIQMEESVVLFLUAMTUT EITRYSFYTFSLLDHLFYFIKMARYNFFIILYPUGVAGELLTIY AALPHVKKTGMFSIRLPNKYNVSFDYYYFLLITMASYTPLFPQL YFFMLRQRRKVLHG\G*L*KMIK*SLQTRCFFQNNQDYLSPSF NNKNKQLCEISWIVWFLKI  5880 1138 1324 SLWCLVAGGGLGFSSONPLORAGTLARPREARGTFSALTACSA SVTSKGKSSGMWPSAASDRDSPVPLRPPGPVQLPSGTGWVLSD *KKKRGRCSS/WLSQPQHEREKEVVLLRRSMABGERRRAASDVL CRSLANETHQLRRTLTATAHMCQHLAKCLDERQHAQRNVGERSP DQSEHTDGHTSVQSVIEKLQEENRLLKQKVTHVEDLNAKKQRYN ASRDEYVRGLHAQLGGLQIPHEPELMRKEISRLNRQLEBKINDC AEVKQELAASRTARDAALERVQMLEQQILAYKDDFMSERADRER AQSRIQELEEKVASLLHQVSWRQDSREPDAGRIHAGSKTAKYLA ADALELMVPGGWRPGTGSQQPEPPAEGGHPGAAQRGQGDLQCPH CLQCFSDEGGELLRVABCCQ CLQCFSDEGGELLRVABCCQ SEVKKPGASVMVSCYVSGYTLTKLSMHWVRQAPGKGLE*MGPFD LQDVETIYPQKPGRRVSMTEETSTETTQ/AYLELSSLRSEDTAV HHCATDTV HHCATDTV SGCVEMLYSHSLEYNPEWISVQSAVAPAQLALNSDGDL*LHSGE RTRRD*QLPEAGGPGLQEPLQLGELDITSDEFILDEVDG\VDLR HYSQVELLELQQIEQKSIRDYIQESENIASLHNQITACDAVLER MEQMLGAPQSDLSSISSETRTLQEQSGAMNIRLRNRQAVRGKLG ELVDSLVVPSALVTAILEAPVTPFRFLEQLQELDAKAAAVREQE ARGTAACADVRGVLDRLRVKAVTKIRFFILQKIYSFRKPMTNYQ IPGTALKKYRFFYQFLLGMERATAKEIRDETYFELSKIYLSYYR SYLGRLMKVQVEEVABKDDLMGVEDTAKKGFFSKPSLRSRNTIF TLGTRGSVISPTELEAPILLVPHTAQRGEQRYPFEALFRSQHYAL LDNSCREYLFTCEFFVVSGPAAMDLFHAVGRGTLSWTLKHLDSV	5879		001	GVPASPYSVKKPPSVTPIFLEPPPKEEGAPGAPEQT
ALAWAR PYMEKGTHRGLYKS JOKTLK PFOTPALLE I LYCLIGIV PTSVI VTGVQVSSRI FMVWLITHSI KPIQNESSVULFI LYVALVEVSRI FMVWLITHSI KPIQNESSVULFI LYVALVEVS PTSVL DALLPYF KWAR YNFFI LLYPVGWAGELLTI Y AALPHVKKTGMFS I RLENKYNVSFDYYYFLLITMASYI PLFPQL YFHMLRQRRKVLHG\G-L*KRMIK*SLOTRCFFQNNODYLSPSF NNKNKOLCETSWI VWFLKI  5880  1138  1324  SLWCLVAGGIGLGPSSONPLQRAGILAR PREARGTFSALTACSA SVTSKOKSSSGWWBSAASDRDSPVPLRPPGPVQLPSGTGWVLSD *KKKRGRCSS / WLSOPQHEREKEVVLLRRSMAEGERARAAS DVL CRSLANETHQLRRILTATAHMCQHLAKCLDERQHAQRNVGERSP DQSEHTDGHTSVQSVI EKLQEENRLLKQKVTHVEDLNAKWQRYN ASRDEYVRGLHAQLRGLQI PHEPELMKKEISRINRQLEEKINDC AEVKQBLAASRTARDAALERVQMLEQQI LAYKDDFMSERADRER AQSRIQELEEKVASLLHQVSWRQDSREPDAGRIHAGSKTAKYLA ADALELMVPGGWRPGTGSQOPEPPAEGGHPGAAQRGQGDLQCPH CLQCFSDEQGEBLLHAVBECCQ CLQCFSDEQGEBLLHVABECCQ SCVKKPGASVMVSCYVSGYTLTKLSMMVVRQAPGKGLE*MGPFD LQDVETIYPQKFQGRVSMTEETSTETTQ/AYLELSSLRSEDTAV HHCATDTV  5882  2407  2216  SGCVEMLYSHSLEYNPEWISVQSAVAPAQLAINSDGDL*LHSGE RTRRD*QLPEAGGPGLQEPLOIGELDITSDEFILDEVDG\VDLR HYSKQVELELQQIEQKSIRDVIQESENIASLHNQITACDAVLER MEQMLGAPQSDLSSISSEIRTLQEQSGANNIRLENRQAVRGKLG ELVDGLVVPSALVTAILEAPVTEPRFLEQLQELDAKAAVREQE ARGTAACADVRGVLDRIKVKAVTKIREFILQKIYSFRKMTINYQ IPQTALKKYRFFYQFLLGNERATAKGIRDEYVETLSKIYLSYYR SYLGRLMKVQYEEVARKDDLMGVEDTAKKGFFSKPSLKRRNTIF TLGTRGSVISPTELEAPILVPHTAQRGEGRYPFEALFRSQHYAL LDNSCRSYLFICEFFVVGGRAAHDLFHAWGRFTI,SMTIKHLDSV			301	RETEAAAAGSGSRAAGWAGSPPTLLPLSPTSPRCAATMASSDED
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*VISKGRSSSGMWPSAASDRDSPVPLRPPGPVQLPSGTGWVLSD *KKKRGRCSS/WLSQPQHEREKEVVLLRRSMAEGERRARASDVL CRSLANETHQLRRTLTATAHMCQHLAKCLDERQHAQRNVGERSP DQSEHTDGHTSVQSVIEKLQEENRLLKQKVTHVEDLNAKWQRYN ASRDEYVRGLHAQLRGLQIPHEPELMREISRLNRQLEEKINDC AEVKQELAASRTARDAALERVQMLEQQILAYKDDFMSERADRER AQSRIQELEEKVASLLHQVSWRQDSREPDAGRIHAGSKTAKYLA ADALELMVPGGWRPGTGSQQPEPPAEGGHPGAAQRGQGDLQCPH CLQCFSDEQGEELLRHVAECCQ GGIHFSPTEAPRAQHLTMDCTWRILFLVAAATGTHAQVQLLQSG SEVKKPGASVMVSCYVSGYTLTKLSMHWVRQAPGKGLE*MGPFD LQDVETIYPQKFQGRVSMTEETSTETTQ/AYLELSSLRSEDTAV HHCATDTV  5882 2407 2216 SGCVEMLYSHSLEYNPEWISVQSAVAPAQLALNSDGDL*LHSGE RTRRD*QLPEAGGPGLQEPLQLGELDITSDEFILDEVDG\VDLR HYSKQVELELQQIEQKSIRDYIQESENIASLHNQITACDAVLER MEQMLGAFQSDLSSISSEIRTLQEQSGAMNIRLRNRQAVRGKLG ELVDGLVVPSALVTAILEAPVTEPRFLEQLQELDAKAAAVREQE ARGTAACADVRGVLDRLRVKAVTKIREFILQKIYSFRKPMTNYQ IPQTALLKYRFFYQFLLGNERATAKEIRDEYVETLSKIYLSYYR SYLGRLMKVQYEEVAEKDDLMGVEDTAKKGFFSKPSLRSRNTIF TLGTRGSVISPTELEAPILVPHTAQRGEQRYPFEALFRSQHYAL LDNSCREYLFICEFFFVSGPAAHDLFHAVMGGTLSMTIKHLDSV	5880	1138	1324	SIWCI-VAGGIGI GRESONDI ODDICAY ADDRESSO
*KKKRGCSS/WLSOPQHEREKEVULLRRSMAEGERARAASDVL CRSLANETHQLRRTLTATAHMCQHLAKCLDERQHAQRIVGERSP DQSEHTDGHTSVQSVIEKLQEENRLLKQKVTHVEDLINAKWQRYN ASRDEYVRGLHAQLRGLQIPHEPELMRKEISRLNRQLEEKINDC AEVKQELAASRTARDAALERVQMLEQQILAYKDDFMSERADRER AQSRIQELEEKVASLLHQVSWRQDSREPDAGRIHAGSKTAKYLA ADALELMVPGGWRPGTGSQQPEPPAEGGHPGAAQRGQGDLQCPH CLQCFSDEQGEELLRHVAECCQ SEVKKPGASVWYSCYVSGYTLTKLSMHWVRQAPGKGLE*MGPFD LQDVETIYPQKFQGRVSMTEETSTETTQ/AYLELSSLRSEDTAV HHCATDTV  5882 2407 2216 SGCVEMLYSHSLEYNPEWISVQSAVAPAQLAINSDGDL*LHSGE RTRRD*QLPEAGGPGLQEPLQLGELDITSDEFILDEVDG\VDLR HYSKQVELELQQIEQKSIRDYIQESENIASLHNQITACDAVLER MEQMLGAPGSDLSSISSEIRTLQEQSGAMNIRLRNQAVRGKLG ELVDGLVVPSALVTAILEAPVTEPRFLEQLQELDAKAAAVREQE ARGTAACADVRGVLDRLRVKAVTKIREFILQKIYSFRKPMTNYQ IPQTALLKYRFFYQFLLGNERATAKEIRDEYVETLSKIYLSYYR SYLGRLMKVQYEEVAEKDDLMGVEDTAKKGFFSKPSLRSRNTIF TLGTRGSVISPTELEAPILVPHTAQRGEQRYPFEALFRSQHYAL LDNSCREYLFICEFFFVSGPAAHDLFHAVMGRTLSMTIKHLDSV	ſ			SVTSKGKSSSGMWPSAASDEDS DUDLEDDGGDUOLDGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
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LADCYDAIAVFLCIHIVLRFRNIAAKRDVPALDRYWEQVLALLW			}	TLGTRGSVISPTELEAPILVPHTAORGEORYPFEALFRSOHVAL.
IMACYMATAVFIX: THIVLRFRNIAAKRDVPALDRYWEQVLALLW				LADOUDA LAVEL CHULE PROVENT NT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHURCH PROVENT CHUR
				THE CITAL AND THE CHILDREN THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTR

SEO	Predicted		
ID	beginning	Predicted end	
NO:	nucleotide	nucleotide	M=Aldnine, C=CVSteine D-Assault a and a
	location	location	Glucamic Acid, F=Phenylalanine C=Clusine
l l	corresponding	corresponding	n=nistidine, l=isoleucine K-lucine
1	to first	to first	Labeucine, Mamethionine, Nabararagine
	amino acid	residue of	P=Proline, Q=Glutamine, P=Arminine
i	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
!	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ĺ	sequence	seducuce	Codon, /=possible nucleotide deletion
	<del> </del>	<del> </del>	\=possible nucleotide insertion)
1		İ	PRFELILEMNVQSVRSTDPQRLGGLDTRPHYITRRYAEFSSALV
1			SINQTIPNERTMOLLGOLOVEVENFVLRVAABFSSRKEQLVFLI
ĺ			NNYDMMLGVLM\E+ERAADDSKEVESFQQLLNARTQEFIEELLS
1		ĺ	PPFGGLVAFVKEAEALIBRGQAERLRGEEARVTQLIRGFGSSWK
1			SSVESLSQDVMRSFTNFRNGTSIIQGALTQLIQ\LYHRFHRV\L
5883	2	1374	SQPQLRALPARAELINIHHLMVELKKHKPNF
ł	1	1 *3/*	EFPGRRFRAVMEAGAGAGAGAGWSCPGPGPTVTTLGSYEASEG
Į	1	ł	CERKKGQRWGSLERRGMQAMEGEVLLPALYEEEEEEEEEEE
		ļ	EEEEQVQKGGSVGSLSVNKHRGLSLTETELEELRAQVLQLVAEL
i			EETRELAGQHEDDSLELQGLLEDERLASAQQAEVFTKQIQQLQG
ŀ			ELRSLREEISLLEHEKESELKEIEQELHLAQAEIQSLRQAAEDS
1			ATEHESDIASLQEDLCRMQNELEDMERIRGDYEMEIASLRAEME
1			MKSSEPSGSLGLSDYSGLQEELQELRERYHFLNEEYRALQESNS
			SLTGQLADLESERTQRATERWLQSQTLSMTSAESQTSEMDFLEP
1	i i		DPEMQLLRQQLRDAEEQMHGMKNKCQELCCBLEELQHHRQVSEE
ſ			EQRRLQRELKCAQNEVLRFQTSHS\SPSHPLPPIPPSSPCLL*A
5884	4261	2522	LVVISALLNCWWAETSS
1			GVLARASARLRVPLTGVRACAEPEVGAEPAKVAGAAEPDEDGGR
	]		SRLRDCGDYTPSERLGPKGAMLWFQGAIPAAIATAKRSGAVFVV
	1		FVAGDDEQSTQMAASWEDDKVTEASSNSFVAIKIDTKSEACLQF
ľ			SQIYPVVCVPSSFFIGDSGIPLEVIAGSVSADELVTRIHKVRQM
İ			HLLXSETSVANGSQSESSVSTPSASFEPNNTCENSQSRNAELCE
ļ			IPSTSDTKSDTATGGESAGHATSSQEPSGCSDQRPAEDLNIRVE
	İ		RLTKKI EERREEKRKEEEQREIKKEIERRKTGKEMLDYKRKQEE
1 .	]		BLTKRMLEERNREKAEDRAARERIKQQIALDRAERAARFAKTKE
1	1		EVEAAKAAALLAKQAEMEVKRESYARERSTVARIQFRLPDGSSF
1	1		TNQFPSDAPLEEARQFAAQTVGNTYGNFSLATMFPRREFTKEDY
I	1		KKKLLDLELAPSASVVLLP/ALFINF*AGRPTASIVHSSSGDIW
	Ì		TLLGTVLYPFLAIWRLISNFLFSNPPPTOTSVRVTSSEPPNPAS
L	1		SSKSEKREPVRKRVLBKRGDDFKKEGKIYRLRTQDDGEDENNTW NGNSTQOM
5885	900	467	
	1		AAGGGRRSRLSRSWFTGPSKSPSGVRCCG\RR\AWEDKDEFLDV IYWFRQIIAVVLGVIWGVLPLRGFLGIAGPCLINAGVLYLYFSN
í	1		YLQIDEEYGGTWELTKEGFMTSFA/IVHGHLDHLLHCHPL*LM
<u> </u>			VYSSQVLPIQSKGPS TVHGHLDHLLHCHPL*LM
5886	86	1341	PFRGRALTLKKQPRPGVAPPSLGTCHKSDPGRPAAQSQPPSPGS
			GTFGLLSFRMVRTKTWTLKKHFVGYPTNSDFELKTSELPPLKNG
j	ľ		EVLLEALFLTVDPYMRVAAKRLKEGDTMMGQQVAKVVESKNVAL
	]	İ	PKGTIVLASPGWTTHSISDGKDLEKLLTEWPDTIPLSLALGTVG
	1		MPGLTAYFGLLEICGVKGGETVMVNAAAGAVGSVVGQIAKLKGC
			KVVGAVGSDEKVAYLQKLGFDVVFNYKTVESLBETLKKASPDGY
]	İ		DCYFDNVGGEFSNTVIGQMKKFGRIAICGAISTYNRTGPLPPGP
i i			PPEIGIYQELRMEAFVVYRWQGDARQKALKDLLKWVLELPYFVI
		}	D*LQANTLVYKSMKSAKPSLEYISEKLVSG\KIQYKEYIIEGFE
احينا		İ	NMPAAFMGMLKGDNLGKTIVKA
5887	1937	104	APGCRGCRATRCPCRGPRWDSLGDEAARSPAAPGGAPGLLGLRE
		1	RPDRCHPGGDDRGPQLHRGSPG/SPSELSRRPGPPGLPGLQGPP
			PAPGLPQSRTL/PVLCVCDLSPAQCDINCCCDPDCSSVDFSVFS
1	ł		ACSVPVVTGDSQFCSQKAVIYSLNFTANPPQRVFELVDQINPSI
	i	1	FCIHITN*NLHYPLLIQKYL/NENNFDTLMKTSDGFTLNAESY
1	1	1	VSFTTKLDIPTAAKYEYGVPLQTSDSFLRFPSSLTSSLCTDNNP
[		}	AAFLVNQAVKCTRKINLEQCEEIEALSMAFYSSPEILRVPDSRK
			KVPITVQSIVIQSLNKTLTRREDTDVLQPTLVNAGHFSLCVNVV
}	İ		LEVKYSLTYTDAGEVTKADLSFVLGTVSSVVVPLQQKFEIHFLQ
1	ł	1	ENTOPVPLSGNPGYVVGLPLAAGFQPHKGSGIIQTTNRYGQLTI
1		1	LHSTTEQDCLALEGVRTPVLFGYTMQSGCKLRLTGALPCQLVAQ
1		ŀ	KVKSLLWGQGPPDYVAPFGNSQGP/ADMLDWVPIHFITQSFNRK
1		<b>j</b> :	DSCQLPGALVIEVKWTKYGSLLNPQAKIVNVTANLISSSFPEAN
1			SGNERTILISTAVTFVDVSAPAEAGFRAPPAINARLPFNFFPPF
		;	V V V V V V V V V V V V V V V V V V V
			-

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
İ	amino acid	residue of	S=Serine, T=Threonine, V=Valine.
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Ston
1	amino acid	sequence	Codon, /=possible nucleotide deletion.
	sequence		\=possible nucleotide insertion)
5888	375	2302	LLCRTPGVAMQRADSEQPSKRPRCDDSPRTPSNTPSARADWSPG
	Ì		LELHPDYKTWGPEQVCSFLRRGGFEEPVLLKNIRENEITGALLD
		1	CLDESRFENLGVSSLGERKKLLSYIORLVOIHVDTMKVINDPIH
1		1	GHIELHPLLVRIIDTPQFQRLRYIKQLGGGYYVFPGASHNRFEH
i	1	ł	SLGVGYLAGCLVHALGEKQPELQISERDVLCVQIAGLCHDLGHG
			PFSHMFDGRFIPLARPEVKWTHEQGSVMMFEHLINSNGIKPVME
1			QYGLIPEEDICFIKEQIVGPLESPVEDSLWPYKGRPENKSFLYE
1			IVSNKRNGIDVDKWDYFARDCHHLGIQNNFDYKRFIKFARVCEV
ļ	J		DNELRICARDKEVGNLYDMFHTRNSLHRRAYQHKVGNIIDTMIT
İ			DAFLKADDYIBITGAGGKKYRISTAIDDMEAYTKLTDNIFLEIL
j			YSTDPKLKDAREILKQIEYRNLFKYVGETQPTGQIKIKREDYES LPKEVASAKPKVLLDVKLKAEDFIVDVINMDYGMQBKNPIDHVS
			FYCKTAPNRAIRITKNQVSQLLP\EKFAEQ\LIRVYCKKVDRKS
1	1		LYA\ARQYFVQW\CADR\NFT\KPQDGRCY*PPTP*HPQKKGW\
L.			NDSTFSPKIPTRLPRRLPKSRV\QLFKDDPM
5889	1831	731	LPAACGRPVTARPRQAPEGRSGRPRDLDPYPPQVFPPRPDRVAI
1			VTGGTDGIGYSTAKHLARLGMHVIIAGNNDSKAKQVVSKIKEET
1	}		LNDKET+VLLCCPGWLCLWNSSDPPTSASRGAGTTGVHHHFLLK
1	1		FGIFIL\DLASMTSIRQFVQKFKMKKIPLHVLINNAGVMMVPQR
			KTRDGFEEHFGLNYLGHFLLTNLLLDTLKESGSPGHSARVVTVS
			SATHYVAELNMDDLQSSACYSPHAAYAQSKLALVLFTYHLORLL
1	,		AAEGSHVTANVVDPGVVNTDLYKHVFWATRLAKKLLGWLLFKTP
[			DEGAWTSIYAAVTPELEGVGGRYLYNKKETKSLHVTYNQKLQQQ
5890	1322	222	LWSKSCEMTGVLDVTL
3030	1322	200	FRRGWSAAGRAVPVAFCSRISASSPRRPRGAVRLQSGTEAACRS
İ	ļ		GRPDPRPASAAGGHAGERMSQRDTLVHLFAGGCGGTVGAILTCP
1			LEVVKTRLQSSSVTLYISEVQLNTMAGASVNRVVSPGPLHCLKV ILEKEGPRSLFRGLGPNLVGVAPSRAIYFAAYSNCKEKLNDVFD
			PDSTQVHMISAAMAGFTAITATNPIWLIKTRLQL*/SQGTAGKR
1			RMGAFECVRKVYQTDGLKGFYRGMSASYAGISETVIHFVIYESI
			KOKLLEYKTASTMENDEESVKEASDFVGMMLAAATSK\LVATTI
			AYPHEVVRTRLREEGTKYRSFFQTLSLLVOEEGYGSLYRGLTTH
			LVRQIP\NTAIMMATYELVVYLLNG
5891	1322	200	FRRGWSAAGRAVPVAFCSRISASSPRRPRGAVRLQSGTEAACRS
1 1			GRPDPRPASAAGGHAGERMSQRDTLVHLFAGGCGGTVGAILTCP
			LEVVKTRLQSSSVTLYISEVQLNTMAGASVNRVVSPGPLHCLKV
<b>]</b>			ILEKEGPRSLFRGLGPNLVGVAPSRAIYFAAYSNCKEKLNDVFD
1	[		PDSTQVHMISAAMAGFTAITATNPIWLIKTRLQL*/SQGTAGKR
			RMGAFECVRKVYQTDGLKGFYRGMSASYAGISETVIHFVIYESI KQKLLEYKTASTMENDEESVKEASDFVGMMLAAATSK\LVATTI
	1		AYPHEVVRTRLREEGTKYRSFFQTLSLLVQEEGYGSLYRGLTTH
			LVRQIP\NTAIMMATYELVVYLLNG
5892	1764	379	VVLRVCGRLSVNSAVSSRTGGWSAGLTCAMQRLQVVLGHLRGPA
ļ ļ	ł		DSGWMPQAAPCLSGAPHASAADVVVVHGRRTAICRAGRGGFKDT
	İ		TPDELLSAVMTAVLKDVNLRPEQLGDICVGNVLQPGAGAIMARI
1	ł	1	AQFLSDIPETVPLSTVNRQCSSGLQAVASIAGGIRNGSYDIGMA
1			CGVESMSLADRGNPGNITSRLMEKEKARDCLIPMGITSENVARR
1	į		FGISREKQDTFALASQQKAARAQSKGCFQAEIVPVTTTVHDDKG
l .			TKRSITVTQDEGIRPSTTMEGLAKLKPAFKKDGSTTAGNSSOVS
1		. 1	DGAAAILLARRSKAEELGLPILGVLRSYAVVGVPPDIMGIGPAY
		İ	AIPVALQKAGLTVSDVDIFEINE\AFASQAAYCVEKLRLPP*EG
		i	*TPLGGASGP*GHPLGLHWGHVQVITLAQ*S*SARGKRAYRSGC
5893	3	1665	PCAIGSWNGSPLPVFEYPWGT
, ,,,,,	-	1653	ILSKRRCQKAKTKELMAKKVAVIGAGVSGLISLKCCVDEGLEPT
		. [	CFERTEDIGGVWRFKENVEDGRASIYQSVVTNTSKEMSCFSDFP
j	}	ſ	MPEDFPNFLHNSKLLEYFRIFAKKFDLLKYIQFQTTVLSVRKCP
	1		DFSSSGQWKVVTQSNGKEQSAVFDAVMVCSGHHILPHIPLKSFP
	i		GMERFKGQYFHSRQYKHPDGFEGKRILVIGMGNLGSDIAVELSK
			NAAQVFISTRHGTWVMSRISEDGYPWDSVFHTRFRSMLRNVLPR TAVKWMIEQQMNRWFNHENYGLEPQNKYIMKEPVLNDDVPSRLL
			CGAIKVKSTVKELTETSAIFEDGTVEENIDVIIFATGYSFSFPP
		<del></del>	- The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lvsine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ł	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
ļ	sequence		\=possible nucleotide insertion)
1	'		LEDSLVKVENNMVSLYKYIFPAHLDKSTLACIGLIQPLGSIFPT
1	]		AELQARWVTRVFKGLCSLPSERTMMMDIIKRNEKRIDLFGESQS
			QTLQTNYVDYLDELALEIGAKPDFCSLLFKDPKLAVRLYFGPCN
			SY*YRLVGPGQWEGARNAIFTQKQRILKPLKTRALKDSSNFSVS
5894	177		FLLKILGLLAVVVAFF\CQLQWS
3094	174	1673	RYSPKKVLQNKESSLKLGMATALVSAHSLAPLNLKKEGLRVVRE
			DHYSTWEQGFKLQGNSKGLGQEPLCKQFRQLRYEETTGPREALS
l			RLRELCQQWLQPETHTKEHILELLVLEQFLIILPKELQARVQEH
j			HPESREDVVVVLEDLQLDLGETGQQVDPDQPXKQKILVEEMAPL
1		•	KGVQEQQVRHECEVTKPEKEKGEETRIENGKLIVVTDSCGRVES
1			SGKISEPMEAHNEGSNLERHQAKPKEKIEYKCSEREQRFIQHLD
			LIEHASTHTGKKLCESDVCQSSSLTGHKKVLS*ERKVIQC\HGV
1			LGKAFQRSSHLVRHQKIHLGEKPYQCNECGKVFSQNAGLLEHLR
1			IHTGEKPYLCIHCGKNFRRSSHLNRHQRIHSQEEPCBCKECGKT FSQALLLTHHQRIHSHSKSHQCNECGKAFSLTSDLIRHHRIHTG
1			EKPFKCNICQKAFRLNSHLAQHVRIHNEEKPYQCSECGEAFRQR
			SGLFQHQRYHHKDKLA
5895	2967	86	HPSLLGAIPFYPPPSSPWPPPLYLFWNSHRKSRHFINQRGIHGE
l i	·		MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT
			RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW
			EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS
		•	RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW
			FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA
1 !			EGKGLSPIEPEEELATLSEEBIAMAVTAWEKGLESLPPLRPQQ
			NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS
1 1			RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPOEICDKYHIIHA
1	•		DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQOLLKRGFVLOD
.			TVEQLRCEHCARF\LADRFVEGVCPFCGYEEARGDOCDKCGKLT
[			NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLEEWLGRTL
1			PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E
1	1		GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ
1 1	Í		FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG
1 1			K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA
1			FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV
1 1			LTPDDQRLLA\HVTLELQIIYIIQ\LLEKVRIRDALRSILTIS\RH
	[		GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML
1 1	[		QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP
1 . [	ļ	·	LFQKLENDQIESLRQRPGGGQAKTSPKPAVVETVTTAKPQQIQA LMDEVTKQGNIVRELKAQKADKNEVAAEVAKLLDLKKQLAVAEG
I. 1			KPPEAPKGKKKK
5896	2967	86	HPSLLGAIPFYPPPSSPWPPPLYLFWNSHRKSRHFINQRGIHGE
			MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT
1			RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW
			EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS
]			RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW
1			FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPOPSPA
1 1	1		EGKGLSPIEPEEEELATLSEEEIAMAVTAWEKGLESLPPLRPOO
			NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS
		ļ	RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIIHA
{	1		DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLOD
	[		TVEQLRCEHCARF\LADRFVEGVCPFCGYEEARGDQCDKCGKLI
	Ì	1	NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLEEWLGRTL
	1		PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E
	]	ļ	GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ
1		ſ	FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG
	j	l l	K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA
.	į.		FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV
	Í		LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH
1		İ	GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML
- 1			QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP LFQKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTAKPQQIQA
	<del></del>		P. MUDDINGALESDRAKLOGOĞAKIZAKNANARIALLAKNÖĞIĞY

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
l	corresponding	to first	N=Leucine, M=Methionine, N=Asparagine,
ſ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W-Transcohen V Menseine, Vavaline,
1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	sequence	Codon, /=possible nucleotide deletion,
	3042000		\=possible nucleotide insertion)
			LMDEVTKQGNIVRELKAQKADKNEVAAEVAKLLDLKKQLAVAEG KPPEAPKGKKKK
5897	2967	86	
2057	2507	00	HPSLIGATPFYPPPSSPWPPPLYLFWNSHRKSRHFINQRGIHGE
1	1		MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT
i			RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW
1			EATELOPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS
			RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW
	1		FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA
i	<b>,</b>		EGKGLSPIEPEEEELATLSEEEIAMAVTAWEKGLESLPPLRPQQ
1	i		NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS
			RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIIHA
1			DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD
			TVEQLRCEHCARF\LADRFVEGVCPFCGYEEARGDQCDKCGKLI
i			NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLEEWLGRTL
1			PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E
1			GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ
1	·		FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG
	ĺ		K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA
1			FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV
1			LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH
1			GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML
-	·		QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP
j i			LFQKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTAKPQQIQA
1		•	LMDEVTKQGNIVRELKAQKADKNEVAABVAKI,LDLKKQLAVAEG
5898	2967		KPPEAPKGKKKK
1 2000	2307	86	HPS_LGATPFYPPPSSPWPPPLYLFWNSHRKSRHFINORGIHGE
			MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT
1			RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGNEQDDLTNQWLEW
1 1	•		EATELOPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS
]			RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEBLSALHSW
1 1			FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA
1 1			EGKGLSPIEPEEEBLATLSEEEIAMAVTAWEKGLESLPPLRPQQ
1 1			NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS
i 1			RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIIHA
	İ		DIY\RWFNISFDIPGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCEHCARF\LADRFVEGVCPFCGYBEARGDQCDKCGKLI
			NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLBEWLGRTL
}			PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E
1 [	i		GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ
1 1	ĺ		FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG
1 1			K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA
1 1			FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV
			LTPDDQRLLA\HVTLELOHYHO\LLEKVRIRDALRSILTI9\RH
l i			GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML
[ ]			QPYMPTVSATIQAQLQLPPPACSILLINFLCTLPAGHQIGTVSP
1			LFQKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTAKPQQIQA
1 }	,		LMDEVTKQGNIVRELKAQKADKNEVAAEVAKLLDLKKQLAVAEG
L		ļ	KPPEAPKGKKKK
5899	326	1078	NCPKSKEPNGVRAPSLPSPLRAAMALSDVDVKKQIKHMMAFIEQ
			EANEKAEBIDAKAEBEFNIEKGRLVQTQRLKIMEYYBKKEKQIE
1 1	İ	j	QQKKILMSTMRNQARLKVLRARNDLISDLLSEAKLRLSRIVEDP
l i			EVYQGLLDKLVLQGLLRLLEPVMIVRCRP\QDLLLVEAAVQKAI
	1		PEYMTISQKHVEV\QIDKEA*LAVECSWEVWEVYSGNQRIKVSN
		1	TLESRLDLSAKQKMPEIRMALFGANTNRKFFI
5900	64	1409	KANSRDSPCLEFCPLCGVSSHDLQHRMWYHRLSHLHSRLQDLLK
ļ į	İ	]	GGVIYPALPQPNFKSLLPLAVHWHHTASKSLTCAWQQHEDHFEL
	ļ	İ	KYANTVMRFDYVWLRDHCRSASCYNSKTHQRSLDTASVDLCIKP
	Ì	ł	KTIRLDETTLFFTWPDGHVTKYDLNWLVKNSYEGQKQKVIQPRI
1		1	LWNAEIYQQAQVPSVDCQSFLETNEGLKKFLQNFLLYGIAFVEN
		ļ	VPPTQEHTEKLAERISLIRETIYGRMWYFTSDFSRGDTAYTKLA
	İ		LDRHTDTTYPQEPCGIQVFHCLKHEGTGGRTLLVDGFYAAEQVL
	<del></del>		Ant cordanienterioring indicat I WEGAP

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			QKAPEEFELLSKSAI\KHEYIEDVGECHQPHDWDWAQS+ISTHG
		Ì	/YKELYLIRYNNYDRAVINTVPYDVVHRWYTAHRTLTIELRRPE
1			NEFWVKLKPGRVLFIDNWRVLHGRECFTGYRQLCGCYLTRDDVL
<u> </u>			NTARLLGLQA
5901	1	2121	VAIEQTSLKMMQAVGGAPARPTGEYICNQCGAKYTSLDSFQTHL
1			KTHLDTVLPKLTCPQCNKEFPNQESLLKHVTIHFMITSTYYICE
ĺ	ŀ		SCDKQFTSVDDLQKHLLDMHTFVFFRCTLCQEVFDSKVSIQLHL
	1		\AVKHSNEKKVYRCTSCNWDFRNETDLQLHVKHNHLENQGKVHK
	i .		CIFCGESFGTEVELQCHITTHSKKYNCKFCSKAFHAIILLEKHL
			REKHCVFETKTPNCGTNGASEQVQKEEVELQTLLTNSQESHNSH
1	1		DGSEEDVDTSEPMYGCDICGAAYTMETLLQNHQLRDHNIRPGES
i	1		AIVKKKAELIKGNYKCNVCSRTFFSENGLREHMQTHLGPVKHYM
			CPICGERFPSLLTLTEHKVTHSKSLDTGNCRICKMPLQSEEEFL
			EHCQMHPDLRNSLTGFRCVVCMQTVTSTLELKIHGTFHMQKTGN
1			GSAVQTTGRGQHVQKLYKCASCLKEFRSKQDLVKLDINGLPYGL
1	ļ		CAGCVNLSKSASPGINVPPGTNRPGLGQNENLSAIEGKGKVGGL
	ĺ		KTRCS*LATFKF*VLKVELPEPHPKPFHRGVSRPDSNSTQLKTP
1	]		QVSPMPRISPSQSDEKKTYQCIKCQMVFYNEWDIQVHVANHMID
1			EGLNHECKLCSQTFDSPAKLQCHLIEHSFEGMGGTFKCPVCFTV
	i		FVQANKLQQHIFSAHGQEDKIYDCTQCPQKFFFQTELQNHTMTQ HSS
5902	712	209	
1	/	209	LKNRRRSRPSIRQSIGSTSVSRWLTSLFTYLDHTADVQ*V*REF
1			IPLXPRQ*ED*MFQSWLHAWGDTLEEAFEQCAMAMFGYMTDTGT
	}		VEPLQTVEVETQGDDLQSLLFHFLDEWLYKFSADEFFIP\GWGE EFSLSKHPQGTEVKAITYSAMQVYNEENPEVFVIIDI
5903	2106	735	DTPGPSLPSTTAPFSLRSLSFPSRPSYLLPGDPQPLQGRGLPTT
			PALFALSAVPGGAASPMPPSGLRLLPLLLPLLWLLVLTPGRPAA
	[		GLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGEVPPGP
1			LPEAVLALYNSTRDRVAGESABPEPEPEADYYAKEVTRVLMVET
1 '			HNEIYDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRL
1			KLKVEQHVELYQKYSNNSWRYLSNRLLAPSDSPEWLSFDVTGVV
J J			RQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGFTTGR\RGDL
i			ATIHGMNRPFLLLMATPLERAOHLOS\SRHROAL\DTNY\CFSF
]			HGGRNCLRC/VHC*HLIFRKDL\GW\KWI\HE\PKGYHANFC\L
1			GPCPYIWSLDTQYSKVLALYNQ\HKPG\ASAAP\CCVPOALEP\
			LPIVYY\VGRKPKVEQLSNMIVRSCKCS
5904	3	1126	MMEEIENAINTFKEEQRLIYEELIKEEKTTNNELSAISRKIDTW
	i		ALGNSETEKAFRAISSKVPVDKVTPSTLPEEVLDFEKFLQQTGG
ł I	1		RQGAWDDYDHQNFVKVRNKHKGKPTFMEEVLEHLPGKTQDEVQQ
			HEKWYQKPLALEERKKESIQIWKTKKQQKREEIFKLKEKADNTP
]	İ		VLFHNKQEDNQKQKEEQRKKQKLAVEAWKKQKSIEMSMKCASQL
1	J		KBEEBKEKKHQKERQRQFKLKLLLESYTQQKKEQEEFLRLEKEI
1 1			RBKAEKAEKRKNAADEISRFQERDLHKLELKILDRQAKEDEKSQ
			KQRRLAKLKEKVENNVSRDPSRLY/NTHQRLGRTNQKDRTNRLW
5905	287	2912	ATSTYPT*GYSNLETRNTEKSMR
[		2,10	MASFPPRVNEKETVRLRTIGELLAPAAPFDKKCGRENWTVAFAP DGSYFAWSQGHRTVKLVPWSQCLQNFLLHGTKNVTNSSSLRL>R
1			QNSDGGQKNKPREHIIDCGDIVWSLAFGSSVPEKQSRCVNIEWH
]			RFRFGQDQLLLATGLNSGRIKIWDVYTGKLLLNLVDHTGVVRDL
f 1			TFAPDGSLILVSASRDKTLRVWDLRDDGN\MMKVLRGHQNWVY\
]	I		SCAFSPDSSMLCSVGASKAVVAAILV*LRLCWHHSHTGATMVLS
			WAERVASLATGLGATFTIG*SNLAFVLQGVLYVHRCWSMSTFCF
			SPFLFFFFKVISPTVKYH+LLSKLIFQFYGIGSLTSETNLM*SI
] ]	İ	1	WLSNGFSVLFFGILSDSRDILRL*FNLKFVLIFF*K*CIVSVQK
			KKKPKRIALLQEERLS*DKPPSSHLI*QTEVNIRILFRAILHS*
	1	ſ	LLIFRI*NCI*TYS*IIDPFYIQMTYDRG*FGKNKMVKF*FIEM
		]	*LYYFHKIAFSFCNVV*HPCCLPKKFHLAVNILFACSICFSS*A
	1	İ	QVGDPSLL*TSDYLKGRCQWSNNLLTLRFLSVYFFKNLVVSGKK
		}	REGGL*YLTLFISVYFS*LVFGINGFQYSFVVKLHCLYFMFRLI
	ł		FKLTFNRNI*NRICMSALINLKTDFNLTMTLSIFFKLLIIYNA*
			YNLN*I*QF*YKMCHFVLCMSE*SYNICLFIAGF\LWNMDKYTM

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine.
Ì	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine.
	to first	amino acid	P-Proline, Q-Glutamine, R-Arginine,
ŀ	amino acid residue of	residue of	S=Serine, T=Threonine, V=Valine,
ĺ	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
j	sequence	sequence	Codon, /=possible nucleotide deletion,
	bequence	<del></del>	\=possible nucleotide insertion)
	ļ		**RKLEGHHHDVVACDFSPDGALLATASYDTRVYIWDPHNGDILM
1			EFGHLFPPPTPIFAGGANDRWVRSVSFSHDGLHVASLADDKMVR FWRIDEDYPVQVAPLSNGLCCAFSTDGSVLAAGTHDGSVYFWAT
			PRQVPSLQHLCRMSIRRVMPTQEVQELPIPSKLLEFLSYRI
5906	146	2038	REGAGSGRMASGA\YNPYIEIIEQPRQRGMRFRYKCEGRSAGSI
1			PGEHSTDNNRTYPSIQIMNYYGKGKV\RITLVTK\NDPYKPHPH
			DLVGKDCRD\GYYEAEFGQE\RRP\LFFQN\LGIRCVKKKEVKE
ľ			A\IITR\IKAGINPFDVP*KQLNDIEDCDLDVVRLWFRVFLPDG
1		1	HGNL\TTALPPV\VSSPIYDNRAPNTAELRVCRVNKNCGSVRGG
			DEIFLLCDKVQKDDIEVRFVLNDWEAKGIFSOADVHROVAIVFK
ļ			TPPYCKAITEPVTVKMQLRRPSDQEVSESMDFRYLPDEKDTYGN
		j	KAKKQKTTLLFQKLCQDHVETGFRHVDQDGLELLTSGDPPTLAS
			QSAGITVNFPERPRPGLLGSIGEGRYFKKEPNLFSHDAVVREMP
			TGVSSQAESYYPSPGPISSGLSHHASMAPLPSSSWSSVAHPTPR
			SGNTNPLSSFSTRTLPSNSQGIPPFLRIPVGNDLNASNACIYNN ADDIVGMEASSMPSADLYGISDPNMLSNCSVNMMTTSSDSMGET
ĺ	ĺ		DNPRLLSMNLENPSCNSVLDPRDLRQLHQMSSSSMSAGANSNTT
			VFVSQSDAFEGSDFSCADNSMINESGPSNSTNPNSHVFVQDSQY
			SGIGSMQNEQLSDSFPYEFFQV
5907	99	1873	TYLLSSWSS**NLDTKIKSQVKV/RKGHKKISWPYPOPAKONGK
1			KATSKVPSAPHFVHPNDHANREAELKKKWVEEMREKOOAAREOE
1			RQKRRTIESYCQDVLRRQEEFEHKEEVLOELNMFPOLDDEATRK
1			AYYKEFRKVVEYSDVILEVLDARDPLGCRCFQMEEAVLRAQGNK
1			KLVLVLNKIDLVPKEVVEKWLDYLRNELPTVAFKASTQHQVKNL
ł	l i		NRCSVPVDQASESLLKSKACFGABNLMRVLGNYCRLGEVRTHIR
			VGVVGLPNVGKSSLINSLKRSRACSVGAVPGITKFMQEVYLDKF IRLLDAPGIVPGPNSEVGTILRNCVHVQKLADPVTPVETILQRC
			NLBEISNYYGVSGFQTTEHFLTAVAHRLGKKKKGGLYSQEQAAK
			AVLADWVSGKISFYIPPPATHTLPTHLSAEIVKEMTEVFDIEDT
1	ĺ		EQANEDTMECLATGESDELLGDTDPLEMEIKLLHSPMTKIADAI
			ENKTTVYKIGDLTGYCTNPNRHQMGWAKRNVDHRPKSNSMVDVC
l i			SVDRRSVLQRIMETDPLQQGQALASALKNKKKMQKRADKIASKL
5908			SDSMMSALDLSGNADDGVGD
3308	247	975	HCGIKKRGEGSGSPSPASGGFQLGCQIPEPSLPSEEETHPHTRA
] . [		:	HTRTLRATLTRRPPRSHSTRLRFPMPLDGDGGLASWK/PMRER*
i I			GWRRPAKAAGASLGVAATGKRGCRMSKRYLQKATKGKLLIIIFI
1			VTLWGKVVSSANHHKAHHVKTGTCEVVALHRCCNKNKIEERSQT VKCSCFPGQVAGTTRAAPSCVDASIVEQKWWCHMQPCLEGEECK
		ļ	VLPDRKGWSCSSGNKVKTTRVTH
5909	1	5002	PAIPGSTIIWAPGSHSAARADGRHGSLPSQSQAPGALCGARAPP
	I	İ	SSNLRADRSMICAQARAGKNLYHNRFLGLAAMAFPSRNSOSLRR
	[		CKEPIRYSYNPDQFHNMDLRGGPHDGVTIPRSTSDTDLVTSDSR
		ĺ	STLMGRSSYYSIGHSQDLVIHWDIKEEVDAGDWIGMYLIDEVLS
	[		ENFLDYKNRGVNGSHRGQIIWKIDASSYFVEPETKICFKYYHGV
]	1		SGALRATTPSVTVKNSAAPIFKSIGADETVQGQGSRRLISFSLS
	ŀ		DFQAMGLKKGMFFNPDPYLKISIQPGKHSIFPALPHHGQERRSK IIGNTVNPIWQABQFSFVSLPTDVLEIEVKDKFAKSRPIIKRFL
[		1	GKLSMPVQRLLERHAIGDRVVSYTLGRRLPTDHVSGQLQFRFEI
			TSSIHPDDEEISLSTEPESAQIQDSPMNNLMESGSGEPRSEAPE
] }		1	SSESWKPEQLGEGSVPDRPGNQSIELSRPAEEAAVITEAGDQGM
		ĺ	VSVGPEGAGELLAQVQKDIQPAPSAEELAEOLDLGEEASALLLE
			DGEAPASTKEEPLEEEATTQSRAGREEBEKEQEEEGDVSTLEOG
			EGRLQLRASVKRKSRPCSLPVSELETVIASACGDPETPRTHYIR
		ļ	IHTLLHSMPSAQGGSAAEEEDGAEEESTLKDSSEKDGLSEVDTV
			AADPSALEEDREEPEGATPGTAHPGHSGGHFPSLANGAAQDGDT
	ļ.,		HPSTGSESDSSPRQGGDHSCEGCDASCCSPSCYSSSCYSTSCYS
		İ	SSCYSASCYSPSCYNGNRFASHTRFSSVDSAKISESTVFSSQDD
	1		EEEENSAFESVPDSMQSPELDPESTNGAGPWQDELAAPSGHVER
	1		SPEGLESPVAGPSNRREGECPILHNSQPVSQLPSLRPEHHHYPT IDEPLPPNWEARIDSHGRVFYVDHVNRTTTWQRPTAAATPDGMR
	1		RSGSIQQMEQLNRRYQNIQRTIATERSEEDSGSQSCEQAPAGGG

Deginning	SEQ	Predicted	Predicted end	
NO: location corresponding to first amino acid residue of anino acid residue of anino acid residue of anino acid sequence sequence anino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence seque		1		
Corresponding to first amino acid residue of simil and acid residue of amino acid sequence   Columnine, Napagragism, Peroline, Geldutamine, Rabginine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, Sequence   Columnine, S	NO:			Glutamic Acid R-Phonulal anima and
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amino acid residue of amino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequen	ł		to first	L-Leucine, M=Methionine, N=Asparagina
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AQLIRALGPVELALISLITLIAGSIAFILEDAYYIYKNTLCP IKRRILIKKSSAPTVVSVLCCFGIM FEVLIVEMITTSYADC FYLLMLVWWEGFGGKEAVLRTLRDTPMMVHTGPCCCCCPCCPRL LLTRKKLQ N°CWALKSTPFS*R*R*PWWACFGSEPTASMTQQTTL RGAQLYGSTLSSA/CSTLLALMTIGIISRQARLHIGEQNMGAKF ALFQVLLILITALQPSIFSVLANGGQIACSPPYSSKTRSQVMNCH LLILETHMVTLTRMYYRKDHKVGYETFSPDLDLNLKALRNM ANTMKGCCTH  CPLAPETCIGGGLEMRSPKFQSFIITSSHSGAGLLVKNPSTPVF CGHRRGAAPKYKPTPVVGPEQRPTGQKHMRGGVSLLSPRLECS GTISAHCNLSLESSINSPADA*LAGITGVCHHAQLIFVFLVET GHHNGQACLELL/MVVTULPRPPKVLGLQA  5912  924  277  MILINRALMIGALALTTVKSPCGGGDIVADHVASYGVNLYQSYGP SGQYSHEPGDEDEPYVDLERKETVWQLPLFRFRRFPDFFATIN LAVLKHALNIVIKRNSTAATNSVPSVTVFSKSPVTLGGPNTLI CLVONIPPVVNITMLSSGHSVTEGVSETRFSSKSDHFILQDQ VTSSFSFF**0L*TAKUGCIGAMFEPLLKHWGAEIPTTL CLVONIPPVVNITMLSSGHSVTEGVSETRFSSKSHFILQDG VTSSFSFF**0L*TAKUGCIGAMFEPLLKHWGAEIPTTL CLVONIPPVVNITMLSSGHSVTEGVSETRFSSKSCHFILGDS DSEKCSYSQSVKRQALYACSTCTPEGGEPAGLKKWGANGKYNDN FFGLYCICKRPYPDBEDEIPDENIQCVVCEDMFHGHLGALPPE SGDPQMFVCQACMKRGSFLAMYAAQLAVISTGMKVNGDN FFGLYCICKRPYPDBEDEIPDENIQCVVCEDMFHGHLGALPPE SGDPQMFVCQACMKRGSFLAMYAAQLAVISTGMKVNGDN FFGLYCICKRPYPDBEDEIPDENIQCVVCEDMFHGHLGALPPE SGDPQMFVCQACMKRGSFLAMYAAQLAVISTGMKNGSLGN R*JODGSVLYPSNGHGHODSTLKKDVPEGGKDDVEEVKVEQNSEP CAGSSESSIDLTVFKNISLMARSKSGCKLQEKKAQLIKKDTAT YWPLNWRSKLCTCQDCMKMYGDLDVLFITDSYDTVLAYENGKI AQATORSDEMDTISSNNRVQOVELIC/GIQ*PED  MIGGSELPFEEALFIQVASNORRVDFYSIEDMINAI/GGRN ENGALSSVETYSPKTDSWSVVAQLFRFTYGRAGTIYKDFVYISG GHDYGTGPYKRLLCYDHRTDVWEERRPMTTAGASDDSCASWDH PHRHLGGSSDDNIESMERFDVLGWEARSPCCNOMTRVAPLLHANSE SGVAVWEGRIYILGGYSWENTAFSKTVQVVDREADKWSRGVDLP KATAGGSAGFIPPSSLGGRYRKKAKARGTRTGASDDSCASWDH PHRHLGGLGRPAATS FFGRPFPSKLGRRRKRARIIQAPHCIISPRPTCPPGALQAPEA PASRAEGEVAVVVNGHTEGPAPARSAR KEPPGLPRPLGSPPCTF PQEDFPALGGCPPRPPSPGFSAVVLLKGTPPPPPFLVPPIS KPPPGFGGLIPSPHPPVSPAPPPPPPGVKPRDLRSPPCTP PQEDFPALGGCPPRPPSGFSAVVLLKGTPPPPPGLVPPIS KPPPGFGGLIPSPHPPVSPAPPPPPPGVKPRDLRSPPCTP PRELIGERPSAHPVHGGLBARRGRAFI TEDSPDSTKGTSGGGR PVIAQHHEHLMHVAGILPPVLHSGLKFATATAQDGWTSQQYPDH PTELLIG-VAATABANLAGLIPSPLLEARARAGGRTGAAH SPRELIGFFRATCHORDHENDEFSGLEGEWPSRT FEBSPDSTKGTSGGGR PVIAQHHEHLM	2310	1526	446	VAEFAAMEPGRTQIKLDPRYTADLLBVLKTNYGIPSACESODDT
IRRRILLMKSSAPTWSVLCCFGLMTPRSLVLVEMTITSFYANC FYLLMLVAWGGGGGKEAVLRTLRDTWAWTGGGCCCCPCCPDL LLTRKKLQ\R-CWALSNTPS-R-R-PWWACCPSCPTASMTQQTFL RGAQLYGSTLSSA/CSTLLALTLGI ISRQARHLGEQMMGAKF AFGQVLLLTALQSSTSVLANGGJACSPPYSSKTRSQVMMCH LLLLETPLMTVTRMYTRRDIIKVGYETFSSPDLDLNLKALRNM AMTMKGCCTH AMTMKGCCTH CHARGAAFKYKPTPVVGPBGRPTGGKHMGGGSLLSPRLECS GTISAHCTLRLPSSSSAPAPAS-LAGITGVCHHAQLIFFLVET GFHHYGQAGLELL/NVVIHLPRPPKVLGLQA  5912  924  277 MILNARALMGALALTYMSPGGGEDIVADHVASYGVNLYQSYGP SQQYSHSFDGDEPPYVDLERKETWQLDFLFRRRRTPDFGFALTN IAVLKHALNIV IRRSSSTAATNEVEVTVFTSKSPYTLGGPNTLI CLVDNIFPPVNTITHUSNGHSYTEGVSSTRSSPYSLGGPNTLI CLVDNIFPPVNTITHUSNGHSYTEGVSSTRSSPYSLGGPNTLI CLVDNIFPPVNTITHUSNGHSYTEGVSTRSSPYSLGGPNTLI CLVDNIFPPVNTITHUSNGHSYTEGVSTRSSPYSLGGPNTLI CLVDNIFPPVNTITHUSNGHSYTEGVSTRSSPYSLGGFALTAL DSSKCSYSGOSVRRQALVACSTCTPEGEEPAGICLAGSTECHGS HKLFELYTKRNFRCDCGMSKFKNLECKLLDPKAKNNSGNKYNDN FFGLYCICKRPYPDPEDEIPPDMICVEGWBFBGHLGAIPPE SGDFGEVVCQACMKRCSFLWAYAAQLAVTKIST\CMMDNGSTLM B*FOLYCICKRPYPDPEDEIPPDMICVEGWBFBGHLGAIPPE SGDFGEVVCQACMKRCSFLWAYAAQLAVTKIST\CMMDNGSTLM B*FOLYCICKRPYPDPEDEDIPPDMICVGTOWFDWFWCGVLEDWFBCHLAGIFP GAGSSSESDLQTVFKNESLNAGSKSGCKLQBLKANGLIKKDTAT YWPLNWRSKLCTCQDCMKMYGDLDVLFLTDEYDTVLAYENGKI AQATNSBDPLMDTLSSMRRVQOVBLIGGTSPPDEDIVAI/GGRN ENGALSSVETYSPKTDSWSVAGLPRFTYGHAGTIYKDFYYISG GHDYGIGPYKRLLCYDHRTDVWEBERMTARGHNSCS-GDS IYSIGGSDNIESMRRPDVLGVRAYSPCCNOWTRVAPLLHANSE SGVAVWEGRIYILGGYSWENTAFSKTVQVVDREDAKWSCVDLP KALAGGSACFIAP*SLGGRTRKKARATRTGASDPSCASWDH PHRHLBGLCRPAATS  5915  1604  703 FFGGFFFFPLLGGRRKRARITQAPHCIISPRPTCPFGALQAPEA PASRAEGDPAVVNGHTEGPAPARSAPKEPPCLVPPIS KPPPGFSGLLSSRHPVNGCLPARRGPLAKARGTRTGASDPSCASWDH PHRHLBGLCRPAATS FFGFFFFLLGGRRKRARITGAFFFTCGFFGALQAPEA PASRAEGDPAVVNGHTEGPAPARSAPKEPPCLVPPIS KPPPGFSGLLSSRHPVNGCLPARRGPLAKARGTRTGASDPSCASWDH PHRHLBGLCRPAATS FFGFFFFLLGGRRKRARITGAFFFTCGFFGALQAPEA PASRAEGDPAVVNGHTEGPAPARSAPKEPPCLYPPGLAPPIS KPPPGFSGLLSSRHPVNGCLPARRGPLAKARGTRTGASDPSCASWDH PHRHLBGLCRPAATS FFGFFFTCHTONGATARGNATHTSGLKDFKFTCGGRFGATCAGAPT  FFGFFTCHTONGATARGNATHTAGHTHAGHTYKDFYTSG FFRFTCHTONGATARGNATHTAGLOPCKFTGATCAGACCAGC TVTGAVHRH				AAQLLRALGPVELALTSILTLLALGSIAIFLEDAVYLVKNTLCD
FYILMINWEGGGKEAVLRITIPPMWATTGCCCCCCCCRL LITEKLG\R-CWALGNTPS-R-R-P-PWAGCTSSPTASMTQQTFL RGACLYGSTLSSA/CSTLLALWTLGI ISRQARLHLGEQMMGAKF ALFQVLLILTALQPSIFSVLANGGJACSPPYSSKTRSQVMNCH LILLETPLMTVITRMYRRKDIKVGYGFTSSPDLDLINLKALRWM ANTMKGCCTH  O_CPLAPCTQGKGLEMRSPKPQSFIRSSHSAGGLLVKNPSTPVF CGHRRGGAAFKYKPTPVVGPEGRPTGCKHMRGGVSLLSPRLECS GTISAHCRLRLPSSSNSPAPAS-LAGITGVCHHAQLIFVFLVET GFHHVGQAGLELL/NVVILHPRPPBVLGLQA  5912  324  277  MILNKALMIGALALTTVMSFCGGEDIVADHVASYGVNLYQSYGP SGQYSHEPDGDEPFYVDLERKETWAQLIPFRRFRFDPGFALTN IAVLKHALNIVIRRSSTAATHEVPEVTVFSKSPVLAGGPNTLI CLVONIFPPVVNITWLSNGHSVTEGVSETRPSSPKSDHFILQDQ VTJSSFFPF**OL*TAKVEQLGAWFEPLLKWAGLIPFTLQDQ VTJSSFFPF**OL*TAKVEQLGAWFEPLLKWAGLIPTTL GLYDNIFPPVVNITWLSNGHSVTEGVSETRPSSPKSDHFILQDQ VTJSSFPFF**OL*TAKVEQLGAWFEPLLKWAGLIPTTL SGBPQBKVCQAGCMKRCSFLWAYAAQLAVTKIST\CMMDMCGTLM FFGLYCICKRPYPDPEDEIPPEMIQCVVCEDWFHGRHLGATPPE SGDPQBKVCQAGKKRCSFLWAYAAQLAVTKIST\CMMDMCGTLM F*/DDQCXIKRPMGFRDDSTLKEDVGSLDVDKEVEQMSEP CAGSSESSDLOTVFKNESLNABSKSGCKLQELKAKQLIKKDTAT YWPLNWRSKLCTCQDCMKKYGDLDUFFLTDSVTVLAYENGGKI AQATDRSDPLMDTLSSMRRVQOVBLUC/GIQ+FED CAGSSESSDLOTVFKNESLNABSKSGCKLQELKAKQLIKKDTAT YWPLNWRSKLCTCQDCMKYGDLDUFFLTDSVTVLAYENGGKI AQATDRSDPLMDTLSSMRRVQOVBLUC/GIQ+FED GHDYQIGPYRKNLLCYDHRTDVWEERPKMTTARGHHSMCSJGDS IYSIGGSDDNIESMRFPDVLGVERAYSPQCONGMTRVAPLLHANSE GHDYQIGPYRKNLLCYDHRTDVWEERPKMTTARGHSMCSJGDS IYSIGGSDDNIESMRFPDVLGVERAYSPQCONGMTRVAPLLHANSE SGVAVWEGRIYILGGVSKENTAFSKTVQVDREADKWSRQVDLP KAIAGGSACFIAP*SLGQRTRKRKARIQAPFCTGASDPSCASWDH PHRHLPGLCRPAATS  5915  1604  703  FFGRPFTRPLKLGGRRKRARIQAPHCHSPRPFCCPPGALQAPPA PASRABGDVAVVNGHTEGPAPARSAPKSPPCLPPPISSFPCT PQEDFFALGGPCPPRMPPSPGSFAVVLLKGTPPPPPGLVPPIS KPPPGFSGLLSSHPI-VSSPAPPPPPPGK/RPRLLPAP/FGLPS PRELIGGEPSAHPVHQCLPARRGPLORVQEBLRGVQTGDDLRS PROLIFERIGHTHANGGILPPWLHSGLKAPATAGAGGCR TVTGAVHRHILMHVAGIIPPWLHSGLKPTAATAQDQWTSQQYPDH PTRLLIQ-HQATABKUN-TTALLQOHAVSPMMAES TTRULCY-HQAVTAKMN-TTALLQOHAVSPMMAES PTRLLIC-HQAVTAKMN-TTALLQOHAVSPMMAES PTRLICHONATAMAN-TTALLOPANTAGOMYSQQYPDH				IKRRTLLWKSSAPTVVSVLCCFGLWIPRSLVLVEMTTTSPVAVC
RGACLYGSTLSSA/CSTLLAUTIGIISRQARLHLGEORMGAKF ALFQVLLILTALQSI FSVLAUTIGIISRQARLHLGEORMGAKF ALFQVLLILTALQSI FSVLAUTIGIISRQARLHLGEORMGAKF ALFQVLLILTALQSI FSVLAUTIGIISRQARLHVKNPSTPVF CCHRRGGAFKYKPTPVVGPQRPTGCKHMRGGVSLLSPRLECS GTISAHCNLRLPSSSNSPAPAS-*LaGITOXCHHAQLIFVFLVET CGHRRGGAFKYKPTPVVGPQRPTGCKHMRGGVSLLSPRLECS GTISAHCNLRLPSSSNSPAPAS-*LaGITOXCHHAQLIFVFLVET GPHHVGQAGLELL/NVVIHLPRPPKVLGLQA  5912  924  277  MILNRALMIGALALTTVMSPCGGEDTVADBVASYGVNLVQSYGP SQCYSHBPGDGEPFYVDLERKETVAQUPLFFRRRFRFDCFALTN IAVLKHNLNIVIKRSNSTAATHEVPEVTVFSKSPVTLGQPNTLI CLVDNIFPPVVNITWLSNGHSVTEGVSETPRSSPKSDHFFLQDQ VYSSFSFFF**DI-TAXVEGLGAMFEPLLKHMCASIPTLI CLVDNIFPPVVNITWLSNGHSVTEGVSETPSSPKSDHFFLQDQ VYSSFSFFF**DI-TAXVEGLGAMFEPLLKHMCASIPTLI CLVDNIFPPVVNITWLSNGHSVTEGVSETPSSPKSDHFFLQDQ PSSKCSYSQSVKRQALYACSTCTPEGGESPAGICLACSYECHGS HKLPELTTKRNFRGCDCGNSKFRNLECKLLPDKAKVNSGNKXNDN PFGLYCLCKRPYPDPEDEITDEMIQCVVCEDWFHGRHLGAIPPE SGDFQEVVCQACMKRCSFLWAYAAQLAVTKIST\CMMDMCGTIM B*/DDGEVIKPEMGENDSTLLEEDPEGGKDDVREVKVEGNSEP CAGSSESDLQTVFKNESINASSKSGCKLQBLKAKQLIKKDTAT YWPLNMRSKLCTCDCMCMKYGDLHFTDSVETVLGENSEP CAGSSESDLQTVFKNESINASSKSGCKLQBLKAKQLIKKDTAT YWPLNMRSKLCTCDCMCMKYGDLHFTDSVETVLGFRYTYGFGTIYGFVYISG GHDVQIGPYKKNLLCYDHRTDVWEERRPMTTAKGMHSMCSLGDS IYSIGSDDNIESMERFDVLGWEAYSPCCNOWTRVAPLLHANSE SGVAVWEGRIYILGGYSWENTIFSKTVQVYDREADKWSGVDLP KALAGGSACFIAP*SLGQRTRKRKAKARGTRTGASDPSCASWDH PHRLPGLCRPAATS PASRAGGPVAVVVNGHTEGPAPARSAR KEPFGLPRPGSFCPT PRELIGGEPSAHPVURGLPARRGAPAH SGSGAPPPPPLKLGRRRKRARITQAPHCISPRPRTCPPGALQAPPA PASRAGGPVAVVVNGHTEGPAPARSAR KEPFGLPRPGSFCPT PRELIGGESPSAHPVRGCLPABRRGAPAHPPPPPQK/RPLLPAP/PGLPS PRELIGGESPSAHPVRGCLPABRRGAPAH SPRUMEIWGPWRRWESFSLEGEWFSRTFEFSPSTKGTSGKCR TVYGAVHRILMINAGIIPWVLHSQLKPTAATAQDQATSQQYDH PTILLIQ-MQATABNIN*TTALLOGRANDARDA		]		FYLLMLVMVEGFGGKEAVLRTLRDTPMMVHTGPCCCCCCCCCCC
ALFQUILITATQPSIFSYLANGGQIACSPPYSKTRSQVMMCH LLILETFIMTVLTRMYTRKDIKVQPETFSSPDLDLNLKALRWM AWTMKGCCTH  GPLAPCIQKGLEMRSPKPGSFIIRSSHSGAGLLVKNPSTPVF CCHRRGGAPKYKPTPVVGPEQRPTGQKHMRGCVSLLSPRLCCS GTISAHCRLRLPSSSNSPAPAS*LAGITGVCHHAQLIFVFLUET GPHNVQQAGLELL/NVVJHLPRPPKVLGLQA  5912  974  277  MILNKALMLGALALTTVMSPCGGDTVADHVASYGVNLYQSYGP SQVSHBPDGDEPTVVLLERKETVWQLPLFRFRRFDDFFALTN LAVLKHLNIVIKRSNSTAATNEVPEVTVPSKSPVTLGQPNTLI CLVONIFPPVVNITWLSNGHSVTGGVSETRPSSPKSDHFILQDQ VTSPSFPFE**DL*TAKVBGLGAWFSPLLKHWGAEIPTTL  5913  46  1198  QLRMAGAEGAARQSELEPVVSLIVDLCLACSYECHOS HKLFELTYRKNFRCDCSNSKFKNLECKLLPDKAKVNSGNKYNDN FFGLYCICKRPYDPEDEIPDEMIQCVEOWFHGRHLGAIPPE SGDFQENVCQACKKRCSFLWAVAAQLAVTKIST\GMMDWGTTLM E*/DDQEVIKPENGERQDSTLKEDVPEGGKDDVREVKVEQNSEP CAGSSSSSDLOTVFKNESLNAESKSGCKLQELKAKQLIKOTAT YWPLNWRSKLCTCQDCMKNYGDLDVFFLOSFDTVLAYSENKGKI AQATDRSDPHMDTLSSMNRVQQVELIC/GIQ*FED  1946  124  NLGGSELPPSEALFIQVASMNQRRVDFYLASIEDMLVAI/GGRN ENGALSSVETYSPKTDSWSYVAGLPRFTYGHAGTIYKDFYYISG GHDYQIGPYKKNLLCYDHRTDVWEERRRHTTARGHMSCSLGDS IYSIGGSDNIESMRFPDVLGFSPOCNOMTRVAPLLHANSE SGVAVWEGRIYILGGYSWENTAFSKTVQV VDREADKWSRCVDLP KALAGGSACFIAP*SLGQRTKKRKAKARGTRTGASDPSCASWDH PHRILPGLCRPAATS  5915  1604  703  FFGRFTRPLKLGRRKREARIIQAPHCUSPRPRTCPPGALQAPEA PASRAEGPVAVVVNCHTEGPAPARSAPKEPGLPRFLGSFPCPT PRELIPGCEPSARVVLNCHTEGPAPARSAPKLPFGLPRFLGSFPCDT PRELIPGCEPSARVVLNCHTEGPAPARSAPKLPFGLPRFLGFPC PRELIPGGEPSARPVLDRAGRASPAREPGLPRFLGSFPCDT PRELIPGCEPSARPVLDRAGRASPAREPGLPRFLGSFPCDT PRELIPGCEPSARPVLDRAGRASPAREPGLPRFLGSFPCTT PRELIPGGEEPSARPVLDRAGRASPAREPGLPRFLGSFPCDT PRELIPGGEEPSARPVLDRAGRASPAREPGLPRFLGSFPCDT PRELIPGGEEPSARPVLDRAGRAGPCONGERRGCCR TVTGAVHRHLEHNAGIIPWULHSQLKPTAATAGOCATSQQYDDH PTISLIJQ*NOATAGNN*TTALLQCLKPTAATAGOCATSQQYDDH PTISLIJQ*NOATAGNN*TTALLQCLKPTAATAGOCATSQQYDDH		l i		LLTRKKLQ\R*CWALSNTPS*R*R*PWWACFSSPTASMTQQTFL
Deeks   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept   Sept		]		RGAÇLYGSTLSSA/CSTLLALWTLGIISRQARLHLGEQNMGAKF
5911 109 595 Q-PLAPCIGK GLEMRS PKPQS FITRS HSGAGLLVKNPSTPVF CGHRRGAAFKYKPTPVVGPBGRPTGQKHMRGGVSLLS PRIECS GTISAHCHLRIESS SINS PAPAS*LAGITGVCHHAQLIF VFLVET GPHHVGQAGLEL //NVVIHLPPKVLGLQA  5912 974 277 MILNKALMLGALALTVMSPCGGEDIVADHVASYGVNLYQSYGP SGQYSHBPGGDEPYVDLERKETVWQLD LFRRFRRFDFOFALTN IAVLKHNINIVIKRS NSTAAFNEVPEVTVYFSKS PVTLGQPNTLI CLVDNIF PPVVNITWLS NSTAAFNEVPEVTVYFSKS PVTLGQD VTSPSFPFF**DL*TAKVEQLGAMFEPLLKHWGAEIPTL CLVDNIF PPVVNITWLSNGHS VTEGVSETRPSSKSDHFFLQDQ VTSPSFPFF**DL*TAKVEQLGAMFEPLLKHWGAEIPTL DESKCSYSQGSVKRQALYACSTCTPEGEEPAGICLACSYECHGS HKLPELYTKRNFRCDCCNSKFWNLECKILPPKAKVNSGNKYNDN PFGLYCLKRPYPDPDEBIEIPAGVVDVLEDEPBGRENDAVLAGS DSEKCSYSQGSVKRQALYACSTCTPEGEEPAGICLACSYECHGS HKLPELYTKRNFRCDCCNSKFWNLECKILPPKAKVNSGNKYNDN PFGLYCLKRPYPDPDEBIEIPAGVVCQACMKRCSFLWAYAAQLAVTKIST\GWMDWGGTLM E*/DDQEVIKPENGEHDDSTLKEDVPEGGKDDVREVKVEQNSBP CAGSSSEDLGTVFKWESLMABESKSGCKLQBLKAKQLIKKDTAT YWPLNWRSKLCTCQDCWKMYGDLDVLFLTDEYDTVLAYENKGKI AQATORSDPLWDTLSSMNRVQQVELLCG/G1Q**PED LYSIGGSDDVATEVKESLMABESKSGCKLQBLKAKQLIKKDTAT YWPLNWRSKLCTCQDCWKMYGDLDVLFLTDEYDTVLAYENKGKI AQATORSDPLWDTLSSMNRVQQVELLCG/G1Q**PED GHDYQIGPYRKNLLCYDHRTDVWEERRFPTTARGWHSMCS/LGDS IYSIGGSDDNIESMRSPDVLGGVRYNAPALLHANSE SGVAVWBGRIYILGGYSWENTAFSKTVQVYDREADKWSKGVDLP KALAGGSACFIAP*SLGQATRKKKAARGTRTGASDPSCASWDH PHRHLPGLCRPAATS  5915 1604 703 FPGRPTPPLKLGRRRKRARIIQAFHCHSPRPTCPPGALQAPEA PASRAEGPVAVVNGHTEGPAPARSAPKBPPGLPRPLGSFPCDT PQEDFFALGGPCPRNPPSSFPSTVVLLKGTPPPPPGLVPPIS KPPPGFSGLLPSPPPPPPPPPCVPPPIS KPPPGFSGLLPSPPPPPPPPPCVPPPIS KPPPGFSGLLPSPPPPPPPPCVPPPIS KPPPGFSGLLPSPPPPPPPPCVPPPIS PPRLFGEREPAHPVLIGGLPARRGPLQRYQEPLRGVGTGPDLRS PPLLGERPSHPPNTGGTPARTAGQVYPDH SPRLFGERSPAHPVLIGGLPARRGPLQRYGPLRGVGTGPDLRS PPLLGERPSAHPVLIGGLPARRGPLQRYGPLRGVGTGPDLRS PPLLGEPGPAGGFFFGL**AAAGPAAH				ALFQVLLILTALQPSIFSVLANGGQIACSPPYSSKTRSQVMNCH
5911 109 595 Q_PLAPCIQGKGLEMRSPKPQSFIIRSSHSGAGLLVKNPSTPVF CGHRRGGAAPKKKPTPVVGPBQRPTGGCHMRGGVSLLSPRLECS GTISAHCULRIPESSSNSPAPAS*LAGITGVCHAQLIFVFLVET GPHHVGQAGLELL/NVVIHLPRPPKVLGLQA  5912 924 277 MILNRALMGALLTTVWSFCGGEDIVADHVASYGVNIJVQSYGP SQQYSHEPGGDEFYVDLERKETVAQLPLFRRFRRFDPQFALTN IAVLKHNLNIVIKRSNSTAATNEVPEVTVFSKSPVTLGQPNTLI CLVONIFPPVNITWLSGHSVTEGVSETRPSSPKSDHFILQDQ VTSPSFPFE**DL*TAKVGLGAFFEPLLKHWGAEIPTTL  5913 46 1198 QLRMAGAEGAAGRGSELEPVVSLVDVLEEDEELENEACAVLGGS DSEKCSYSQGSVKRQALYACSTCTPEGEEPAGICLACSYECHGS KKLFSLYTKRNFRCDCGNSKFKNLECKLLPDKAKVNSGNKYNDN PFGLYCICKRPYPDPEDEIPDEMIQCVVCEDWFHGRHLGAIPPE SGDPCBFVVCQACMKRCSFLWAYAAQLAVTKIST\GMMDWCGTLM E*/DDGEVIKPENGEHODSTLKECVLPDKAKVNSGNKYNDN PFGLYCICKRPYPDPEDEIPDEMIQCVVCEDWFHGRHLGAIPPE SGDPCBFVVCQACMKRCSFLWAYAAQLAVTKIST\GMNDWCGTLM E*/DDGEVIKPENGEHODSTLKECVLPDKVLKVEQNSBP CAGSSSESDLQTVFKNESLNAESKSGCKLQELKAKQLIKKDTAT YWPLNMRSKLCTCQDCMKMYGDLDVLFITDSYDTVLAYENKGKI AQAATDASDPLMDTLSSNNRVQQVELLC/G1Q*FED  1924 NLGGSELPPEEALFIQVASMNQRRVDFYLASIEDMLVAI/GGRN ENGALSSVETYSPKTDSWSVVAGLPRETYGHAGTIYKDFVYISG GHDVQIGPYKKNLLCYDHRTDVWEERPFMTTAKGMISMCS'LGDS IYSIGGSDDNIESMERFDVLGVEANSPQCCPMTVAPLLHANSE SGVAVMEGRIYILGGYSWENTAFSKTVQVVDREADKWSRGVDLP KAIAGGSACFIAP*SLGQRTRKKKAARGTRTGASDPSCASWDH PHRHLBGLCRPAATS  5915 1604 703 FFGRPTRPJKLGGRRKRARIIQAPHCISPRPRTCPPGALQAPEA PASRAEGPVAVVVNGHTEGPAPARSAPKEPPCLPRPLGSFPCDT PQSDFPALGGPCPPRNPPSBGPSAVVLLKGTPPPPPGLLVPIS KPPPGFSGLLPSPHPPSPGPSAVVLLKGTPPPPPGLVPIS KPPPGFSGLLPSPHPPSPGPSAVVLLKGTPPPPPPGLVPIS KPPPGFSGLLPSPHPPSPGPSAVVLLKGTPPPPPGLVPIS KPPPGFSGLLPSPHPPSPGPSAVVLLKGTPPPPPGLVPIS KPPPGFSGLLPSPHPPSPGPSAVVLLKGTPPPPPGLVPIS KPPPGFSGLLPSPHPPSPGPSAVVLLKGTPPPPPGLVPIS KPPPGFSGLLPSPHPPSPGDFSRAVPLLKGTPPPPPGLVPIS KPPPGFSGLLPSPHPPSPGBAPARAPKPPCLPRPLGSFPCDT PVLQELPGPAGGEFPEGL**AAAGPAAH  5916 256 633 SPRMEIWGDWHRWESFSLEGEWPSRIPESPPDSTKGTSGKGC TVTGAVHRHLHNAGIIPWLMSGLKPTAATAQQVFMDH		i		AWTMKGCCTH AWTYKKENIKVGYETFSSPDLDLNLKALRNM
CCHRRGGAFKYKPTPVOFEORPTGCKHRRGGYSLLSPRIECS GTISAHCNILFESSNSPADAS*LAGITGVCHHAQLIFVFLVET GPHHVGQAGLELL/NVVIHLPRPPKVIGLQA  974 277 MILNKALMIGALALTTVMSPCGGEDTVADHVASYGVNLYGSYGP SQQYSHEFDGDEPYYADLEKTVWQLPLFRRFRRFDPOFALTN IAVLKHNLNIVIKRSNSTAATHEVPSVTVFSKSPVTLGQPNTLI CLVDNIFPPVVNITHLSNGHSVTEGVSETRPSSPKSDHFILQDQ VTSPSFPFE**DL*TAKVGAMETPSLLKHWGAEIPTTL CLVDNIFPPVVNITHLSNGHSVTEGGEDELENERAGAVLGGS DSEKCSYSQGSVKRQALVACSTCTPSGESPAGICLAGSYECHGS HKLFSLTYKRMFRCDCGNSKFKNLECKLLPDKAKVMSGNKYNNN PFGLYCICKRPYPDPEDBIPDEMIQCVVCEDWFHGHLLGAIPPE SGDFQBVVCQACMKRGSFLWAVAQLAVTKIST\GMMDMCGTLM B*/DDGEVIKPSGHDDSTLKEDVPEQGKDDVREVKVEQNSBP CAGSSSESDLQTVFKNESLNARSKSGCKLQELKAKQLIKKDTAT YWPLNMRSKLCTCQDCMKMYGDLDVLFITDEYDTVLAYENKGKI AQATRSDPLMDTLSSMMRVQOVELIC/GIQ*FED  124 NLGGSELFPEEALFIQVASMRVQDVVLLGTGFPD ENGALSSVETYSPKTDSWSYVAGLPRFTYGHAGTIYKDFVYISG GHDYOIGPYRKNLCYDHRTDVWEERPMTTARGHSMCSLGDS IYSIGGSDDNIESMERPDVLGVERYSPCCNOMTRVAPLLHANSE SGVAVWEGRIYILGSWENTAFSKTVQVYDREADKWSRGVDLP KAIAGGSACFIAP*SLGQRTRKRKAKARGTRTGASDPSCASWDH PHRHLBGLCRPAATS  5915 1604 703 FFGRPTRPLKLGRRRKARATIQAPHCHSPRPTCFPGALQAPEA PASRAEGPVAVVVNGHTEGFAPARASARKEPBCLPRFLSFFCPT PQEDFFALGGPCPRMPPSPFGFSAVVLLKGTPPPPPECLYPPIS KPPPGFSGLLPSPHP\DVSPAPPPPPPDK/RPILPPPPPELVPPIS KPPPGFSGLLPSPHP\DVSPAPPPPPPPDK/RPILPPPPPELVPPIS KPPPGFSGLLPSPHP\DVSPAPPPPPPPDK/RPILPPPPPPPDK/PPIS PPRLUGLPGPAGGFFPBCL**AGGPAH  5916 256 633 SPRMBEWGPWHRWESFSLEGEWPSRIPEPSPDSTKGTSGKGCR TVTGAVHRHINHVAGIIPWVHSGLKPTAATAGODQWTSQQYPDH FTILLIQ*NQATHANN*TTALLOPHOLLVSPMATAGODQWTSQQYPDH FTILLIQ*NQATAGNN*TTALLOPHOLLVSPMATAGODQWTSQQYPDH	5911	109	595	
5912 974 277 MILNKALMLESSSNSPAPAS*LAGITGVCHHAQLIFVFLVET GPHHVQQACIELL/MVVIHLPRPPKVLGLQA  MILNKALMLGALALTTVMSPCGGEDTVADHVASYGVNLYQSYGP SQQYSHEFGGDEFYYDLERKETVWQLPLFRRFRFDPOFALTN IAVLKHNLNIVIKRSNSTAATNEVPEVTVYSKSPVTLGQPNTLI CLVONIFPPVVNITHLSNGHSYTEGVSETRYSSPKSHFFLQDQ VTSPSFPFE**DL*TAKVEOLGAWFEPLLKHWGAEIPTTL  5913 46 1198 QLRMAGAEGAGGSELEPVVSLVVDLEEDEELBEACAVLGGS DSEKCSYSQGSVKRQALVACSTTPFGGEFDAGICLACSYECHGS HKLFELYTKRNFRCDCGNSKFKNLECKLLPDKAKVNSGNKYNDN PFGLYCICKRPYDPDEDEIPDEMIQCVVCEDWFHGHLGAIPPE SGDPCBVVQACMMKCSFLWAVAQLAVTKIST\GMMDNCGTLM E*/DDQEVIKPENGEHQDSTLKEDVPEQCKDDVREVKVEQNSRP CAGSSSSDLQTVFKNESLNARSKSGCKLQELKAKQLIKKDTAT YWPLNMRSKLCTCQDCMMYGDLDVLFLTDEYDTVLAYENKGKI AQATDRSDPLMDTLSSMNRVQQVELIC/GIQ*FED  124 NLGGSELPPEEALFIQVASMNQORVDFYLASIEDMLVAI/GGRN ENGALSSVETYSPKTDSWSVVAGFTYGHAGTIYKDFVYISG GHDYQIGPYRKNLLCYPHRTDVWEERRFMTTARGHHSMCSLGDS IYSIGGSDDNIESMERFDVLGVEAYSPQCNQWTRVAPLLHANSE SGVAVWEGRIYILGGYSWENTAFSKTVQVYDREADKWSRGVDLP KATAGGSACFIAP*SLGGRTRKKAKARGTRTGASDPSCASWDH PHRHLPGLCRPAATS  5915 1604 703 FFGRPTRPLKLGRRRKRARIQAFHCISPRPT-CPPGALQAPEA PASRAEGPVAVVNGHTEGPAPARSAPKEPPCLPRPLGSFPPCF PAGRAEGPVAVVNGHTEGPAPARSAPKEPPCLPRPLGSFPPCF PAGRAEGPVAVVNGHTEGPAPARSAPKEPPCLPRPLGSFPPCF PQEDFPALGGPCPPRMPPSPGFSAVVLLKGTPPPPPPECLVPPIS KYPPGFSGLLPSHPVVQGLPAERRGPLQRVQEPLRRVQTGPDLRS KYPPGFSGLLPSHPVVQGLPAERRGPLQRVQEPLRRVQTGPDLRS KYPPGFSGLLPSHPVVQGLPAERRGPLQRVQEPLRRVQTGPDLRS PVLQELPGBEGSFPPGL**AAGPAAH  5916 256 633 SPRMWEIMGWHRWEGFSLEGEWPSRIPEPSPDSTKGTSGKGCR TVTGAVHRHLINIVAGIIPWVLHSQLKYTAATAQOQWTSQQYPDH  5917LILQ*NQATADKNN*TTALOOPHORLVYSPMAEA				CGHRRGGAAFKYKPTDIAGDEODDTCOVUMBGGUGL GDD
5912 924 277 MILNKALMIGALALTTVMSPCGGEDIVADHVASYGVNLYQSYGF SGQYSHEFDGDEFYVDLERKETVWQLPLFRFRRRDPOPRALTN IAVLKHNLMIVIKRSMSTAATNEVPEVTVFSKSPVTLGGPNTLI CLVDNIFPPVVNITWLSNGHSVTEGVSETRPSSPKSDHFILDDO VTSPSFPFE**DL*TAKVEOLGAWFEPLLKHWGAEIPTTL CLVDNIFPPVVNITWLSNGHSVTEGVSETRPSSPKSDHFILDDO VTSPSFPFE**DL*TAKVEOLGAWFEPLLKHWGAEIPTTL GLYCHDIFPPVVNITWLSNGHSVTEGVSETRPSSPKSDHFILDDO VTSPSFPFE**DL*TAKVEOLGAWFEPLLKHWGAEIPTTL GLYCHDIFPPVVNITWLSNGHSVTEGVSETRPSSPKSDHFILDDO VTSPSFPFE**DL*TAKVEOLGAWFEPLLKHWGAEIPTTL GLYCHGGE DASHCACAVLGGS DSEKCSYSGGSVKRQALYACSTCTPEGEEPAGICLACSYECHGS HKLFELYTKRNFRCDCGNSKYKNLDKCSTLMFFGYGGCVVCEDWFHGRHLGAIPPE SGDFQEMVCQACMKRGSFLWAYAAQLAVTKIST\GMMDNCGTLM E*/DDGVIKPMGEHQDSTLKEDVPEQGKDDVREVKVEQNSEP CAGSSSESDLCTVFKNESLNAESKSGCKLQELKAKQLIKKDTAT YWPLNWRSKLCTCQDCMKMYGDLDVLFITDSYDTVLAVENKKKI AQATORSDPLMDTLSSMNZVQQVELIC/GIQ*FED NLGGSELPPEEALFIQVASMNZVQVELIC/GIQ*FED NLGGSELPPEEALFIQVASMNZVQVEFLIC/GIQ*FED SGGALSSVETYSPKTDSWSYVAGLPRFTYGHAGTIYKDFVYISG GHDYQIGPYRKNLLCYDHRTDVWEERR PMTTARGWHSMCSLGDS IYSIGGSDDNIESMERFDVLGWEARSPQCNQWTRVAPLLHANSE SGVAVWEGIISMENTAFSKTVQVYDREADKWSRGVDLP KAIAGGSACFIAP*SLGQRTRKRKAKARGTRTGASDPSCASWDH PHRHLGCLCRPAATS  5915 1604 703 FPGRPTRPLKUGRRRKRARIIQAPHCHISPRPRTCPPGALQAPEA PASRAGGPVAVVVNGHTEGPAPARSAPKEPPGALQAPEA PASRAGGPVAVVVNGHTEGPAPARSAPKEPPGALQAPEA PASRAGGPVAVVVNGHTEGPAPARSAPKEPPGALQAPEA PASRAGGPVAVVVNGHTEGPAPARSAPKEPPGALQAPEA PASRAGGPVAVVVNGHTEGPAPARSAPKEPPGALQAPEA PASRAGGPVAVVVNGHTEGPAPARSAPKEPPGALQAPEA PASRAGGPVAVVVNGHTEGPAPARSAPKEPPGALQAPEA PASRAGGPVAVVVNGHTEGPAPARRAPLEPPPPGALQAPEA PASRAGGPVAVVVNGHTEGPAPARRAPLEPPPPPGLVPPIS KPPGFSGLLPSPHP\PVSPAPFPPPPPQK/RPRLIPAP/PGLPS PPLELPGEPSSALPVHQGLPAERRGPLQRVQCPLRGVQTGPDLRS PVLQELPGPAGGEFPECL**AAGPAAH  5916 256 633 SPRMWBIWGPWHRWESFSLEGEWPSRIPEPSDSTKGTSGKGCR TVTGAVHRHLNHVAGIIPWVLALLQPHORLVVSPBMARA				GTISAHCNLRLPSSSNSPAPAS+LAGITGVCHHAOLTGUETVET
MILINKALMIGALALTTVMSFCGEDIVADHVASYGVNLYQSYGF SGQYSHEFDGDEPFYVDLERKETVWQLPLFRERREDPOPALTN IAVLKHILMI VIKRSMSTAATMEVPEVTVYFSKSPVTLGQPNTLI CLVDNIFPPVNITWLSNGHSVTEGVSETRPSSPKSDHFILQDQ VTSPSFPFF**DL*TAKVEQLGAMFEPLLKHWGAEIPTTL  5913  46  1198  QLRMAGAEGAARGYSELEPVVSLVDVLEEDEELENEACAVLGGS DSEKCSYSQGSVKRQALYACSTCTPEGEEPAGICLACSYECHGS HKLFELYTKRNFRCDGMSKFKNLECKLLPDKAKVMSGNKYNDN PFGLYCIKGRPYPDPEDEIPDEMIQCVVCEDMFHGRHLGAIPPE SGDFOEMVCQACMKRCSFLWAYAAQLAVTKIST\CMMDNCGTLM E*/DDQEVIKPBNGBRQDSTLKEDVPEQGKDDVREVKVEQNSEP CAGSSSESDLQTVFKNESLNAESKSGCKLQSLKAKQLIKKDTAT YWPLNMRSKLCTCQDCMKYVGDLDVLFITDSYDTVLAYENKGKI AQATDRSDPLMDTLSSMNRVQQVELIC/GIQ*FED  124  NLGGSLSPETEALFTQVASMNRRVDFYLASIEDMLVAI/GGRN ENGALSSVETYSPKTDSWSVVAGLPRFTYGHAGTIYKDFVYISG GHDYQIGPYRKNLCYDHRTDWEERRFMTTARGWHSNCSLGDS IYSIGGSDDNIESMERFDVLGVEAYSPQCNGWTRVAPLLHANSE SGVAVWEGRIYILGGYSWENTAFSKTVQVVDREADKWSRGVDLP KALAGGSACFIAP*SLGQRTRKRKAKARGTRTGASDPSCASWDH PHRHLPGLCRPAATS  5915  1604  703  FFGRPTRPLKLGRRRKRARITQAPHCHSPRPR*CPPGALQAPEA PASRAEGPVAVVVNGHTSGPAPARSAPKEPPGLPRPLGSFPCPT PQEDFPALGGPCPPRMPPSPGFSAVVLLKGTPPPPPEGLVPPIS KPPPGFSGLLPSPHP\PVSPAPPFPPPPCLVPPIS KPPPGFSGLLPSPHP\PVSPAPPFPPPPCLVPPIS KPPPGFSGLLPSPHP\PVSPAPPFPPPPCLVPPIS KPPPGFSGLLPSPHP\PVSPAPPFPPPPCLVPPIS KPPPGFSGLLPSPHP\PVSPAPPFPPPQLRVCQEPLRGVQTGPDLRS PRLOGEPSALPVANGALTSGLEWFRTPPPPPGTARGVTGPDLRS FPRELGGEPSALPVANGLTSGLEWFTAATAQDQMTSQQYPDH PTRLIQ*NOATADKNN*TTALLQPHORGLYVSPBMBRA				GFHHVGQAGLELL/NVVIHLPRPPKVLGLOA
SGQYSHEFOGDEFYYOLERKETVWQLPLFRFFRFFDPOFALTN IAVLKHNLNIVIKRSNSTAATNEVPEVTVFSKSPVTLGQPNTII CLVONIFPPVVNTTWLESGHSVTEGVSETRPSSPKSDHFILQDQ VTSPSFPFF***DL*TAKVEQLGAWFEPLLKHWGAEIPTTL  1198 QLRMAGAEGAAGRGSELEPVUSLVDVLEEDBELENEACAVLGGS DSEKCSYSGGSVKRQALYACSTCTPEGEEPAGICLACSYECHGS HKLFELYTKRNFRCDCGNSKFKNLECKLLPDKAKVNSGNKYNDN FFGLYCICKRPYPDPEDEIPDEMIQCVVCEDWFHGRHLGAIPPE SGDFQEMVCQACMKRCSFLWAYAQLAVTKIST\GMMDNCGTIM B*/DDQEVIKPENGEHQDSTLKEDVPEQGKDDVREVKVEQNSEP CAGSSSESDLQTVFKNESLNAESKSGCKLQELKAKQLIKKDTAT YWPLNWRSKLCTCQDCMKMYGDLDVLFLTDEYDTVLAYENKGKI AQATDRSDPLMDTLSSMNRVQQVELIC/GIQ*FED PINGLGSVETYSPKTDSWSYVAGLPRFTYGHAGTIYKDFVYISG GHDYQIGPYRKNLLCYDHRTDVWEERRPMTTARGWHSMCSLGDS IYSIGGSDDIESMERFDVLGVEAYSPQCNQWTRVAPLLHANSE SGVAVWEGRIYILGGYSWENTAFSKTVQVYDREADKWSRGYDLP KAIAGGSACFIAP*SLGQRTRKRKAKARGTRTGASDPSCASWDH PHRHLPGLCRPAATS  5915 1604 703 FFGRPTRPLKLGFRRRKRARITQAPHCHSFRPTCPPGALQAPEA PASRAEGPVAVVNGHTEGPAPARSAPKEPPCLPRFLGSFPCPT PQEDFPALGGPCPPRMPPSPGFSAVVLLKGTPPPPPPGLVPPIS KPPPGFSGLLPSPHP\PVSPAPPPPPPPCK/RPRLPAP/PGLPS PASRAEGPVAVVNGHTEGPAPARSAPKEPPCLPRFLGSFPCPT PGEDFPALGGPCPPRMPPSPGFSAVVLLKGTPPPPPPGLVPPIS KPPPGFSGLLPSPHP\PVSPAPPPPPPPCK/RPRLPAP/PGLPS PRELPGGEFSAHPVHQGLPAERRGPLQRVQCPPGPLRS PVLQELPGPAGGEFPEGL**AAGPAAH  5916 256 633 SPRMWEIWGFWHRWESFSLEGEWFSRIPEFSPDSTKGTSGKGCR TVTGAVVHRLINHVAGIIPWULNSTALLQOKPTBAATAQQQYTSQQPDH PTRLIQ*NQATABKNY*TTALLQOKPTBAATAQQQYTSQQPPDH PTRLIQ*NQATABKNY*TTALLQOKPTBAATAQQQYTSQQPPDH	3312	924	277	MILNKALMLGALALTTVMSPCGGEDIVADHVASYGVNLYOSYGP
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5914 960 124 NLGGSELPPEALFIQVASMOQRVDFYLASIEDMLVAI/GGRN ENGALSSVETYSPKTDSWSYVAGLPRFTYGHAGTIYKDFYYISG GHDYQIGPYRKNLLCYDHRTDVWEERRPMTTARGWHSMCSLGDS IYSIGGSDDNIESMERFDVLGVEAYSPQCNQWTRVAPLLHANSE SGVAVWEGRIYILGGYSWENTAFSKTVQVYDREADKWSRGVDLP KAIAGGSACFIAP*SLGQRTRKRKAKARGTRTGASDPSCASWDH PHRHLPGLCRPAATS FPGRPTRPLKLGRRRKRARITQAFHCHSPRPTCPPGALQAPEA PASRAEGPVAVVNGHTEGPAPARSAPKEPPGLPRPLGSFPCPT PQEDFPALGGPCPPRMPPSPGFSAVVLLKGTPPPPPPGLVPPIS KPPPGFSGLLPSPHP\PVSPAPPPPPQK/RPRLLPAP/PGLPS PRELPGEEPSAHPVHQGLPAERRGPLQRVQEPLRGVQTGPDLRS PVLQELPGAGGEFPEGL**AAGPAAH  5916 256 633 SPRWEIWGPWHRWESFSLEGEWPSRTPEPSPDSTKGTSGKGCR TVTGAVHRHINHVAGIIPWVLHSQLKPTAATAQDQWTSQQYPDH PTRLILQ*NQATADKNN*TTALLOPHORL\VSPRMAFA	ľ	1		YWPLNWRSKLCTCQDCMKMYGDLDVLFLTDEYDTVI.AVENKGYT
NLGGSELPPEEALFIQVASMNQRRVDFYLASIEDMLVAI/GGRN ENGALSSVETYSPKTDSWSYVAGLPRFTYGHAGTIYKDFVYISG GHDYQIGPYRKNLLCYDHRTDVWEERRPMTTARGWHSMCSLGDS IYSIGGSDDNIESMERPDVLGVEAYSPQCNQWTRVAPLLHANSE SGVAVWEGRIYILGGYSWENTAFSKTVQVYDREADKWSRGVDLP KAIAGGSACFIAP*SLGQRTRKRKAKARGTRTGASDPSCASWDH PHRHLPGLCRPAATS  5915 1604 703 FPGRPTRPLKLGRRRKRARIIQAPHCHSPRPRTCPPGALQAPEA PASRAEGPVAVVVNGHTEGPAPARSAPKEPPGLPRPLGSFPCFT PQEDFPALGGPCPPRMPPSPGFSAVVLLKGTPPPPPFLVPPIS KPPPGFSGLLPSPHP\PVSPAPPPPPPCWKRPRLLPAP/PGLPS PRELPGEEPSAHPVHQGLPAERRGPLQRVQEPLRGVQTGPDLRS PVLQELPGPAGGSFPEGL**AAGPAAH  5916 256 633 SPRWEIWGFWHRWESFSLEGEWPSRIPEPSPDSTKGTSGKGCR TVTGAVHRHLNHVAGIIPWVLHSQLKPTAATAQDQWTSQQYPDH PTRLILQ*NQATADKNN*TTALLOPHORL\VSPRMAFA	F014			AQATORSDPLMDTLSSMNRVQQVELIC/GIO*FED
ENGALSSVETYSPKTDSWSYVAGLPRFTYGHAGTIYKDFVYISG GHDYQIGPYRKNLCYDHRTDVWEERRPHMTARGWHSMCSLGDS IYSIGGSDDNIESMERFDVLGVEAYSPQCNQWTRVAPLLHANSE SGVAVWEGRIYILGGYSWENTAFSKTVQVYDREADKWSRGVDLP KAIAGGSACFIAP*SLGQRTRKRKAKARGTRTGASDPSCASWDH PHRHLPGLCRPAATS FPGRPTRPLKLGRRRKRARITQAPHCHSPRPRTCPPGALQAPEA PASRAEGPVAVVVNGHTEGPAPARSAPKEPPGLPRPLGSFPCTT PQEDFPALGGPCPPRMPSPGFSAVVLLKGTPPPPPFLVPPIS KPPPGFSGLLPSPHP\PVSPAPPFPPPQK/RPRLLPAP/PGLPS PRELPGEEPSAHPVHQGLPAERRGPLQRVQEPLRGVQTGPDLRS PVLQELPGPAGGEFPEGL**AAGPAAH  5916 256 633 SPRWEIWGPWHRWESFSLEGEWPSRTPEPSPDSTKGTSGKGCR TVTGAVHRHLNHVAGIIPWVLHSQLKPTAATAQDQWTSQQYPDH PTRLILQ*NQATADKNN*TTALLOPHORL\VSPRMAFA	2314	960	124	NLGGSELPPEEALFIQVASMNQRRVDFYLASIEDMI.VAT/GCDN
GHDYQIGPYRKNLLCYDHRTDVWEERRPMTTARGWHSMCSLGDS IYSIGSDDNIESMERFDVLGVEAYSPQCNQWTRVAPLLHANSE SGVAVWEGRIYILGGYSWENTAFSKTVQVYDREADKWSRGVDLP KAIAGGSACFIAP*SLGQRTRKRKAKARGTRTGASDPSCASWDH PHRHLPGLCRPAATS  5915  1604  703  FPGRPTRPLKLGRRRKRARITQAPHCHSPRPT:CPPGALQAPEA PASRAEGPVAVVVNGHTEGPAPARSAPKEPPGLPRPLGSFPCPT PQEDFPALGGPCPPRMPPSPGFSAVVLLKGTPPPPPPGLVPPIS KPPPGFSGLLPSPHP\PVSPAPPPPPPQK/RPRLLPAP/PGLPS PRELPGEEPSAHPVHQGLPAERRGPLQRVQEPLRGVQTGPDLRS PVLQELPGPAGGEPEGL**AAAGPAAH  5916  256  633  SPRMWEIWGPWHRWESFSLEGEWPSRIPEPSPDSTKGTSGKGCR TVTGAVHRHLNHVAGIIPWVLHSQLKPTAATAQDQWTSQQYPDH PTRLILQ*NQATADKNN*TTALLOPHORL\VSPRMAEA	- 1	•		ENGALSSVETYSPKTDSWSYVAGLPRFTYGHAGTIYKDFVYISG
1YSIGGSDDNIESMERFDVLGVEAYSPQCNQWTRVAPLLHANSE SGVAVWEGRIYILGGYSWENTAFSKTVQVYDREADKWSRGVDLP KAIAGGSACFIAP*SLGQRTRKRKAKARGTRTGASDPSCASWDH PHRHLPGLCRPAATS  1604 703 FPGRPTRPLKLGRRRKRARIIQAPHCHISPRPRTCPPGALQAPEA PASRAEGPVAVVVNGHTEGPAPARSAPKEPPGLPRPLGSFPCPT PQEDFPALGGPCPPRMPPSPGFSAVVLLKGTPPPPPPGLVPPIS KPPPGFSGLLPSPHP\PVSPAPPPPPPQK/RPRLLPAP/PGLPS PRELPGEEPSAHPVHQGLPAERRGPLQRVQEPLRGVQTGPDLRS PVLQELPGPAGGEFPEGL**AAGPAAH  5916 256 633 SPRMWEIWGPWHRWESFSLEGEWPSRIPEPSPDSTKGTSGKGCR TVTGAVHRHLNHVAGIIPWVLHSQLKPTAATAQDQWTSQQYPDH PTRLILQ*NQATADKNN*TTALLOPHORL\VSPRMAEA	[			GHDYQIGPYRKNLLCYDHRTDVWEERRPMTTARGWHSMCS; CDS
SGVAVWEGRIYILGGYSWENTAFSKTVQVYDREADKWSRGVDLP KAIAGGSACFIAP+SLGQRTRKRKAKARGTRTGASDPSCASWDH PHRHLPGLCRPAATS  FPGRPTRPLKLGRRRKRARITQAPHCHSPRPRTCPPGALQAPEA PASRAEGPVAVVVNGHTEGPAPARSAPKEPPGLPRPLGSFPCPT PQEDFPALGGPCPPRMPPSPGFSAVVLLKGTPPPPPPGLVPPIS KPPPGFSGLLPSPHP\PVSPAPPPPPPQK/RPRLLPAP/PGLPS PRELPGEEPSAHPVHQGLPAERRGPLQRVQEPLRGVQTGPDLRS PVLQELPGPAGGEFPEGL**AAGPAAH  5916 256 633 SPRMWEIWGPWHRWESFSLEGEWPSRIPEPSPDSTKGTSGKGCR TVTGAVHRHLNHVAGIIPWVLHSQLKPTAATAQDQWTSQQYPDH PTRLILQ*NQATADKNN*TTALLOPHORL\VSPRMAFA	-			IYSIGGSDDNIESMERFDVLGVEAYSPOCNOWTRVADILHANGE
KAIAGGSACFIAP*SLGQRTRKRKAKARGTRTGASDPSCASWDH PHRHLPGLCRPAATS FPGRPTRPLKLGRRRKRARITQAFHCHSPRPRTCPPGALQAPEA PASRAEGPVAVVVNGHTEGPAPARSAPKEPPGLPRPLGSFPCPT PQEDFPALGGPCPPRMPPSPGFSAVVLLKGTPPPPPPGLVPPIS KPPPGFSGLLPSPHP\PVSPAPPPPPPQK/RPRLLPAP/PGLPS PRELPGEEPSAHPVHQGLPAERRGPLQRVQEPLRGVQTGPDLRS PVLQELPGPAGGEFPEGL**AAGPAAH  5916 256 633 SPRMEIMGPWHRWESFSLEGEWPSRIPEPSPDSTKGTSGKGCR TVTGAVHRHLNHVAGIIPWVLHSQLKPTAATAQDQWTSQQYPDH PTRLILQ*NQATADKNN*TTALLOPHORL\VSPRMAFA		į		SGVAVWEGRIYILGGYSWENTAFSKTVOVYDREADKWSPGVDLD
FPGRPTRPLKLGRRRKRARI TQAPHCHISPRPRTCPPGALQAPEA PASRAEGPVAVVVNGHTEGPAPARSAPKEPPGLPRPLGSFPCPT PQEDFPALGGPCPPRMPPSPGFSAVVLLKGTPPPPPPGLVPPIS KPPPGFSGLLPSPHP\PVSPAPPPPPPQK/RPRLLPAP/PGLPS PRELPGEEPSAHPVHQGLPAERGPLQRVQEPLRGVQTGPDLRS PVLQELPGPAGGEFQL**+AAGPAAH  5916 256 633 SPRMWEIWGPWHRWESFSLEGEWPSRIPEPSPDSTKGTSGKGCR TVTGAVHRHLNHVAGIIPWVLHSQLKPTAATAQDQWTSQQYPDH PTRLILQ*NQATADKNN*TTALLOPHORL\VSPRMAEA	1	1	1	KAIAGGSACFIAP*SLGQRTRKRKAKARGTRTGASDPSCASWDH
FPGRPTRPLKLGRRRKRARI IQAPHCIISPRPRTCPPGALQAPEA PASRAEGPVAVVVNGHTEGPAPARSAPKEPPGLPRHLGSFPCPT PQEDFPALGGPCPPRMPPSPGFSAVVLLKGTPPPPPGLVPPIS KPPPGFSGLLPSPHP\PVSPAPPPPPPDQK/RPRLLPAP/PGLPS PRELPGEEPSAHPVHQGLPAERRGPLQRVQEPLRGVQTGPDLRS PVLQELPGPAGGEFPGL**AAGPAAH  5916 256 633 SPRMEIMGPWHRESFSLEGEWPSRIPEPSPDSTKGTSGKGCR TVTGAVHRHLNHVAGIIPWVLHSQLKPTAATAQDQWTSQQYPDH PTRLILQ*NQATADKNN*TTALLOPHORL\VSPRMAFA	5915	1604	705	PHRHLPGLCRPAATS
PASRAEGPVAVVVNGHTEGPAPARSAPKEPPGLPRPLGSFPCPT PQEDFPALGGPCPPRMPPSPGFSAVVLLKGTPPPPPPGLVPPIS KPPPGFSGLLPSPHP\PVSPAPPPPPPQK/RPRLLPAP/PGLPS PRELPGEEPSAHPVHQGLPAERGPLQRVQEPLRGVQTGPDLRS PVLQELPGPAGGEFPEGL**AAGPAAH  5916 256 633 SPRMWEIWGPWHRWESFSLEGEWPSRIPEPSPDSTKGTSGKGCR TVTGAVHRHLNHVAGIIPWVLHSQLKPTAATAQDQWTSQQYPDH PTRLILQ*NQATADKNN*TTALLOPHORL\VSPRMAEA		2003	/03	FPGRPTRPLKLGRRRKRARI IQAPHCHSPRPRTCPPGALQAPEA
KPPPGFSGLLPSPHP\PVSPAPPPPPPQK/RPRLLPAP/PGLPS PRELPGEEPSAHPVHQGLPAERGGPLQRVQEPLRGVQTGPDLRS PVLQELPGPAGGEPPEGL*+AAGPAAH  5916 256 633 SPRMWEIWGPWHRWESFSLEGEWPSRIPEPSPDSTKGTSGKGCR TVTGAVHRHLNHVAGIIPWVLHSQLKPTAATAQDQWTSQQYPDH PTRLILQ*NQATADKNN*TTALLOPHORL\VSPMAEA	1	1	j	PASRAEGPVAVVVNGHTEGPAPARSAPKEPPGLPRPLGSEPCPT
PRELPGEEPSAHPVHQGLPAERRGPLQRVQEPLRGVQTGPDLRS PVLQELPGPAGGEFPEGL**AAGPAAH  5916 256 633 SPRMWEIWGPWHRWESFSLEGEWPSRIPEPSPDSTKGTSGKGCR TVTGAVHRHLNHVAGIIPWVLHSQLKPTAATAQDQWTSQQYPDH PTRLILQ*NQATADKNN*TTALLOPHORL\VSPRMAEA	ł	[	J	PQEDFPALGGPCPPRMPPSPGFSAVVLLKGTPPPPPPBGLVPDTC
5916 256 633 SPRMEIMGEMENT FERSTREAM  TYTGAVHRILINDAGI I PWVLHSQLKPTAATAQDQWTSQQYPDH  PTRLILQ*NQATADKNN*TTALLOPHORL\VSPRMAFA			İ	REFERENCE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROP
SPRMWEIWGPWHRWESFSLEGEWPSRIPEPSPDSTKGTSGKGCR TVTGAVHRHLNHVAGIIPWVLHSQLKPTAATAQDQWTSQQYPDH PTRLILQ+NQATADKNN+TTALLOPHORL\VSPRMAEA		1		PVIORI DEPACE PROPERTY + A REPORT OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPE
TVTGAVHRHLHVAGIIPWVLHSQLKPTAATAQDQWTSQQYPDH PTRLILQ*NQATADKNN*TTALLOPHORL\VSPMAFA	5916	256	633	SPDMUTTWCDWUDWEGEST PORTURAL
PTRLILQ*NQATADKNN*TTALLOPHORL\VSPRMAEA		1		TVTGAVHRHINHVAGTIPHVILHGOT VERMA AND CONTROL
5917 1343 827 AHOILTYLED/TCLUDAURYLDURY TOUR TOUR				PTRLILO*NOATADKNN*TTALLOPHOPI \1200000
	5917	1343	827	AHQILTYLEP/ICLVVNYNKILTVFLTKSVLBI*KFIHTPQTYR

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ļ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
-	to first	amino acid	P-Proline, Q-Glutamine, R-Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	1	\=possible nucleotide insertion)
1	•		F*NDFFGIKEVYVSRRLRKTSF/RLAVTFLEQAVVSKECVPVDQ
1	ľ		FMEHLLPSLLSLASDPVPNVRVLLAKALRQMLLBKAYFRNAGNP
5918	<del> </del>		HLEVIBETILALQSDRDQDVSFFAALEPKRRNIIDTAVLEKQN
3918	13	1247	EGAQVARRRSRRQWRAGRCGRGGGRRAERTGGRGPPGRPRPLP
Į.			PGPARRGRRRMETPFYGDEALSGLGGGASGSGGTFASPGRLFPG
ŀ			APPTAAAGSMMKKDALTLSLSEQVAAALKPAPAPASYPPA\ADG
		i	APSAAPPDGLLASPDLGLLKLASPELERLIIQSNGLVTTTPTSS
1		ļ	QFLYPKVAASEEQEFAEGFVKALEDLHKONQLGAGRAAAAAAA AGGPSGTATGSAPPGELAPAAAAPEAPVYA\NLSSY\AGGCRGL
		· ·	RGGAAT\VAFAAEPVPFPPPPPPPGALGPRRP/RLALQGRRPQTV
			PDVP\SFGESP\PLSPIET\DTPRRI\KAKRKL\RNPQIRAPK
1	ļ	ì	PASRKLGAQSRALBRESEDPS*SPEHGSLASTASLLREQVAQLK
i		1	QKVLSHVNSGCQLLPQHQVPAY
5919	1	4254	TSVQGDSQGTPTSSQGSINMRHWISQAIHGSTTSTTSSSSTQSG
		ļ:	GSGAAHRLADVMAQTHIENHSAPPDVTTYTSEHSIQVERPQGST
			GSRTAPKYGNAELMETGDGVPVSSRVSAKIQQLVNTLKRPKRPP
		,	LREFFVDDFEELLEVQQPDPNQPKPEGAQMLAMRGEOLGVVTNW
			PPSLEAALQRWGTISPKAPCLTTMDTNGKPLYILTYGKLWTRSM
			KVAYSILHKLGTKQEPMVRPGDRVALVFPNNDPAAFMAAFYGCL
J.			LAEVVPVPIEVPLTRKDAGSQQIGFLLGSCGVTVALTSDACHKG
			LPXSPTGBIPQFKGWPKLLWFVTESKHLSKPPRDWF\PHIKDAN
	,		NDTAYIEYKTCK\DGSVLGVTVTRTALLTHCQALTQACGYTEAE TIVNVLDFKKDVGLWHGILTSVMNMHVISIPYSLMKVNPLSWI
			QKVCQYKAXVACVKSRDMHWALVAHRDQRDINLSSLRMLIVADG
		•	ANPWSISSCDAFLNVFQSKGLRQEVICPCASSPEALTVAIRRPT
			DDSNQPPGRGVLSMHGLTYGVIRVDSEEKLSVLTVQDVGLVMPG
		,	AIMCSVKPDGVPQLCRTDEIGELCVCAVATGTSYYGLSGMTKNT
			PEVFAMTSSGAPISEYPFIRTGLLGFVGPGGLVFVVGKMDGLMV
1 1			VSGRRHNADDIVATALAVEPMKFVYRGRIAVFSVTVLHDERIVI
			VAEQRPDSTEEDSFQWMSRVLQAIDSIHQVGVYCLALVPANTLP
			KTPLGGIHLSETKQLFLEGSLHPCNVLMCPHTCVTNLPKPRQKQ
			PEIGPASVMVGNLVSGKRIAQASGRDLGQIEDNDQARKFLFLSE
1			VLQWRAQTTPDHILYTLLNCRGAIANSLTCVQLHKRAEKIAVML
			MERGHLQDGDHVALVYPPGIDLIAAFYGCLYAGCVPITVRPPHP QNIATTLPTVKMIVEVSRSACLMTTQLICKLLRSREAAAAVDVR
		,	TWPLILDTDD*PKKRPAQICKPCNPDTLAYLDFSVSTTGMLAGV
			KMSHAATSAFCRSIKLQCELYPSREVAICLDPYCGLGFVLWCLC
		• •	SVYSGHQSILIPPSELETNPALWLLAVSQYKVRDTFCSYSVMEL
1	·	•	CTKGLGSQTESLKARGLDLSRVRTCVVVAEERPRIALTQSFSKL
1			FKDLGLHPRAVSTSFGCRVNLAICLQGTSGPDPTTVYVDMRALR
! <u>.</u> .			HDRVRLVERGSPHSLPLMESGKILPGVRIIIANPETKGPLGDSH
		•	LGEIWVHSAHNASGYFTIYGDESLQSDHFNSRLSFGDTQTIWAR
Í		*	TGYLGFLRRTELTDANGERHDALYVVGALDEAMELRGMRYHPID
1.	• 1		IETSVIRAHKSVTECAVFTWTNLLVVVVELDGSEQEALDLVPLV
	1		TNVVLEEHYLIVGVVVVVDIGVIPINSRGEKQRMHLRDGFLADQ
5920	1381	1499	LOPIYVAYNM
		21//	QLGAVAHAGVSRIPP+LFPPLHPTFLSLWCLHHKLP/HPPGASM VRPPVVPRRPPAHISSVRQASTQVPRTVPHTQRVANIGTQTTGP
	İ		SGVGCCTPGRPLLPCKCSSAAHSTYRVQBPAVHIPGQEPLTASM
,			LAAAPLHEQKQMIGERLYPLIHDVHTQLAGKITGMLLEIDNSEL
			LLMLESPESLHAKIDEAVAVLQAHQAMEQPKAYMH
5921	727	157	VCPGTGGE*GLWGQLGGLPKETPLKPMDAFTGSGLKRKPDDVDV
İ	ļ		GSSVSNSDDEISSSDSADSCDSLNPPTTASFTPTSILKROKOLR
i			RKNVRFDQVTVYYFARRQGFTSVPSQGGSSLGMAQRHNSVRSYT
	ļ	.	LCEFAQEQEVNHREILREHLKEEKLHAKKMKLTKNGTVESVEAD
1	. 1	ļ	GLTLDDVSDEDIDVENVEVDDYFFLQPLPTKRRRALLRASGVHR
ł		ļ	IDAEEKQELRAIRLSREECGCDCRLYCDPEACACSOAGIKCOVD
			RMSFPCGCSRDGCGNMAGRIEFNPIRVRTHYLHTIMKLELESKR
			Q\GAAQQPQ*GALPDCQLQPDRSTGL*DPSWIGSKGLSFTGKG AAATHLIILRVIENRGAEGKRK
5922	2475	495	SYSNWGLFPSVFIQVPRSRTGNLKPIFLFYSYYE\CMETLKG\T
			TOTAL TENE TOTAL TOTAL TOTAL TENE TENE TENE TENE TENE TENE TENE TEN

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
ł	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
- {	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
j	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /-possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			CLYNATOYKVCSPRNDRPDACYNPSEPAATTVFEIRTGLLIGDT
1			SKIITRTBEKEIPKQITLRFDACAAINSKKLEIGCGSLN*ERS*
ı			RVENKYVCHESGVCKNCAYWPCVI*AT*KKNKNDSVYLOKGEAN
ł	ł	1	PSCAAGHCNPLELIITNPLDPHWKKGERVTLGINRTGLKPOVVT
			LIKGEVHKCSPKPVFQTFYEELNLPAPELLKKTKNLFLOLAENV
1	}	l	IFLLNGTSCYVRGGTTIGDRWPWEA*ELVPTDPAPDIIPT*KAR
1		ĺ	ASNF+VLKTSIIRQYCIAREGKDFIIPVGKPNCIGOKLYNSTTK
			TIT**DLNHTEKNPFSKFSKLKTA*AHAESH*DWTVPSGLY*IC
1			RHRAYFRLPNKWADSCVIGTIKPSFFLLPIKMGELLGFSVYASR
1 .			EKKGIVIGNWKDNEWPRERIIQYYGPATWAQDGSWGYR/TP/VY
1			MLNWIIRLQAILEIISNETGRALTVLAWQETQMRNAIYQNRLAL
			DYLLVAEGGVCRKFNLTNCCLQINDQGQVVKNIVRDMTKLAHVP
Ì	1		IQVWHKFDPESLFGKWFPAIGGFKTLIVGVLLVIRTCLLLPCVL
ł			PLLFQMIKGIVATLVHQKTSAHVNYMNHYRSISQRDSKSEDESE
5923	137	638	NSH
	1	636	QLCGRRGQRFRTSIKRMHPI*RTCPNTNL/IILLSQENTQIRDL
1	1		QQENRELWISLEEHQDALELIMSKYRKQMLQLMVAKKAVDAEPV
	j		LKAHQSHSAEIESQIDRICEMGEVMRKAVQVDDDQFCKIQEKLA
5924	274	2146	QLELENKELRELLSISSESLQARKENSMDTASQAIK
		4210	EKGKVKDAGAEQWISLSLSCKGSWETQFSNHLNSLTPPTSVRRM
1			PLITTVTLLKMVARHHMKLLCSKAFSTQLQQKIFLHSQMGIHHQ SVCMKLKPNTSHIISILMGQPMALVQLETLAPLTIIIQKFQTQD
1 .			HMKFWKNLPLHSHHLTPSVPQTVIPKKTGSPEIKLKITKTIQNG
1			RELFESSLCGDLLNRVQASE\Q*NQSIESRKEKRKKSNKHDSSR
1 .			SEERKSHKIPKLEPEEQNRPNERVDTVSEKPREEPVLKEGSPSS
1	}		ANTIFCSNNGSVHW\FKFQVGDLVWSKVGTYPWWPCMVSSDPQL
	1		EVHTKINTRGAREYHVQFFSNQPERAWVHEKRVREYKGHKQYEE
			LLAEATKQASNHSEKQKIRKPRPQRERAQWDIGIAHAEKALKMT
1 1	!		REERIEQYTFIYIDKQPERALSQAKKSVASKTEVKKTRRPRSVL
1			NTQPEQTNAGEVASSLSSTEIRRHSQRRHTSAEEEEPPPVKIAW
1 1	,		KTAAARKSLPASITMHKGSLDLOKCNMSPVVKIEOVPALONATG
] !			DGKFIDQFVYSTKGIGNKTEISVRGODRLIISTPNORNEKPTOS
1 1			VSSPEATSGSTGSVEKKQQRRSIRTRSESEKSTEVVPKKKIKKE
5925			QVGFLHVES
3925	216	1911	MMTAESREATGLSPQAAQEKDGIVIVKVEEEDEEDHMWGQDSTL
1 1			QDTPPPDPEIFRQRFRRFCYQNTFGPREALSRLKELCHOWLRPE
í i			INTKEQILELLVLEQFLSILPKELOVWLOEYRPDSGEEAVTLLE
] [			DLELDLSGQQVPGQVHGPEMLARGMVPLDPVOESSSPDLHHEAT
i i			QSHFKHSSRKPRLLQSRALPAAHIPAPPHEGSPRDQAMASALFT
1 1			ADSQAMVKIEDMAVSLILEEWGCQNLARRNLSRDNRQENYGSAF
	ł		PQGGENRNENEESTSKAETSEDSASRGETTGRSQKEFGEKRDQE
1 1	i		GKTGERQQKNPEEKTRKEKRDSGPAIGKDKKTITGERGPREKGK
1			GLGRSFSLSSNFTTPEEVPTGTKSHRCDECGKCFTRSSSLIRHK
1 1	1		I IHTGEKPYECSECGKAF\SLNS\NLVLHQRI\HTGEKPHECNE
1			CGKAFSHSSNLILHQRIHSGEKPYECNECGKAFSQSSD\LTKHQ
1	i		RIHTGEKPYECSECGKAFNRNSYLILHRRVHTREKPYKCTKCGK \AFTRSSTLTLHHRIHARERASEYSPASLDAFGAFLKSCV
5926	2	233	DRCLMLKQGSQPGSPPAT/CEPPAPPVYQAPCQSCPEPPGAHEP
		,	SDSPHHTPVHPPPEHSAACPAPATCCPPPRSSMS
5927	4146	1248	KHFSKFGSQALYQLKRPASGQNSISVMPAQKITKPAAKYGIPLA
			YKKYGDKKLHEKKPLQKHKQAHQTPEKRVNTGEERRKISEEAAR
			KRRLEFIEKEKKQKDQIISLMKAEQMKRQEKERLERINRAREQG
		j	WRNVLSAGGSGEVKAPFLGSGGTIAPSSFSSRGQYEHYHAIFDQ
			MQQQRAEDNEAKWKREIYGRGLPERQKGQLAVERAKQVEEFLQR
1		:	KREAMQNKARAEGHMGILQNLAAMYGGRPSSSRGGKPRNKEEEV
!	l	}	YLARLRQIRLQNFNERQQIKAKLRGEKKEANHSEGQEGSEEADM
1		. [	RRKK\IESLKAHANARAAVLKEOLERKRKEAYEREKKVWEEHLV
ŀ	. 1	Į.	AKGVKSSDVSPPLGQHETGGSPSKQQMRSVISVTSALKEVGVDS
	ļ	1	SLIDTREISEEMOKINNAISSKREILRRLNENLKAGEDEKGKON
ľ		į	LSDTFEINVHEDAKEHEKEKSVSSDRKKWEAGGOLVIPLDELTI.
			DTSFSTTERHTVGEVIKLGPNGSPRRAWGKSPTDSVLKILGEAE

SEQ	Predicted	Predicted end	Daning poid
ID	beginning	nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, R=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
Ì	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
-	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
i	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid	1	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	sequence	Codon, /=possible nucleotide deletion
	sequence	<u> </u>	\=possible nucleotide insertion)
1	1	İ	LQLQTELLENTTIRSEISPEGEKYKPLITGEKKVQCISHEINPS
1	ĺ	1	AIVDSPVETKSPEFSEASPOMSLKLEGNLEEPDDLETETLORDS
1			GTNKDE\SLPCTITDVWISBEKETKETOSADRITIOENEVSEDG
ł	1		VSSTVDQLSDIHIEPGTNDSQHSKCDVDKSVOPEPFFHKVVHSE
ì		Į.	HLNLVPQVQSVQCSPEESFAFRSHSHLPPKNKNKNSLLIGLSTG
1	1		LFDANNPKMLRTCSLPDLSKLFRTLMDVPTVGDVRQDNLEIDEI
			EDENIKEGPSDSEDIVFEETDTDLQELQASMEQLLREQPGEEYS
}		İ	EEEESVLKNSDVEPTANGTDVADEDDNPSSESALNEEWHSDNSD
i	ļ		GEIASECECDSVFNHLEELRLHLEQEMGFEKFFEVYEKIKAIHE
L	1		DEDENIEICSKIVQNILGNEHQHLYAKILHLVMADGAYQEDNDE
5928	4146	1248	KHFSKFGSQALYQLKRPASGQNSISVMPAQKITKPAAKYGIPLA
1			YKKYGDKKLHEKKPLQKHKQAHQTPEKRVNTGEERRKISEEAAR
	<u> </u>		KRRLEFIEKEKKQKDQIISLMKAEQMKRQEKERLERINRAREQG
· I			WPMVLSAGGGGGUVA DET GGGGTTA DAGGEKERLEKINRAREQG
1	[		WRNVLSAGGSGEVKAPFLGSGGTIAPSSFSSRGQYEHYHAIFDQ
j	[		MOQQRAEDNEAKWKREIYGRGLPERQKGQLAVERAKQVEEFLQR
1			KREAMONKARAEGHMGILONLAAMYGGRPSSSRGGKPRNKEEEV
j	]		YLARLRQIRLQNFNERQQIKAKLRGEKKEANHSEGQEGSEEADM
i	}		RRKK\IESLKAHANARAAVLKEQLERKRKEAYEREKKVWEEHLV
1			AKGVKSSDVSPPLGQHETGGSPSKQQMRSVISVTSALKEVGVDS
	,		SLTDTRETSEEMQKTNNAISSKREILRRLNENLKAQEDEKGKQN
			LSDTFEINVHEDAKEHEKEKSVSSDRKKWEAGGQLVIPLDELTL
			DTSFSTTERHTVGEVIKLGPNGSPRRAWGKSPTDSVLKILGEAE
			LQLQTELLENTTIRSEISPEGEKYKPLITGEKKVQCISHEINPS
1	i		AIVDSPVETKSPEFSEASPQMSLKLEGNLEEPDDLETEILQEPS
1 1	,		GTNKDE\SLPCTITDVWISEEKETKETQSADRITIQENEVSEDG
			VSSTVDQLSDIHIEPGTNDSQHSKCDVDKSVQPEPFFHKVVHSE
1 1			HLNLVPQVQSVQCSPEESFAFRSHSHLPPKNKNKNSLLIGLSTG
1 1	• .		LFDANNPKMLRTCSLPDLSKLFRTLMDVPTVGDVRQDNLEIDEI
1 1			EDENIKEGPSDSEDIVFEETDTDLQELQASMEQLLREQPGEEYS
1 1	. [		EEEESVLKNSDVEPTANGTDVADEDDNPSSESALNEEWHSDNSD
	·		GELASECECDSVFNHLEELRLHLEQEMGFEKFFEVYEKIKAIHE
5929	3	1550	DEDENIEICSKIVQNILGNEHQHLYAKILHLVMADGAYQEDNDE
	J 1	1558	LDFSMTTQLPAYVAILLFYVSRASCQDTFTAAVYEHAAILPNAT
1 1	ľ		LTPVSREEALALMNRNLDILEGAITSAADQGAHIIVTPEDAIYG
] }			WNFNRDSLYPYLEDIPDPEVNWIPCNNRNRFGQTPVQERLSCL\
1 1			AKNNSIYVVANIGDKKPCDTSDPQCPPDGRYQYNTDVVF\DSQG
1	1		KLVARYHKQNLFMGENQFNVPKEPEIVTFNTTFGSFGIFTCFDI
Į /			LFHDPAVTLVKDFHVDTIVFPTAWMNVLPHLSAVEFHSAWAMGM
	1		RVNFLASNIHYPSKKMTGSGIYAPNSSRAFHYDMKTEEGKLLLS
j Í	İ		QLDSHPSHSAVVNWTSYASSIEALSSGNKEFKGTVFFDEFTFUK
1 1	1.		LTGVAGNYTVCQKDLCCHLSYKMSENIPNEVYALGAFDGLUTTE
1 1	1		GRYYLQICTLLKCKTTNLNTCGDSAETASTRFEMFSI.SGTPGTO
	[		YVFPEVLLSENQLAPGEFQVSTDGRLFSLKPTSGPVLTVTLFGP
5930	112		LYEKDWASNASSGLTAQARIIMLIVIAPIVCSI.SW
2230	113	6082	RGNCFWIVPFTMAQRTGLEDPERYLFVDRAVIVNPATOADWTAK
1 1	-		KLVWIPSERHGFEAASIKEERGDEVMVRIAENGKKAMVNKDDIO
j i			KMNPPKFSKVEDMAELTCLNEASVLHNLKDRYYSGI.TYTYSGI.F
			CVVINPYKNLPIYSENIIEMYRGKKRHEMPPHTYAISESAVDCM
			LQDREDQSILCTGESGAGKTENTKKVIOYLAHVASSHKGRKDHN
1			IPGE\LERQLLQANPILESFGNARTVONDNSSRFGKFTPTNEDV
		•	TGYIVGANIETYLLEKSRAVROAKDERTFHIFYOLLSG\AGEHI.
1	}	İ	KSDLLLEGFNNYRFLSNGYIPIPGO\ODKGNFRGDPGEAMHTMG
1	1	l	FSHEEILSMLKVVSSVLQFGNISFKKERNTDOASMPRNTVAOKT.
- 1	ļ	i	CHLLGMNVMEFTRAILTPRIKVGRDYVCKAOTKEOADFAVEALA
1	ļ	l	KATYERLFRWLVHRINKALDRTKROGASFIGILDIAGFEIERLN
J	1		SFEQLCINYTNEKLQOLFNHTMFILEOEEYOREGIEWNFIDEGI.
		ļ	DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ
1		ļ	GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND
ļ	ĺ	ļ	NVATLLHQSSDRFVAELWKDVDRIVGLDQVTGMTETAFGSAYKT
j			KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK
			LDPHLVLDQLRCNGVLEGIRICRQGFPNRIVFQEPRQRYEILTP
			- TOTAL DOLLAR TANGET MAN TANGET TOTAL

	SEQ	Predicted	Predicted end	I have a self-se
	ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	ĺ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
		corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
		to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
		amino acid	residue of	S=Serine, T=Threonine, V=Valine,
		residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown t=Ston
		amino acid	sequence	Codon, /=possible nucleotide deletion,
		eednesce	<u>L</u>	\=possible nucleotide insertion)
		,		NAIPKGFMDGKQACERMIRALELDPNLYRIGOSKIPEPAGYLAU
i	ı	1	ļ	LEEERDLKITDIIIFFQAVCRGYLARKAFAKKOOOLSALKULOB
				NCAAYLKLRHWQWWRVFTKVKPLLOVTROEELOAKDEELLKUV
٠ ا				BROTKVEGELEEMERKHOOLLEEKNILAEOLOAFTRI.FAFAFFM
ı				RARLAAKKQELEEILHDLESRVEEEEERNOILONEKKKMOAHTO
- 1			1	DLEEQLDEBEGARQKLQLEKVTAEAKIKKMEEETLLLEDONGKE
- [			j	IKEKKLMEDRIAECSSQLAEEBEKAKNLAKIRNKORVMISDLEE
-		!	1	RLKKEEKTRQELEKAKRKLDGETTDLODOIARLOAOTDELVIOL
- 1		ł	İ	AKKEEELQGALARGDDETLHKNNALKVVRELOAGTAELGEDERG
- [		ļ	ļ.	EKASRNKAEKQKRDLSEELEALKTELEDTLDTTAACOELPTKRE
1				USVAELKKALEEETKNHEAQIODMRORHATALEELSEOLEOAKD
				FKANLEKNKQGLETDNKELACEVKVLOOVKAESEHKRKKLDAOV
-				QELHAKVSEGDRLRVELAEKASKLONELDNYSTIJERAEKKGIK
-		İ.		FAKDAASLESQLQDTQELLQEETRQKLNLSSRIRQLEEEKNSLQ
-		ļ		EQQEEEEEARKNLEKQVLALQSQLADTKKKVDDDLGTIESLEEA
-				KKKLLKDAEALSQRLEBKALAYDKLEKTKNRLQQELDDLTVDLD
٠ ا				HOROVASNLEKKO\KKFDQLLAEEKSISARYAEERDRAEAEARE
ļ	1			KETKALSLARALEEALEAKEEFERQNKQLRADMEDLMSSKDDVG
				KNVHELEKSKRALEQQV\EEMRTQLEELEDELQATEDAKLRLEV
ı		į.		MMQAMKAQFERDLQTRDEQNEEKKRLLIKQVRELEAELEDERKQ RALAVASKKKMEIDLKDLEAQIEAANKARDEVIKQLRKLQAQMK
1				DYQRELEEARASRDEIFAQSKESEKKLKSLEAEILQLQEELASS
ı				ERARRHAEQERDELADEITNSASGKSALLDEKRRLEARIAQLEE
				ELEEEQSNMELLNDRFRKTTLQVDTLNAELAAERSAAQKSDNAR
				QQLERQNKELKAKLQELEGAVKSKFKATISALEAKIGQLEEQLE
1				QEAKERAAANKLVRRTEKKLKEIFMQVEDERRHADQYKEQMEKA
		İ		NARMKQLKRQLEEAEEEATRANASRRKLQRELDDATEANEGLSR
1				EVSTLKNRLRRGGPISFSSSRSGRRQLHLEGASLELSDDDTESK
$\perp$	5931			LISDANRIĞEPÇSE
I	2931	113	6082	RGNCFWIVPFTMAQRTGLEDPERYLFVDRAVIYNPATQADWTAK
1				KLVWIPSERHGFEAASIKEERGDEVMVELAENGKKAMUNKDDIO
		1		KMNPPKPSKVEDMAELTCLNEASVLENLKDRYYSGI.TVTVSGI.F
1	1			CVVINPYKNLPIYSENIIEMYRGKKRHEMPPHIYAIGEGAVRCM
1				LQDREDQSILCTGESGAGKTENTKKVIOYLAHVASSHKGPKDUN
	i			IPGE LERQLLQANPILESFGNARTVONDNSSREGKETPINEDU
				TGYIVGANIETYLLEKSRAVROAKDERTFHIFYOLLSG\AGEHL
	1			KSDLLLEGFNNYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG
Ĺ	1	}		FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL
ı		1		CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFBLN
ı	j			SFEQLCINYTNEKLQQLFNHTMFILEQBEYQREGIEWNFIDFGL
1	1			DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ
1		ŀ		GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND
1	1			NVATLLHQSSDRFVAELWKDVDRIVGLDQVTGMTETAFGSAYKT
ĺ	ľ	ļ		KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHFKPACK
	- 1			LDPHLVLDQLRCNGVLEGIRICROGFPNRIVFOEFRORVEILTD
ì	-		İ	NAIPKGFMDGKQACERMIRALELDPNLYRIGOSKIEFPACU AU
				LEEERDLKITDIIIFFQAVCRGYLARKAFAKKOOOLSALKULOR
			1	NCAAYLKLRHWQWWRVFTKVKPLLOVTROEEELOAKDERLLVIV
	- 1	}		EKQTKVEGELEEMERKHOOLLEEKNILAEOLOAFTEL PAPARE
			ļ	RARLAAKKQELEEILHDLESRVBEEEERNOILONEKKKMOAHTO
	1	}	J	DEEEQLDEEEGAROKLOLEKVTAEAKIKKMEEETIJI.EDOMCVP
	1			IKEKKLMEDRIAECSSQLAEEEEKAKNLAKIRNKQEVMISDLEE
	- 1	1	. 1	RLKKEEKTRQELEKAKRKLDGETTDLQDQIAELQAQIDELKLQL
	1			AKKEEELQGALARGDDETLHKNNALKVVRELQAQIAELQEDFES
			1	EKASRNKAEKQKRDLSEELEALKTELEDTIDTTAAQQELRTKRE QEVAELKKALEEETKNHEAQIQDMRQRHATALEELSEQLEQAKR
	1		]	FKANLEKNKQGLETDNKELACEVKVLQQVKAESEHKRKKLDAQV
			1	QELHAKVSEGDRLRVELAEKASKLQNELDNVSTLLEEABKKGIK
	- 1			FAKDAASLESQLQDTQELLQEETRQKLNLSSRIRQLEEEKNSLQ
				EQQBEEEEARKNLEKQVLALQSQLADTXKKVDDDLGTIESLEEA

mo: mo: mo: mo: mo: mo: mo: coation corresponding to first damino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Octation   Corresponding to first amino acid sented acid   February   Corresponding to first amino acid sented acid   Section   Corresponding to first amino acid sented acid   Sequence   Corresponding to first amino acid sequence   Coden,   February   Coden,   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   February   F	ID	beginning		(A=Alanine C=Cvsteine D=Aspartic Acid P-
Cortesponding   to first   amino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   ma	NO:	nucleotide		Glutamic Acid. F=Phenylalanine G-Glycine
LeLeucipe, M-Mothdonine, N-Asparagine, for first amino acid amino acid residue of amino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence		location	I .	H=Histidine TaTsoleucine K-Lygine
Do first   residue of amino acid residue of amino acid mino acid mino acid mino acid amino acid amino acid amino acid sequence   S-Se-Fire, T-Threenine, V-valline, S-Se-Fire, T-Threenine, V-valline, S-Se-Fire, T-Threenine, V-valline, M-Tryptophan, Y-Tyrosine, X-Unknown, *-Stop Codon, /-possible mucleotide insertion)   No.	1	corresponding		LeLeucine MeMothionine NeAspassing
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residue of amino acid sequence    Martyptophan, Y-Tyvosine, X-Eukhonn, *-Stop Codon, /-possible nucleotide daletion, /-		amino acid		SeSerine T-Threenine V-Valine,
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ERARRIAGORIDELADETINSAGKISALLDEKRELEARIAQLER ELEEGGNINELLNORFRITTUQUTLINELASAGKISANA QUERGNIKELKAKLIQELEGAVESKYRATISALERAKIQCEEGLE QEARGRAANKLIVARTEKLEKLEFTIMVEDERRAGVESMERA NARKIQLKROLEGAEEATRANASRIKLQEELDDATEANGGISR EVSTLINBLIRKGOFISFSSRSGRQCHLEGASLELSDDDTESK TDUNETOPPOSE  133 572 PELEETCEFLYGKORILLISGEPREESGUPRETGGLHVKAEANMO FOATLANGLITIVLSVYTIIICFTCSCCCLYKTCGRRPV\APP PHPP/PVHAPYPGPFJPSVPSYPGBSYGGYTHMPPGPGWAAPY PMQYPPPRAQPWSPPAYHELAGGAAPYPASGPYNFAYMDA PRAAL  5933 1 3190 GTRELECHAVESGSKASKTRSSDVHSSGSSDAMDASGPSD SOMPSHTRKSPRKINYNNESARESLCDSPHONISRPLLEINLIK APSIGMSTARATISKREGELEKKEDEKARILEKELELKALE SOMSKVTFVAGGVUNAAKEEHSTDEKRGKIYKPSSEPADOKNP PNQSSERPPSLLVIETKKEPLKKEDEKARILEKELELKALE GERDERHITTUGGAPAPYPSLAFTHENINGEM MERPINLIGGGAAPYPSHAPTHENINGERSELKKEDEKARILEKELELKOL DDYAPGSHUVODSPST\NFTLININGMAMAKEELEKELEKUT DDYAPGSHUVODSPST\NFTLININGMAMAKEELEKELEKUT DDYAPGSHUVODSPST\NFTLININGMAMAKEELEKELEKELE LASVKIMMPRTDEERARERNCGFVAFMRRDABRALKININGMI MEFPINLIGGGAAPYPEPPTITIPPSMMETLOFFALLYVER LASVKIMMPRTDEERARERNCGFVAFMRRDABRALKININGMI MERPINLIGGGAAPYPEPTITIPPSMMETLOFFALLYVER LASVKIMMPRTDEERARERNCGFVAFMRRDABRALKININGMI MERPINLIGGGAAPYPEPTITIPPSMENDERTINAPHTYPHANASEE LASVKIMMPRTDEERARERNCGFVAFMRRDABRALKININGMI MERPINLIGGGAPPFEAMINGFUNGERINGFAHVYNINGBEQ ETERAFVEPSEKKALKEERORIKARIELINGHANGTAALVYNINGBEQ TERAFVEPSEKKALKEERORIKHEILINGHTPAHVYNEN KLYSILOGOSPTINHTEDFRINGFRENDENINGHANGKOW TOFRAABELVUCITESISILKFPIP,KKIARIYILVSDVLINISSA KVANASYTREFFTIKLOJI SEAGATYTSKELEF QHEESEERORIKARESISSISSISSISSISSISSISSISSISSISSISSISSIS	İ			RALAVASKKKMEIDLKDLEAQIBAANKARDEVIKQLRKLQAQMK
ELEEEGNMELLHORFRETTICQUTITUSLALABERSAQKSDNAR QULERGNMELKAKIQELEGAUKSPKAPIATISLAEKSAQKSDNAR QULERGNMELKAKIQELEGAUKSPKAPIATISLEKHRIGOEGAL CARKERAANKLURRTCKLKEIFMUSDERRHADGUTEME RAMMOLKROLEABEREATRANSSRKIRGELDATERHSGUSS EVSTLINBILREGGISFSSSRSGRRQLHLEGASLELSDDDTESK TSDUMETOPGOS  FILLEEICFLFLQKGRKLKLSGPRWEEGKPRGTGGLWVKAEANMG FOATLAVGLTIFULSVUTIIIGFTGSCCCLYNTGRRPRV/APP PHPP/PVURLPYPOPPSVPPSGPSQGYMPOGMPAAPY PMQYPPPYPAQPSVPPSGPSQGYMPOGMPAAPY PMQYPPPYPAQPAPPPATHETLAGGAAPYPASQPPYNPAYMDA FRAAL  5933  1 3190  GTRKLIKGADKTFGGSQKASSKTRSSDVHSSGSSDAHMDASGFSD SOMPSKTRPKSPRKHYNNESARESLCDSPHONJSRPLLENCLK AFSIGKNSTAKRTLSKRQEELKKKEDEKAAAFYVEFTAAPEG SOGKWKTFVARGOVARAKEHETDERKGFLYPSSFADGKNP PMGSSBRSPBLLVIETKKPPLKKGEKKKKSNLELFKELKOI QEREDRHKTKRGLSFRPPPOEDSDOQRESHDRSPRNSSSOVL DDYAPGSHDVODPSTT/NFYLGNINPOPMLKKCCCQEFGRFGP LASVKLMMPRTDEERARERNGEVAPMNRRDABEALKONINGEMI MSFEMKLGRGKAVPIPPHFIYIPPSMHEHTLDSATKVYYRM KLYSILGGSBTKWRTENDFRRFKLAGAIVKWYIPTERHILALI HEMIETVVREGHPFEAMIMNREINNPWRFLERMOTTAMVYYRM KLYSILGGSBTKWRTENDFRRFKLAGAIVKWYIPTERHILALI HEMIETVVREGHPFEAMIMNREINNPWRFLERMOTTAMVYYRM KLYSILGGSBTKWRTENDFRRFKLAGAIVKWIPTERHYLLAGU GAPIEBELGAPHETSKKAALKEGALBLELKVNKTODELSGKRRKKELP CAPTEREBERDRAFKLORGESBESDELDVOIT BLOTATTTICGHLQSENFKORW ORDESSEERBONGEBESBEERDTOSSKSEERHLYSHDIEDBAM TCFRAMEDHAITYPSFFILKQUTHTSTBOTTSTBOTTSKRELPD QHEESSEERBONGEBESBEERDTOSSKSEERHLYSHDIEBRIKELP QHEESSEERBONGEBESBEERDTOSSKSEERHLYSHDIEBRIKEL SKFSKYSEMSEERRAKLREIELKVAKTODELSGKRRKKELP SKFSKYSEMSEERRAKLREIELKVAKTODELSGKRRKKELP SKRSKSRSSKSSKSPHRSHKSSKNTNTGKRPSSKSDAMBASGRFSD COCQURHYDRULGPREKELEERBERDKOKERSSRSDAMDASGRFSD SDMPSRTPPSRFRIKHTURKDESELERBERDKOKERSSRSCH DECTPTREKRKRHSTSSFSPSRSSGRRVKSPSPKSRSKELF SKRSKSRSSRSSHKOSPRDVSKARAFSSSGRRWKSPSPKSRKELF SKRSKSRSSRSSHKOSPRDVSKARAFSSSGRRWKSPSPKSRKELF SKRSKSRSSRSSHKOSPRDVSKARAFSSSGRRWKSPSPKSGVL APSIGMSTARKTLSKKEDEELERBERDROKOCHESSKODKKE DECTPTREKRKRHSTSSFSPSRSSGRRWKSPSRSSGNI OERDBERHKTKGRLSRFEPPOSDSLOGRRSMADSRRWRSGGVI DDYAPGSBUDDBOTTNYPLUNGSSSFDAMDASRRWSGGVI DDYAPGSBUDDBOTTNYPLUNGSSFBRDPPTLINGNSEG DERDBERHKTKGRLSRFEPPOSDSLOGRRSMADSRRWSSG	ļ	l .		DYQRELEBARASRDEIFAQSKESEKKLKSLEAEILQLQEELASS
QQLERQNKELKAKLQELEGAVESKPKATISALEAKIQGLEGQLE QEARERAANKLVRETEKLEET IMVØDERAEDOVTEKDMEKS RARKKQLKRQLEGAEEATRANASRRKLQELDDATEANSGLSR EVSTLINBLIRKGG ISFSSRSGRQLHLEGASLELSDDDTESK TSDVAETQPQSB RHLEETCFLFLQKGRKLKLSGPRWEEGKPRGTGGLWVKAEANMG ROATLAVGLTIFVLSVTI IIGTGSCCCLYKTGRRPV\APP PHPP / EVVILAPYPQPBSVPSSYSGSYGGYHTMPPQGPWAAPY PROMYPPPYRAPPMSPPSYPSSYGGSYGGHTMPPQGPWAAPY PROMYPPPYRAPPMSPPSYPSSYGGSYGGHTMPPQGPWAAPY PROMYPPPYRAPPMSPPSYPSSYGGSKGSSDAMMDASGPSD SMPSRTPRKSPRKHNYNNSSAESLCDSPHONLSPLLENKLK APSIGMSTRPKSPRKHNYNNSSAESLCDSPHONLSPLLENKLK APSIGMSTRPKSPRKHNYNNSSAESLCDSPHONLSPLLENKLK APSIGMSTRPKSPRKHNYNNSSAESLCDSPHONLSPLLENKLK APSIGMSTRPKSPRKHNYNNSSAESLCDSPHONLSPLLENKLK APSIGMSTRPKSPRKHNYNNSSAESLCDSPHONLSPLLENKLK APSIGMSTRPKSPRKHNYNNSSAESLCDSPHONLSPLLENKLK APSIGMSTRPKSPRKHNYNNSSAESLCDSPHONLSPLLENKLK APSIGMSTRPKSPRKHNYNNSSAESLCDSPHONLSPLLENKLK APSIGMSTRPKSPRKHNYNNSSAESLCDSPHONLSPLLENKLK APSIGMSTRPKSPRKHNYNNSSAESLCDSPHONLSPLLENKLK APSIGMSTRPKSPRKHNYNNSSAESLCDSPHONLSPLLENKLK APSIGMSTRPKSPRKHNYNNSSAESLENKONLSPLKELKOOL DDYAPOSHUVOGDSTT'AFFLON'L YNCHAMA MSFEMLGKGKAPFIPPLYTIPSSMEHTLDPPPSGLPFNAQP REELKAPANANDHPPHNXLSPERTLSQATVTSKMLSCCOEPERGRP LASYKLMMPRTDEERARERKORGVAFNRKONSPRPPITTERMILLAIL HEMIEFUVEGOPHFEAMIMNEINNPHRRELPENGTPAHVYTRW KLYSILGGGSPTKHRTEDPFRKPKONSPRPPITTERMILLAIL HEMIEFUVEGOPHFEAMIMNEINNPHRRELPENGTPAHVYTRW KLYSILGGGSPTKHRTEDPFRKPKONSPRPPITTERMILLAIL HEMIEFUVEGOPHFEAMIMNEINNPHROLSERICHTORY CORPAREDALTYPEPTLIKUPITTERMILAIL HEMIEFUVRGOPHFEAMIMNEINNPHROLSERICHTORY CORPARIBANCH FERTALTYPEPTLIKUPITTERMILLAIL GAPIEEELDGAPLEUVDGIPIDATFIDLICHYTIKSDDDLDGAWPC LINNABAELIUCHTEKSELLEKTENKONCHESSESSER SKRKSSMSSERSKRKSSGNSSERSKRSSGNKKSPSKSSRSSERSER SKRKSSMSSERSKRSSGNKKSPSSGSSGAAMMADSGRFSD OGENDERHKTKGRLSPRFSGSSGSGRAWASSFRSSERSER SKRKSSRSSGRSPHRSHKKSKKSTTTGRKPFKKARSRSGSGV DECTPTREKRANDKTPGGSGXASSKTRSSGVHSGSGSDAHMDASGPFD SOMNSKTRPSGLVLTEKKELLEKKRENKLEFFRENKONKERS SCHNKKKRFSGSGRSPHRSHKKSKSKTTTGRKPFKKARSRSGSGV DDAYAGSBUDGDBSTTVNFTLORMSTELLTSHLANGLINGKJENGE PROSSNERPPSILVETKKELPTLEKKARLYTEPHALKALUTVIRMS LASVLLGGDSFTKWRTDERRHENGERPEPDJOBL	1	1		ERARRHAEQERDELADEITNSASGKSALLDEKRRLEARIAQLEE
QEARERAAMKLURRIPKKLEITMUYBDERRHADOYKEOMBEN NARMKLUKRULEBABERATHANSRIKLUGELTRANGTRUNGEL 1932  5932  33  572  RILBETCFLFLOKGREKLKLSGPRHEEGKPERTGELMVKAEANMG FOATLANGLITTULSVYTIIICFTCSCCCLYKTCREREV\APP PHPP/PVHAPYPCPPSVPSYNGESKQSHTMPPGMPAAPY PHPP/PVHAPYPCPPSVPSYNGESKQSHTMPPGMPAAPY PHPP/PVHAPYPCPPSVPSYNGESKQSHTMPANGEPSUMPKAEANMG FOATLANGLITTULSVYTIIICFTCSCCCLYKTCREREV\APP PHPP/PVHAPYPCPPSVPSYNGESKQSHTMPANGEPSUMPANGEPSD PHPP/PVHAPYPCPPSVPSYNGESKQSHTMPANGEPSUMPANGEPSD PHPP/PVHAPYPCPPSVPSYNGESKQSHTMPANGEPSUMPANGEPSD PHPP/PVHAPYPCPPSVPSYNGESKQSHTMPANGEPSUMPANGEPSD PHPP/PVHAPYPCPPSVPSYNGESKQSHTMPANGEPSUMPANGEPSD PHPP/PVHAPYPCSSHTMPANGESKGSTENDHONGSRPLLENNIK APSIGKMSTARRILSKRQEELKKKEOBKAARETVEFFLAPEG SLGKKVTTAVRGUMPAKEKETDERKGETVSSPPADOKNP PNOSSBERPBSLLVIETKKPPLKKGEKKKKSNLELFKELKOI QEERBERHKTKRISLSFPPDGSDORGRESHALNINGKMI MSFEMLGKGKAVFIPPLYIPPSOSDORGRESHALNINGKMI MSFEMLGKGKAVFIPPLPYIPPYIPPSOSDORGRESHALNINGKMI MSFEMLGKGKAVFIPPLPYIPPSOSDORGRESHALNINGKMI MSFEMLGKGKAVFIPPLPYIPPSOSDORGRESHALNINGKMI MSFEMLGKGKAVFIPPLPYIPPTYIPPSOLDFRONDTOMPSOC RERLKMPNAPHLPPPNKEDFBHFINGDFAVYYINGSA KVANASYTKRFFFTLKCQISTOLANTYTTICGHLQSENFKORVM KLISILQCISFTKWRTEDFBHFINGDFANTYTKSLDDLDLGY LINNEAABEIVOCITESISILKTPLPKKIARITVINSDIVINSSA KVANASYTKRFFFTLKCQISTOLANTYTTICGHLQSENFKORVM TCFRAMEDMAITPSFFTLKQUIPTTFRODITGDAMVFFC UPARTBELKGAPAPTTSKARLFFTLKCQISTOLANTYTTICGHLGSENFKORVM TCFRAMEDMAITPSFFTLKQUIPTTFRODITGDAMVFFC SKFSKYSEMSEEKRAKLREIELKVOKKODELESGKRFKROGSF OEOVBHYRDKLOREKEKELEERBERKOKKESFSBDENFKORVM TCFRAMEDMAITPSFFTLKQUIPTTFRODITGDAMVFFC SKFSKYSEMSEEKRAKLREIELKVOKKODELESGKRFKROGSF OEOVBHYRDKLOREKEKELEERBERKOKKESFSKDKKELF SKFSKYSEMSEEKRAKLDFRONGSKSERSPRKNESFSER SKRKKSSKSSSSRSPHRSHKKSKBKTMTGKRFPFKANTYKKCDLE SKFSKYSEMSEEKRAKLDFRONGSKSERSPRKNESFSER SKRKKSSKSSSSRSPHRSHKKSKBKTMTGKRFPFKANTYKKCDLE PROSSINERPPSILVITKKRPTLKKAREGERSFIXKKE APSICKMTAARTILSKKEDEELERBERKOKKTUKSSSFTLARGKRSSVI LCPERSVE SCHALWARADHTPGGSQKASSKTRSSDVHSSGSSDAHMAASGRFDD SOMPKRTPGGVVNAAKEEHTDERKKTUKYNSESFRONGSVI OERBERHKTKKRLSFFSPPOSDSLOGRRSMAASRRNESSGVI DDAYAGSHDUPDDOTTNINTERLEKTERLEKTARLKUN		1		ELEEEQSNMELLNDRFRKTTLQVDTLNAELAAERSAAQKSDNAR
NARWIQLKQLEGAEEEATRANASRRILQELDDATEANGLISE  FUSTLINKRIRGGI ISSSSSSGRQLHLEGAELELSDDTESK  TSDVNETOPPOSE  RHEETCFLFLQKGRKIKLISGFRWEEKKPGTGGLWVKAEANMG FGATLAVGLTIFVLSVYTI IICPTCSCCCLYKTCRRPRPV\APP PHPP/PVHAPPYPOPBVPPSVPPSYPOFYGGYHTMPPGGRPAPAY PMOYPPPYPARAPPYPOPBVPPSYPOFYGGYHTMPPGGRPAPAY PMOYPPPYPARAPPYPOPBVPPSVPPSYPOFYGGYHTMPPGGRPAPAY PMOYPPPYPARAPPYPOPBVPSVPSYPOFYGGYHTMPPGGRPAPAY PMOYPPPYPARAPPYPOPBVPSVPSYPOFYGGYHTMPPGGRPAPAY PMOYPPPYPARAPPYPOPBVPSVPSYPOFYGGYHTMPPGGRPAPAY PMOYPPPYPARAPPYPENKSSKITESDVHSSGSSDAHMDASGFSD SDMSSTRPKSPRKHYRMESARSSLCDSPHONLSSPLLENKLK APSIGMSTARKTLSKKEGELKKKEGEEKKYKYSSSSPALMDASGFSD SDMSKTYPKGSVNAAKEEHETDEKRGKYYKSSSPALMDASGFSD SGMKKTYPKGGVVNAAKEEHETDEKRGKYYKSSSPALMDASGFSD SGMKKTYPKGGVVNAAKEEHETDEKRGKYYKSSSPALMDASGFSD SGMKKTYPKGGVVNAAKEEHETDEKRGKYYKSSSPALMDASGFSD SGMKKTPVRGGVVNAAKEEHETDEKRGKYYKSSSPALMSRNSSGVL DDYAPGSHOVGOSTYNTYSCHPYLKMGSKANLELFKEELKOI QERDBERHATKGRLSFFEPPOSDSGQRRSMDASRRNSSGVL LASVKIMMPRTDEERARERNCGFVAPHNRDABRALKNINKGKMI MSFBMKLGMGRAVPIPPHEIVIPSMMEHTLDPPDSGLPFNAVYYKW KLYSILQGDSFTKMRTEDFRFKNGGFFPDHYPVHIMMSEEQ ETRAPVEBSKKGALKBEGRRKLEELLKOHTPKNOIDGAMYFC LNNAEAAEIVOCTTESLS LKYTLPKKTKAILYVSDVLYNSSA KVANASYYRKFFETKLCQIFSDLANTYRIQGHLGSENFKGRWM TCFRAMEDBALYPPFLIKLONIPLGLAWIF GAPIEBELGAPLEDVOG IP IDAPY LODLDGVP IKSLDDDLDGV PLDATTDSKKMPIPFKKLQIFFDAMYTRIQGHLGSENFKGRWM TCFRAMEDBALYPPFLIKLONIPLGLAWKFQDELEGGKRYKDOGSF QECVBHYRKDKLAPKEKELERREREDKDKKKLISSRSKDKKK DECTPTRKERRRHSTSSSPSPSSSGRRVKSSPSPKSRSKKK SKKSKSSGSSPHRSKKKSKKTNTGRRPFKKAVTYWKCDLP CYCRASUM APSIGKMSTAKRTLSKKGQELKKKBEKKKSNLELFEELKQI DECERSIV PNOSSNERPSLVITETKKYPLKKEKKKKKSNLELFFEELKQI DECERSIV PNOSSNERPPSLVITETKKKTCLGATVKGVIPPENLILALI HRMIETVVREGMYNAAKEEHETDEKGKYYPPENADPRAPAY MSSEKLLGMGAVDTPOHTYLOHINGKAMAABITEELLAAPEG SCINKVKTYVRGGVVNAAKEEHETDEKGKYYPPENADPRAPAYDY MSSEKLLGMGAVDTPOHTYLOHINGKAMAABITEELKAAPEG SCINKVKTYPGGVVNAAKEEHETDEKGKYYPKKSSLLLFEELKQI DDYAGSSMUODBSTT\NFYLIGKINGKYKKSSLLLFEELKQI DDYAGSSMUODBSTT\NFYLIGKINGKYKKSSLLLFEELKQI LASVKIMMPRTDEERARRNGGVAPMRRABABALKYLLINGXMU MSEKKLLGMGAVADP PROPECTIFIGGAMPEC LINGRABED LINGRAMATUR	1	•		QQLERQNKELKAKLQELEGAVKSKFKATISALEAKIGQLEEQLE
5932  33  572  RILBEIGFIFLQKGRKIKLIGGFRWEEKKPRGTGGLHWYARANMG FOATLANGLIFVILSVUTIIIOFTCSCCLYKTGRPFRV\APP PHPP/PVULAPYPQPSVPPSYPESYCGSTUTMPPQPGMPAAPY PHPP/PVULAPYPQPSVPPSYPESYCGSTUTMPPQPGMPAAPY PHPP/PVULAPYPQPSVPPSYPESYCGSTUTMPPQPGMPAAPY PMQYPPPYPAQPMSPPAYHETLAGGAARYPASQPPYNAYMDA FSAAL  5933  1 3190  GTRILKMADKTFGGSQKASSKTRSSDVHSGSSDAHMDASGFSD SOMPSTITPKFFSFRKHNYTNESARSLICDSPHONLSRPLLENKIK APSIGMSTARRILSKEQEELKKEDEKAARIYPESPLAPEG SOMSKTRYBYRGGVWAAREBEETDEKEKPIKYSSENPLOKEN DIVAPGSHOVDPSTT\NPYLGNI\NPOMABSKRSKOORSKRSSGVL DUYAPGSHOVDPSTT\NPYLGNI\NPOMABSKRSKOORSKRSSGVL LASVKLMMPRTDEERARENGGFWAPMINRDABFALKNINGKMI MSFEMKLIGGKAVPIPPHFIYPSMMEKKCCQEERGRGF LASVKLMMPRTDEERARENGGFWAPMINRDABFALKNINGKMI MSFEMKLIGGKAVPIPPHFIYPSMMEKKCCQEFGRGF LASVKLMMPRTDEERARENGGFWAPMINRDABFALKNINGKMI MSFEMKLIGGKAVPIPPHFIYPSMMEKKCCQEFGRGF ERAFVEEPSKKGALKEGRONKLEELINGLTFRKNDIGDAMVFC LINNAEAAEEIVDCITESLSILKTPLPKKIARLYINGSDVLYVSNS KVANASYTRKFFSTKLCGIFSDLNATYRTIGGHLGSEMKKGRW TCRAMEDOMA YPEPFLIKLGNIFLGLWIH IBEKETEOUPDDLD GAPIESELGGAPLEDVOGIPIDATYRIOGHLOGAMVFC LINNAEAAEEIVDCITESLSILKTPLPKKIARLYINSBVLYTSNS KVANASYTRKFFSTKLCGIFSDLNATYRTIGGHLGSEMKGRW TCRAMEDOMA YPEPFLIKLGNIFLGLWIH IBEKETEOUPDDLD GAPIESELGGAPLEDVOGIPIDATYPIDDLOGVIYKSKELFO QHEESSEEEMONQEESSGDEDVYSSKARNSFSSTEVRSRSKELFO QHEESSEEENONQEESSGDEDVYSSKARNSFSSTEVRSRSKELFO QHEESSEERSKOKKEEITRGLARPKWOOSSKELERGAVTTSKWELFO QHEESSEERSKOKKEEITRGLARPKWOOSSKEEKKE DECTPTRKERKRRSTSPSPSBSSGRRVKSSPSKEKERSKEK SHKESSRSRSSHOSSFRVSKKRNSSGRPKKKEK DECTPTRKERKRRSTSPSPSSSSSTEVRSRSRSRSSGV NAGSKKSRSGSRSPHSHSKKKSKGKTTTGRKFPKKAVTTWKCDLF CECRSVF PNQSSNERPPSLLVIETKKFPLKKREEKEKKKSNLELFFEELKGI QERNBERHKTKGRLSRFSPPQSDSOGGRRMAAPSRRRSGGVI DVARGSHUVDDFSTT\NFYLGNIN/POMIKKCCCQFFGREP LASVKIMMPRTDEERARRSRNGGFVAPMBRRABRADGRD PNQSSNERPPSLLVIETKKRPLENGERINGSFUNAPYYINM MSFEMLLGGKAVTTFUNGEN HENTENTENDETENTLAD.I HRM1SFWLLGGKGAVTPTPHYTIPSMMENTENTPPPSGLPFNAQD RELLKNPAMMLPBTDEERARRSRNGGFVAPMBRRABRANGSEQ LASVKIMMPRTDEERARRSRNGGFVAPMBRRABRANGSEQ ETEAFVEEPSKROKGVAPTENTENTPPPSGLPFNAQD RELKNPAMBABEELUORDESTT\NFYLGNINGENOTMANDAL HRM1SFWCLGGGAPTATHE	1			QEAKERAAANKLVRRTEKKLKEIFMQVEDERRHADQYKEQMEKA
5932  33  572  RILBEIGFIFLQKGRKIKLIGGFRWEEKKPRGTGGLHWYARANMG FOATLANGLIFVILSVUTIIIOFTCSCCLYKTGRPFRV\APP PHPP/PVULAPYPQPSVPPSYPESYCGSTUTMPPQPGMPAAPY PHPP/PVULAPYPQPSVPPSYPESYCGSTUTMPPQPGMPAAPY PHPP/PVULAPYPQPSVPPSYPESYCGSTUTMPPQPGMPAAPY PMQYPPPYPAQPMSPPAYHETLAGGAARYPASQPPYNAYMDA FSAAL  5933  1 3190  GTRILKMADKTFGGSQKASSKTRSSDVHSGSSDAHMDASGFSD SOMPSTITPKFFSFRKHNYTNESARSLICDSPHONLSRPLLENKIK APSIGMSTARRILSKEQEELKKEDEKAARIYPESPLAPEG SOMSKTRYBYRGGVWAAREBEETDEKEKPIKYSSENPLOKEN DIVAPGSHOVDPSTT\NPYLGNI\NPOMABSKRSKOORSKRSSGVL DUYAPGSHOVDPSTT\NPYLGNI\NPOMABSKRSKOORSKRSSGVL LASVKLMMPRTDEERARENGGFWAPMINRDABFALKNINGKMI MSFEMKLIGGKAVPIPPHFIYPSMMEKKCCQEERGRGF LASVKLMMPRTDEERARENGGFWAPMINRDABFALKNINGKMI MSFEMKLIGGKAVPIPPHFIYPSMMEKKCCQEFGRGF LASVKLMMPRTDEERARENGGFWAPMINRDABFALKNINGKMI MSFEMKLIGGKAVPIPPHFIYPSMMEKKCCQEFGRGF ERAFVEEPSKKGALKEGRONKLEELINGLTFRKNDIGDAMVFC LINNAEAAEEIVDCITESLSILKTPLPKKIARLYINGSDVLYVSNS KVANASYTRKFFSTKLCGIFSDLNATYRTIGGHLGSEMKKGRW TCRAMEDOMA YPEPFLIKLGNIFLGLWIH IBEKETEOUPDDLD GAPIESELGGAPLEDVOGIPIDATYRIOGHLOGAMVFC LINNAEAAEEIVDCITESLSILKTPLPKKIARLYINSBVLYTSNS KVANASYTRKFFSTKLCGIFSDLNATYRTIGGHLGSEMKGRW TCRAMEDOMA YPEPFLIKLGNIFLGLWIH IBEKETEOUPDDLD GAPIESELGGAPLEDVOGIPIDATYPIDDLOGVIYKSKELFO QHEESSEEEMONQEESSGDEDVYSSKARNSFSSTEVRSRSKELFO QHEESSEEENONQEESSGDEDVYSSKARNSFSSTEVRSRSKELFO QHEESSEERSKOKKEEITRGLARPKWOOSSKELERGAVTTSKWELFO QHEESSEERSKOKKEEITRGLARPKWOOSSKEEKKE DECTPTRKERKRRSTSPSPSBSSGRRVKSSPSKEKERSKEK SHKESSRSRSSHOSSFRVSKKRNSSGRPKKKEK DECTPTRKERKRRSTSPSPSSSSSTEVRSRSRSRSSGV NAGSKKSRSGSRSPHSHSKKKSKGKTTTGRKFPKKAVTTWKCDLF CECRSVF PNQSSNERPPSLLVIETKKFPLKKREEKEKKKSNLELFFEELKGI QERNBERHKTKGRLSRFSPPQSDSOGGRRMAAPSRRRSGGVI DVARGSHUVDDFSTT\NFYLGNIN/POMIKKCCCQFFGREP LASVKIMMPRTDEERARRSRNGGFVAPMBRRABRADGRD PNQSSNERPPSLLVIETKKRPLENGERINGSFUNAPYYINM MSFEMLLGGKAVTTFUNGEN HENTENTENDETENTLAD.I HRM1SFWLLGGKGAVTPTPHYTIPSMMENTENTPPPSGLPFNAQD RELLKNPAMMLPBTDEERARRSRNGGFVAPMBRRABRANGSEQ LASVKIMMPRTDEERARRSRNGGFVAPMBRRABRANGSEQ ETEAFVEEPSKROKGVAPTENTENTPPPSGLPFNAQD RELKNPAMBABEELUORDESTT\NFYLGNINGENOTMANDAL HRM1SFWCLGGGAPTATHE	1	}		NARMKQLKRQLEEAEEEATRANASRRKLQRELDDATEANEGLSR
5932  33  572  RILBETCFLFLJKGRKLKLISGFRWEEKKPCTGGLWYKAEANMG FGATLAVGLTIFULGVYTIICFTCSCCCLYKTCRRPRPV\APP PHPP/PVVHAPPYPQPBVPPSYPPSYPGSYGGYHTMPPGGMPAAPY PHPP/PVVHAPPYPQPBVPPSYPGSYGGYHTMPPGGMPAAPY PHPP/PVVHAPPYPQPBVPPSYPGSYGGYHTMPPGGMPAAPY PHPP/PVVHAPPYPQPBVPPSYPGSYGGYHTMPPGGMPAAPY PHPP/PVVHAPPYPQPBVPPSYPGSYGGYHTMPGGMPAAPY PHPP/PVVHAPPYPQPBVPPSYPGSYGGYHTMPGGMPAAPY PHPPPYPAQPMPPPAYHETLAGAAAPYPASQPPYNPSYMDA FKAAL  5933  1 3190  GTRLKKAADKTFGGSQKASSKTRSSDVHSGGSDAHMDASGFSD SOMPSRTRPKSPRKHYRMESARSLCDSPHQHLSRPLLENLKLK APSIGMATAVATLSKREGELKKKSNLELFYBELLAFEG GERDERHKTKGRISHFEPPGSDGDGGRAMAPSTRNASSGVL DDYAPGSHOVGDPSTT\NPYLGHI\NPQCMLKKCCCGEFGRGFGP LASVKLMPRTDERRAFENCGFVPPMRGAEALKNINGKMI MSFRMKLGRGKAVEIPPHIYIPPSMMEHTLDPPPSGLPFNAQM REFLKMPNAPHIPPPKNKEDFPKTLSQLYKWVIPPERNILALI HEMLEFVVBEGPMPEMAINNREINNPMFRPLFENQTPAHVYYRW KLYSILQGDSPTKWRTEDFRVPKNGSFWPPPHIPYLHGMSEGG ETARFVEBPSKKGALKERGFROKBEEILGHGAGALVFVIRN KLYSILQGDSPTKWRTEDFRVPKNGSFWPPPHIPYLHGMSEGG ETARFVEBPSKKGALKERGFROKBEEILGHGAGSENFKQRVM TCFRAMEDMAIYPPELIKLONIFIGJAVNIESEKPTEUPPDLD GAPIEBELGAPLEDUGG IPDAPPIDLOFY SKLDDULTYSKS KWANASYYKRFFSTKLCGIFSDLMATYTRIPKNIGGSHWPKPCOGSF QECVBHYROKLLQREEKELBERERERDKKOKEKLENGVERSDKKKE DECTPTKERKRRHSTSSFSPSSGSRKFWSSFOKKEK DECTPTKERKRRHSTSSFSPSSSGSRKPKSSFOKKEK DECTPTKERKRRHSTSSFSPSSSGSRKPKSSFOKKEK DECTPTKERKRRHSTSSFSPSSSSGSKFKNSSFOKKEK DECTPTKERKRRHSTSSFSPSSSSGSKFKNSSFOKKEK DECTPTKERKRRHSTSSFSPSSSSGSSFOKKERSSOKKEK SKSKYSBMEEKRALKERSFSRSSSSKOKKEK DECTPTKRERKRRHSTSSFSPSSSSGSRAMPABASGFSD KKSGKKERSSGRSFHRSKKKSKSKTYNGKRPFKKAVTYMKCDLF LCPRSVF  3190  GTRKLWADKTFGGSGKASSKTRSSCVHSGSSSAAABHTUSFLAAPEG SOMNKKTTVRGGVNAAKEEHTTDEKRKYTYPSSRPADGKDP PNGSNERPPSILVITETKKPLIKGREKEKKKSHLELFKERKGI DDYARGSHDVODPSTT\NFYLIGNINDFARRASGRGSC LASVKIMPPRTDEERARERNGGFVRFMRRABASRAKRNSGGU MSEPMLLGWGKAVPIPPHIPITIPINSPHAPRIFINDTDAHVYVRW KLYSILGGDSFTKWITEDFRHPKNGSFWRPPPLNPILHIALI HRMISFVVREGORPFETENTENGFVRPPPPROTPAHVYNR KLYSILGGDSFTKWITEDFRHPKNGSFWRPPPLNPILHGMSEGQ ETEAFVEEP PSKKGALKEEGTBUKLEEILGGLTVFKWOIDDAMVC LANGAABEUVOLTSSLIKTTEDFRHPKNGSFWRPPPLNPILHOBMEG LANGABEUVOLTSSLIKTTEDFRH	1	[		EVSTLKNRLRRGGPISFSSSRSGRRQLHLEGASLELSDDDTESK
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APSIGKMSTAKRTLSKKEGEELKKEDEKAARIYEEFLAAFEG SGGKVKTFVRGGGVVANAKEEIDEKGKIYKPSSRFADGKNP PNQSSNERPPSLLVIBTKKPPLKKGEKEKKKSNLELFKEELKGI GERDERHKTKGKLSKFEPPCSDSDGGRSMDAPSRRNRSSGVL DDYAPGSHDVOEPSTT\NFYLGINI\NPOMNLKKCCGEFGFGF LASVKIMWFRIDEERARERNCGFVAPMNRDAERALKKLNGKMI MSFEMKLGWGKAVVIPPHPIYIPPSMMEHTLPPPPSGLPFNAQP RERLKNENAPMLPPFINKEDFFRKTLSQAIVKVVIPTERNLLALL HRMTEFVVRGPMFEAMINNREINNPMFFLFFENGTPAHYYKR KLYSILGGDSPTKMRTBDFRMKNGSFRPPPLMFYLKMSBEG ETEAPVEEPSKKGALKEEGRDKLEBILGLTPRKNDIGDAMVFC LNNAEAAREIVDCITESLSILKTPLPKKIARLYLVSDVVLNSSA KVANASYYRKFFSTKLCQIFSDLNATYRTIGGHLQSENFKORVM TCFFAMBDMAIYPEPFLIKLQNIFGGLWATYSKMELPD QHEESEEEENQWGEEESBDEDTGSKSEEHLLYSBIPKEMTE SKISKYSEMSEEEEENQWGEEESBDEDTGSKSEEHLLYSBIPKEMTE SKISKYSEMSEEEEENQWGEEESBDEDTGSKSEEHLLYSBIPKEMTE SKISKYSEMSEEERAKLERIELKVMKFGDELESGKRPKKBGGSF QEQVBHYNDKLLQREKEKBLERERERDKKDKEKLESRSKDKKEK DECTPTTKERKKRHSTSPSPSSGRRVKSPSPKSERSERSER SKKSKSSGSRSPHRSHKKSKGKTNTGRKFFKKAVTYWKCOLF LCERSVF  5934  1 3190  GTRKLMADOKTPGGSQKASSKTRSSDVHSGSSDAHMDASGPSD SDMSRTPFLKLVIETKRPLKKKBEEKBKARAETISEFLAAFEG SDGNKVKTFVRGGVVNAAKEEHETDEKGKIYKPSGRFAAFG SDGNKVKTFVRGGVVNAAKEEHETDEKGKIYKPSGRFARNRSSGVL DDYAPGSHDVGDPSTT\NFYLGTKYRNIKKKSKNLELFKEELKQI QEERDERHKTKGRLSRFEPPQSDSDGGRRSMDAPSRRNRSSGVL DDYAPGSHDVGDPSTT\NFYLGTKYNGTVANMIKKCCQGEFGREGP HASVKLMBPTDEERARRNCGFVAPMNRDAERALKNINGKMI MSFEMLLGGKAVPIPPHIYIPPSMLFHLAPLFROGTPAHVYYRW KLYSILQGBSPTKMRTEGFRAPKNGGSWPPPLNFYLLHAMSEG ETEAFVEEPSKKGALKEEGRKEETDUPDLLD HRHIEFVVREGFMFEAMINNEEINLEBLERGLIPPRHYNGSMPPLNPYLHMGSEG ETEAFVEEPSKKGALKEEGRKEETDUPDLLD LNAMAAEEIVDCITESLSILKTPLPKKIARLYLVSDVLYNSSA KVANASYYKRFFETKLCQIFBLUNATYTIGGHLGSENFKGRW	5933	1	3190	GTRKLKMADKTPGGSQKASSKTRSSDVHSSGSSDAHMDASGPSD
SGGNVKTTYRGGGVNAMAKEHETDEKGKIYKPSSRFADQKNP PNQSSNERPPSLLVIETKKEPLKGETLEKKELKGIL DDYAPGSHDVGDESTT\NFYLGNI\NFOMNLKKCCCGEFGFGFG LASWKIMPRIDEERARENCGFVAFMNRRDABERNRSSGVL DDYAPGSHDVGDESTT\NFYLGNI\NFOMNLKKCCCGEFGFGFG REFIKLGGKGAVPIPPHTYIPPSMMEHTLPPPPSGLPFNAQP RERLKNPNAPMLPPPKNKEDFEKTLSQAIVKVVIPTERNILALI HRMIEFVVREGPMFEAMINNREINNPMFRELFENQTPAHYYFR KLYSILQGDEPTKHRTBDFRMKNGSFWRPPLHPYLHGMSEG BTEAFVEEPSKKGALKEEQROKLEELRGLTPRKNDIGDAMVFC LINNAEAAEEIVDCITESLSILKTPLPKKIARLYLVSDVLYNSSA KVANASYTRFFETKLCQIFSDLNATYRTIQGHLQSENFKQRVM TCFFAAMEDMAIPPEFILKLOHISLGAVNITSKELED GAPIEELDGAPLEDDUGIPIDATPIDDLDGVPIKSLDDDLDGV PLDATEDSKNEPIFKVAPSKKEAUDESELEAQAVTTSKWELED QHEESEEENQMQEEESBDEEDTQSKSEEHHLYSNPIKEEMTE SKFSKYSEMSEKRALKRIELKVWKFODELESGKRPKKPGQSF QEQVEHYRDKLLQREKEKELEREREDKKDKKEKLESRSKDKKEK BECTPTRKERKRHSTSSPSSSSGRRVKSPSFSSERSERSER SHKESSRSRSSKNDSFRDVSKKAKRSPSGSSTPKRSRRSRSSP KKSGKKSRSGSRSPKSSKNSPSSSSSGRRVKSPSFSERSERSER SHKESSRSRSSKNDSFRDVSKKAKRSPSGSTPKRSRRSRSSP KKSGKKSRSGSRSPKSHKSKSKTTTGRKPFKKAVTYWKCDLF LCPERSVF  5934  1 3190 GTRKLKMADKTPGGSQKASSKTRSSDVHSSGSSDAHMDASGPSD GTRKLKMADKTPGGSQKASSKTRSSDVHSSGSSDAHMDASGPSD GTRKLKMADKTPGGSQKASSKTRSSDVHSSGSSDAHMDASGPSD GTRKLKMADKTPGGSQKASSKTRSSDVHSSGSSDAHMDASGPSD GTRKLKMADKTPGGSPTNAKEHETDEKRGKIYKPSSRFADQKNP PNOSSNERPPSLLVIETKKPPLKKGKKKKKKKKLLEFKEELKQI QERDBRHKTKGRLSFRFPQDSDSDGGRRSMDAPSRRNRSSGVL DDYAPGSHDVGDPSTT\NFYLGNI\NPQMNLKKCCQEFGRGGP PNOSSNERPPSLLVIETKKPPLKKGKKKKKNELEFKEELKQI QERDBRHKTKGRLSFRFPQDSDSDGGRRSMDAPSRRNRSSGVL DDYAPGSHDVGDPSTT\NFYLGNI\NPQMNLKKCCQEFGRGGP RELKMPNAPMLPPPKNEDGFFAFNADABRPPLNFYLLALI HRMIEFVVREGPMFEAMIMNREINNPMFRPLEFNQTPAHVYIRW KLYSLLQGDSPTKMTEDFRNFKNGSFWRPPPLNFYLLALI HRMIEFVVREGPMFEAMIMNREINNPMFRPLEFNQTPAHVYIRW KLYSLLQGDSPTKMTEDFRNFKNGSFWRPPPLNFYLLALI HRMIEFVVREGPMFEAMIMNREINNPMFRPLEFNQTPAHVYIRW KLYSLLQGDSPTKMTEDFRNFKNGSFWRPPPLNFYLLALI HRMIEFVREGPBFERGNUGBSEWRPPPLNFYLLALI HRMIEFVREGPBFERGRUGBFERGFWGRVM KLYSLLQGDSPTKMFTEDFRNFKNGSFWRPPPLNFYLLALI HRMIEFVREGPBFERGNCDFRHFKNGSFWRPPLNFYLLALI LNARAAEELUDCTTESLSILKTPLPKKLARLYLVSDVLYNSSA KVANASYYRKFFETKLCQIFBLDNATYRTIQGHLOSEMFKQRVM	1			SDMPSRTRPKSPRKHNYRNESARESLCDSPHQNLSRPLLENKLK
PROSSNERPPSILVIETKKPPLKKGEKEKKKSNLELFKEELKOI  QEERCHRHKTKGRLSRFEPPQSDSGQRRSMDAPSRNRSSGVL  DDYAPGSHDVGDPSTT\NPYLGNI\NPOMNLKKCCCGEFGFFGF  LASVKIMMPRTDEERARERNCGFVAFMURRDAERALKNINGKMI  MSFEMKLGWGKAVDIPPHIYIPPSMMEHTLPPPPSGLPFNAQP  RERLKNPNAPMLPPPKNKEDFBKTLSQAIVKVVIPTERNLLALI  HRMTEFVVRBGPMFEAMINNREINDRWFRFLFENGTPAHVYYKW  KLYSILQGDBPTKHRTBDFRWKNGSFWRPPLHFWYLFKMBEEQ  ETEAPVEEPSKKGALKBEQRDKLEEILRGLTPRKNDIGDAMVEC  LNNAEAABEIVDCITESLSILKTPLPKKLAGIYLVSDVILVINSSA  KVANASYYRKFFTKLKQIFSDLAVTYFKINGLOSENFKORVW  TCFRAWBDMAIYPEPFLIKLQMIFJGLVNIIBEKETEDVPDDLD  GAPIBEELDGAPLEDVDGIPIDATPIDJDGVPIKSLDDDLDGV  PLDATEDSKKNEPIFKVAPSKWAVDESELBAQAVTTSKWELPP  QHEESBEERNQNQEESSBDEEDTQSSKSBEHELVSNPIKBEMTE  SKFSKYSEMSEEKRAKLREIELKVMKFQDELESGKRPKKPGGSF  QEQVBHYRDKLLQREKEKELEERERDKKDKEKLESRSKDKKKK  DECTPTTKERSKRRHSTSPSPSRSSGGRPKKSSPSPKSERSRSR  SHKESSRSRSSHKDSPROVSKXAKRSPSGSSDAHMDASGPSD  SCHEKKMADKTPGGSQKASSKTRSSDVHSSGSSDAHMDASGPSD  SCHEKKMADKTPGGSQKASSKTRSSDVHSSGSSDAHMDASGPSD  SCHEKKMADKTPGGSQKASSKTRSSDVHSSGSSDAHMDASGPSD  SCHEKKMADKTPGGSQKASSKTRSDVHSSGSSDAHMDASGPSD  SCHEKKMADKTPGGSQKASSKTRSSDVHSSRSFRFLEERIKG  GERDBRHKTKGRLSFFSPPGSDSDGGRRSMAPSRNRSSGVIL  DDYAPGSHDVGDPSTT\NPYLGTKRGKIYKPSSRFADGKNP  PNQSSNERPPSLLVIETKKPPLKKGEKEKKKKSNLELFKEELKQI  GERDBRHKTKGRLSFFSPPGSDSDGGRRSMAPSRRNRSGGVIL  DDYAPGSHDVGDPSTT\NPYLGT \NPQMMLKKCCCGFGFGFGP  LASVKIMWPRTDEERARERNCGFVAFMNRRDAERALKNLNGKMI  MSFEMKLGWGKAVPIPPHIYIPPSMKEDFFKLSQAIVKVIPPERMLALII  HRMIEFVVREGFMFFEAMIMNREINNPMFRFLFENQTPAHVYYRW  KLYSILQGDSTTKWRTEDFRMFKNGSFWRPPLNPFLHEMSEEQ  PETEAFVEEPSKKGALKEEGRUKLEEILKGLTPRHVMSEEQ  ETEAFVEEPSKKGALKEEGRUKLEEILKGLTPRHVMSEEQ  ETEAFVEEPSKKGALKEEGRUKLEELLEGLTPRKNIGHLAMWFC  LNNARABEIVDCTEESLSILKTPLPKKARLYLJVSDVJYNSSA  KVANASYYRKFFETKLCQIFSDLANTTIGGHLOSENFKGRVM  TCFRAWEDWAYYRKFFETKLCQIFSDLANTTIGGHLOSENFKRGRVM  TCFRAWEDWAYYRKFFETKLCQIFSDLANTTIGGHLOSENFKRGRVM  TCFRAWEDWAYYRKFFETKLCQIFSDLANTTIGGHLOSENFKRGRVM  TCFRAWEDWAYYRKFFETKLCQIFSDLANTTIGGHLOSENFKRRN				AFSIGKMSTAKRTLSKKEQEELKKKEDEKAAAEIYEEFLAAFEG
QERDERHKTGRISRFEPPQSDBGQRSMDAPSRRNRSSGUL DDYAPGSHIDUDDPSTT\NFYLGNI\NPQMILKKCCCQEFGRFGP LASVKIMWPRTDEERAPERNCGFVAFMINRIDAERALKILINGKMI MSFEMKLGWGKAVPIPPHFIYIPSMHHTTLPPPPSGLPFNAQP RERLKNPNAPMIPPPKKKEDPEKTLSQAIVKVIPTERNILALI HRMIEFVVREGPMFEAMIMNREINNPMFRFLFENQTPAHVYYRK KLYSILQGDSPTKMFREDFRHFKNGGFWRPPPLNPYHGMSEEQ ETEAFVZEPSKKGALKEQFDRLEEILRGTPRKNDIGGAMVFC LINNEAABEIVDCITESLSILKTPLPKKIARLYILVSDVLYNSSA KVANASYYRKFFETKLCQIFSDLNATYRTIQGHLGEENFKQRVM TCFRAWEDMAIYPEPFLIKLONIFLGLWNIIBEKETEUPUPDLD GAPIBEELDGAPLEDVDGIPIDATPIDDLDGVPIKSLDDDLDGV PLDATEDSKUNEPIFKVAPEKAVDESELEAQAVTTSKWELFD QHEESEEENQNQEEESEDEDTQSKSEEHHLYSNPIKEMTE SKFKYSEMSEEKRAKLREIELKVMKYQDELBSGKRPKKLEGP QEQVEHYNDKLLOREKKELBERRERGVKOKKEKLESRSKOKKKK DECTPTRKERKRRHSTSPSPSRSSGRRVKSPSPKSERSERSER SHKESSRSSHKDSPRDVSKKAKASPSGSTTYKSRSRSRSSSP KKSKKSRSGSRSPHRSHKKSKKKTNTGRKPFKKAVTYWKCDLF LCPERSVF  5934  1 3190  GTRKLKMADKTFGGSQKASSKTRSSDVHSSGSSDAHMDASGFSD SDMPSTRPKSPRKHNYRNESARESLCDSPHONLSRPLLENKIK AFSIGKMSTAKRTLSKKEQBELKKKBDEKAAAEIYEFLAAFEG SDGNKVKTPVRGGVVNAAKEEHSTDEKRKIYKPSSRFADQKND PNQSSNERPPSLLVIETKKPPLKKEGKEKKKSNLELFKEELQI OEERDBRHKTKGRLSRFEPPQSDSDGGRSMAAPSRRNRSSGVI DDVAPGSHDVOPDSTT\NPYLGNI\NPQMNLKKCCCQEFGRFGP LASVKIMWPRTDEERARENCGFVAFMNROABERALKINGKMI MSFEMKLIGGKAVPIIPPHIYIPPSMMEHTLPPPPSGLFFNAQP REELKMPNAPMLPPPNKKGEKTLSGAIVKVIPPERNLLALI HRMIEFVVREGPMFEAMIMNREINNPMFRFLFENQTPAHVYYRW KLYSILQGSPTKMRTEDFRMYKNGSPRSPPPINFYLHGMSEEQ GETABRHTKKGALKFEDFRMYKNGSPRSPPPINFYLHGMSEEQ ETEAFVEEPSKRAALEEUCHSBLIKRTPLKKUSDLAWFU KLYSILQGSPTKMRTEDFRMYKNGSPRSPPPINFYLHGMSEEQ ETEAFVEEPSKRAALEEUCHSBLIKTPLPKKUTGRAWFC LINNEAABEIVDCITESLSILKTPLPKKLARIYLVSDVLYNSSA KVANASYYRKFFETKLCQIFSDLNATYTTIQGHLQSBMFKQRVM TCFRAMEDMAIYPBFLIKLQNIFGLVNIIEEKSTEDVDDLD	1 1			SDGNKVKTFVRGGVVNAAKEEHETDEKRGKIYKPSSRFADQKNP
DDYAPGSHDVGDPSTT\NFYLGNI\NPOMNLKXCCCGEFGRFGG LASVKIMMPRTDEERARERNCGPVAFMNRRDAERALKNILMGKMI MSFEMKLGWGKAVPIPPHPYIPPSMHEHTLPPPPSGLPFNAQP RERLKNPNAPMLPPFKKEDFEKTLSQAIVKVVIPTERNILALI HRMLEFVVREGDMPEAMIMNREINNPMFRPLFENQTPAHVYYRW KLYSILQGDSPTKWRTEDFERNFKNGSFWRPPPLNPYLHGMSEEQ ETEAFVEEPSKKGALKBEQRDKLBEILRGITPRKNDIGDAMVFC LNNAEABEIVDCITELSILKTPLPKKIARLYLVSDVLYNSSA KVANASYYRKFFETKLCQIFSDLNATYRTIQGHLQSENFKQRVM TCFRAMEDWAIYPEPFLIKLQNIFLGLVNIIBEKETEDVPDDLD GAPIBEBLGAD-LEDUNGIPDATPID-LDGVPIKSLDDDLDGV PLDATEDSKKNEPIFKVAPSKWEAVDESELEAQAVTTSKWELFD QHEESSEEERNQNEESSEDEDTQSSKSEHHLYSMPIKEEMTE SKFSKYSEMSEEKRALKREIELKVMKFODELESGKEPKKPGOSF QEQVEHYRDKLLQREKEKBLERERERDKKDKKEKESSKSKKKE DECTPTRKERKRHSTSFSFSSSSGRVKSSPSPKSERSERSER SHKESSRSRSSKNDSPDTWSKKAKRSPSSSTPKSSRSSRSSP KKSGKKSRSQSRSPHRSHKKSKGKTNTGRKPFKKAVTYWKCDLF LCPERSVF  5934  1 3190 GTRKLKMADATPGGSQKASSKTRSSDVHSGSSDAHMDASGPSD SDMSKRTRPKSPRKHNYRNESARESLCDSPHQNLSRPLLENKLK AFSIGKMSTAKATLSKKEQEELKKKBDEKAAAEIYEEFLAAFEG SDGNKVKTFVRGGVVMAAKETEDEKRGKIVKPSSRFADQKNP PNQSSNERPPSLLVIETKKPPLKKGEKKKSNLELFKEELKQI QEERDBRHTKKGLAGFEPPGGDSDGGRSMADASRRNRSSGVL DDYAPGSHDVGDPSTT\NPTLONI\NPQNNLKKCCQEGFREGP LASVKIMPRTDEERARERNCGFVAPMNRRDAERALKNLNGKMI MSFEMKLGWGKAVPIPPHPIYTPDENKMEKTLEPPPSGCFFNAQP RELKMPNAPMLPPPKNKEDFEKTGSQAIVKVITFURGLILALI HRMIEFVVREGPMFERMINNREINNPRFFLFENQTPAHVYYRW KLYSILQGDSTYKNETDFRKYKNSFRPPPLNFYLHGMESEQ ETTAFVEEPSKKGALKEEQGDBLIEEILRGLTPRKNDIGGAMVYC LINNARABEIVDCTTESLSILKTPLPKKLARLYLVSUVLYNSSA KVANASYYRKFFETKLCQIFSCLNATYRTIQGHLQSENFKQRVM TCFRAMEDBAITPBFFILLCQNIFIGLNATYRTIQGHLQSENFKQRVM TCFRAMEDBAITPBFFILLCQNIFIGLNATYRTIQGHLQSENFKQRVM TCFRAMEDBAITPBFFILLCQNIFIGLNATYRTIQGHLGSENFKQRVM TCFRAMEDBAITPBFFILLCQNIFIGLNATYRTIQGHLGSENFKQRVM TCFRAMEDBAITPBFFILLCQNIFIGLNATYRTIQGHLGSENFKQRVM TCFRAMEDBAITPBFFILLCQNIFIGLNATYRTIQGHLGSENFKQRVM TCFRAMEDBAITPBFFILLCQNIFIGLNATYRTIQGHLGSENFKQRVM TCFRAMEDBAITPBFFILLCQNIFILGNATYRTIQGHLGSENFKQRVM				PNQSSNERPPSLLVIETKKPPLKKGEKEKKKSNLELFKEELKQI
LASVKIMMPRTDEERARERNCGFVAPMNRRDAERALKNINGKMI MSFEMKLGWGKAVPIPPHFIYIPPSGLPFNAQP RERLKNPMAPMLPPPKNKEDFEKTLSQATVKVVIPPERNILALI HRMIEFVVREGPMFRAMIMNREINNPMFRPLFENQTPAHVYYRW KLYSILQGSPTKWRTBDFRWKKNGFWRPPPHPNPTHHGMSEQ ETEAFVEEPSKKGALKERGPDKLBEILRGLTPRKNDIGDAMVFC LINNAEASEIVDCITESLSILKTPLPKKTARIJUSDVLYNSSA KVANASYYRKFFETKLCQIFFDLNATYRTIQGHLQSENFKQRVM TCFRAWEDWATYPEFFILKLONIFIGLVNIIBEKETEGUPDDLDG GAPIBEBLDGAPLEDVOGIPIDATPIDDLDGVPIKSLDDDLDGV PLDATEDSKKNEPIFKVAPSKWEAVDESELERQAVTTSKWELFD OHEESBEEERNONGEESBDEEDTQSSKSEEHLLYSNPIKEEMTE SKFSKYSEMSEEKRAKLREIELKVWKFQDELESGKRPKKPGQSF QEQVBYRDKLLQREKEKEELERERERDKKOKKEKLESRSKOKKEK DECTFTRKERKRHSTSFSPSRSSGRRVKSFSPKSERSERSER SHKESSRSRSSHKDSPRDVSKKAKRSPSGSRTPKRSRRSRSP KKSGKKSRSGSRSPHRSHKKSKGKTNTGRKFFKKAVTYWKCDLF LCPERSVF  5934  1 3190 GTRKLKMADKTFGGSQKASSKTRSDVHSSGSSDAHMDASGFSD SDMSKTRFNSPRCHNYRNESARESLCDSPHQNLSRPLLLENKIK AFSIGKMSTAKRTLSKKGQELKKKBDEKKADAEIVEEPLAAPEG SCMKVKTFVRGGVVNAAKEEHETDEKRGKIYKPSSRFADOKNP PNGSSNERPPSLLVIETKKPPLKKGEKEKKKSNLELFKEELKQI QEERDBRHKTKGGLSFREPPQSDSDGGRRADAPSRRNRSSGVL DDYAPGSHDVGDPSTT\NFYLGNI\NPQMNLKKCCCQEFGREGP LASVKIMWPRTDEERAERNGGFVAFMNRRDAERALKNINGKMI MSFEMKLGWGKAVPIPPPHPIYIPPSGLPFNAQP RERLKNPNAPMLPPPKNKEEFEKTLSQAIVKVVIPTERNILALI HRMIEFVVREGPMFEAMIMREINDMFFFLFENOTPAHVYYRW KLYSILQGDSPTKWRTEDFRRKNGSFWRPPPLNFYLHGMSEEQ ETEAFVEEPSKKGALKEEGRDKLEEILRGITPRRNDIGDAWFC LNNABAYERFFEKLLCQIFFSLNATYTTQGHLQSENKKORVM TCFRAWEDWAIYVEFFETKLCQIFJCBLNATYTTIQGHLQSENKKORVM TCFRAWEDWAIYVEFFETKLCQIFJCBLNATYTTIQGHLQSENKKORVM TCFRAWEDWAIYVEFFETKLCQIFJCBLNATYTTIQGHLQSENKKORVM TCFRAWEDWAIYVEFFETKLCQIFJCBLNATYTTIQGHLQSENKKORVM TCFRAWEDWAIYVEFFETKLCQIFJCBLNATYTRTIQGHLQSENKKORVM TCFRAWEDWAIYVEFFETKLCQIFJCBLNATYTRTIQGHLQSENKKORVM TCFRAWEDWAIYVEFFETKLCQIFJCBLNATYTRTIQGHLQSENKKORVM TCFRAWEDWAIYVEFFETKLCQIFJCBLNATYTRTIQGHLQSENKKORVM TCFRAWEDWAIYVEFFETKLCQIFJCBLNATYTRTIQGHLQSENKKORVM TCFRAWEDWAIYVEFFETKLCQIFJCBLNTITEERETEDVPDDLD	[	· .		QEERDERHKTKGRLSRFEPPQSDSDGQRRSMDAPSRRNRSSGVL
MSFEMKLGWGKAVPIPPHFIYIPPSMLEHTLPPPPGGLPFNAQP RERLKNPNAPMLPPPKNKEDFEKTLSQAIVKVVIPTERNILALI HRMLEFVVREGPMFEAMIMNREINNPMFRFLFENOTPAHVYYRW KLYSILQGDSPTKHRTEDFRMFKNGSFWRPPPLNPVLHGMSEEQ ETEAFVEEPSKKGALKEEQRDKLBEILRGLTPRKNDIGDAMVFC LNNAEAAEIVDCITESLSILKTPLPKKTARIYLVSDVLYNSSA KVANASYYRKFFETKLCQIFSDLNATYRTIQGHLQSENFKQRVM TCFRAWEDMAIYPEPFLIKLQNIFLGLVNIIBEKETEUVPDDLD GAPIBELDGAPLEDVOI PIDATPIDDLDGVPIKSLDDDLDGV PLDATEDSKKNEPIFKVAPSKWEAVDESELRAQAVTTSKWELFD QHEESEEERQNQEEESEDEEDTQSSKSEEHLLYSNPIKEEMTE SKFSKYSEMSEEKRAKLREILKVMKFQDELESGKRPKKPGQSF QEQVBHYRDKLLQREKEKBLERERERDKKDKSKLESRSKDKKSK DECTPTRKERKRRHSTSSPSSSSSTRYKSSRSKSER SHKESSRSSSHKDSPRDVSKKAKRSPSGSSTPKRSRSRSSRS KKGKKSRSQSRSPHRSHKKSKGKTNTGRKPFKKAVTYWKCDLF LCPERSVF  5934  1 3190 GTRKLKMADKTPGGSQKASSKTRSDVHSSGSSDAHMDASGFSD SDMSKTRPKSPRKHNYRNESARESLCDSPHQNLSRPLLENKLK APSIGKMSTAKRTLSKKEQEELKKKEDEKARAEIYEEPTLAAPEG SDONKVKTFVRGGVNNAAKEEHETDEKRGKTYKESSRFADOKNP PNQSSNERPPSLLVIETKKPPLKKGEKEKKKSNLELFKEELKQI QEERDBRHKTKGRLSRFEPPQSDSDGQRRSMDAPSRRNRSSGVL DDYAPGSHDVGDBSTT\NFYLGNI\NPQMNLKKCCQEFGRFGP LASVKLMWPRTDEERAERNCGFVAPMNRRDAERALKNLNGKMI MSFEMKLGWGKAVPIPPPHIYIPPSGLPFKAQP REELKMPNAPMLPPPKNKEPFEKTLSQAIVKVYIPTERNLLALI HRMIEFVVRSGPMFEAMIMNREINNPMFFLFENOTPAHVYYRW KLYSILQGDSPTKWRTEDFRRKNGSFWRPPPLNFYLHGMSEEQ ETEAFVEEPSKGALKEEGORKLEEILERGLTPRNOIDGNAWFC LNNABAYEKFFETKLCQIFSDLNATYRTIQGHLQSENKKGRVM TCFRAWEDMAIYWEPFILKLQNIFIGGLNATYRTIQGHLQSENKKGRVM				DDYAPGSHDVGDPSTT\NFYLGNI\NPQMNLKKCCCQEFGRFGP
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TCFRAWEDWAIYPEPFLIKLQNIFIGLVNIIEEKETEDVPDDLD		}		LNNALAAEEIVDCITESLSILKTPLPKKIARLYLVSDVLYNSSA
TCFRAWEDWAIYPEPFLIKLQNIFLGLVNIIEEKETEDVPDDLD GAPIEEELDGAPLEDVDGIPIDATPIDDLDGVPIKSLDDDLDGV		į		KVANASYYRKFFETKLCQIFSDLNATYRTIQGHLQSENFKQRVM
GAPIEERLDGAPLEDVDGIPIDATPIDDLDGVPIKSLDDDLDGV				TCFRAWEDWAIYPEPFLIKLQNIFLGLVNIIEEKETEDVPDDLD
				GAPIEEELDGAPLEDVDGIPIDATPIDDLDGVPIKSLDDDLDGV

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1.0.	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
Ĭ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	
	sequence	pedaence	Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
<u> </u>	Bequence		
1	1		PLDATEDSKKNEPIFKVAPSKWEAVDESELEAQAVTTSKWELFD
ļ		<u> </u>	QHEESEEEENQNQEEESEDEEDTQSSKSEEHHLYSNPIKEEMTE
			SKFSKYSEMSEEKRAKLREIELKVMKFQDELESGKRPKKPGQSF
			QEQVEHYRDKLLQREKEKELERERERDKKDKEKLESRSKDKKEK
			DECTPTRKERKRRHSTSPSPSRSSSGRRVKSPSPKSERSERSER
		-	SHKESSRSRSSHKDSPRDVSKKAKRSPSGSRTPKRSRSRSRSP
ł		1	KKSGKKSRSQSRSPHRSHKKSKGKTNTGRKFFKKAVTYWKCDLP
5935	<del> </del>		LCPERSVF
2932	3	4493	SYWLSGWRLSRPPRQFWAGWRGIGRFGTMAPVHGDDCEIGASAL
1		•	DECENT VESTARRERISKRONGEADER DRAMAGERIKIEVEDE
		ł	TGVYEEVDEEQYSKLVQARQDDDWIVDDDGIGYVEDGREIFDDD
		}	LEDDALDADEKGKDGKARNKDKRNVKKLAVTKPNNIKSMFIACA
	J	ĺ	GKKTADKAVDLSKDGLLGDILQDLNTETPQITPPPVMILKKKRS
1	1		IGASPNPFSVHTATAVPSGKIASPVSRKEPPLTPVPLKRAEFAG
			DDVQVESTEEEQESGAMEFEDGDFDEPMEVEEVDLEPMAAKAWD
		j	KESEPAEEVKQEADSGKGTVSYLGSFLPDVSCWDIDQEGDSSFS
1		İ	VQEVQVDSSHLPLVKGADEEQVFHFYWLDAYEDQYNQPGVVFLF
1	j		GKVWIESAETHVSCCVMVKNIERTLYFLPREMKIDLNTGKETGT
	1		PISMKDVYEEFDEKIATKYKIMKFKSKPVEKNYAFEIPDVPEKS
ļ			EYLEVKYSAEMPQLPQDLKGETFSHVFGTNTSSLELFLMNRKIK
)	1	i	GPCWLEVKKSTALNOPVSWCKVEAMALKPDLVNVIKDVSPPPLV
l			VMAFSMKTMQNAKNHQNEIIAMAALVHHSPALDKAAPKPPFQSH
l			FCVVSKPKDCIFPYAFKEVIEKKNVKVEVAATERTLLGFFLAKV
1			HKIDPDIIVGHNIYGFELEVLLQRINVCKAPHWSKICRLKRSNM
i			PKLGGRSGFGERNATCGRMICDVEISAKELIRCKSYHLSELVQQ
	1		ILKTERVVIPMENIQNMYSESSQLLYLLEHTWKDA\KFILQIMC
			ELNVLPLALQITNIAGNIMSRTLMGGRSERNEFLLLHAFYENNY
			IVPDKQIFRKPQQKLGDEDEEIDGDTNKYKKGRKKGAYAGGLVL
			DPKVGFYDKFILLLDFNSLYPSIIQEFNICFTTVQRVASBAQKV
1			TEDGEQEQIPELPDPSLEMGILPREIRKLVERRKQVKQLMKQQD
			LNPDLILQYDIRQKALKLTANSMYGCLGFSYSRFYAKPLAALVT
1		ı	YKGREILMHTKEMVQKMNLEVIYGDTDSIMINTNSTNLEBVFKL
			GNKVKSEVNKLYKLLEIDIDGVFKSLLLLKKKKYAALVVEPTSD
Ì			GNYVTKQELKGLDIVRRDWCDLAKDTGNFVIGQILSDQSRDTIV
			ENIQKRLIEIGENVLNGSVPVSQFEINKALTKDPQDYPDKKSLP
			HVHVALWINSQGGRKVKAGDTVSYVICQDGSNLTASQRAYAPEQ
			LQKQDNLTIDTQYYLAQQIHPVVARICEPIDGIDAVLIATGWEL
	]		\DPTQFKVHHYHKDEENDALLGGPAQLTDEEKYRDCERFKCPCP
,	ļ		TCGTENIYDNVFDGSGTDMEPSLYRCSNIDCKASPLTFTVQLSN
] :			KLIMDIRRFIKKYYDGWLICEEPTCRNRTRHLPLQFSRTGPLCP
			ACMKATLQPEYSDKSLYTQLCFYRYIFDAECALBKLTTDHEKDK
			LKKQFFTPKVLQDYRKLKNTAEQFLSRSGYSEVNLSKLFAGCAV
			KS
5936	1124	139	RGEEQFDAEFRRFACLGFGERLQEFSRLLRAVHRSRAWTCYLAI
			RMLMATCCPSPTTTACTGPWQRAPPLRLLVQKREADSSGLAFAS
			NSLQRRKKGLLLRPVAPLRTRPPLLISLPQDFRQVSSVIDVDLL
			PETHRRVRLHKHGSDRPLGFYIRDGMSVRVAPQG\LERVPGIFI
			SRLVRGGLAESTGLLAVSDEILEVNGIEVAGKTLNQVTDMMVAN
			SHN\LIVTVKPANQRNNVVRGASGRLTGPPSAGPGPAEPDSDDD
			SSDLVIENRQPPSSNGLSQGPPCWDLHPGCRHPGTRSSLPSLDD
		,	QEQASSGWGSRIRGDGSGFSL
5937	31	1600	PTSLLKSTVQLMCRLLQDKRYQCVYSLAEIFKVLASFYVILVIL
	ŀ		YGLTSSYSLWWMLRSSLKQYSFEALREKSNYSDIPDVKNDFAFI
			LHLADQYDPLYSKRFSIFLSEVSENKLKQINLNNEWTVEKLKSK
			LVKNAQDKIELHLFMLNGLPDNVFELTEMEVLSLELIPEVKLPS
ŀ	į		AVSQLVNLKELRVYHSSLVVDHPALAFLEENLKILRLKFTEMGK
	ļ		IPRWVFHLKNLKELYLSGCVLPEQLSTMQLEGFQDLKNLRTLYL
l l	1		KSSLSRIPQVVTDLLPSLQKLSLDNEGSKLVVLNNLKKMVNLKS
	1		LELISCOLERIPHSIFSLNNLHELDLRENNLKTVEEIISFQHLQ
	1		NLSCLKLWHNNIAYIPAQIGALSNLEQLSLDHNNIENLPLQLFL
ļ	ì		CTKLHYLDLSYNHLTFIPEEIQYL\SNLQYFAVTNNNIEMLPDG
	<del></del>	<del></del>	

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
ĺ	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
ł	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	amino acid	L=Leucine, M=Nethionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
1	amino acid		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	eedneuce	Codon, /=possible nucleotide deletion,
<u> </u>	sequence		\=possible nucleotide insertion)
1	i	Į.	LFQCKKLQCLLLGKNSLMNLSPHVGELSNLTHREPIG\NYLETL
F030			PPELEGCQSLKRNCLIVEENLLNTLPLPVTERLOTCLDKC
5938	395	1865	YKGEGFFCNQEARGERRKKKKAMSSPNIWSTGSSVYSTPVFSQK
			MTVWILLLSLYPGFTSQKSDDDYEDYASNKTWVLTPKVPEGDV
1	i		TVILNNLLEGYDNKLRPDIGVKPTLIHTDMYVNSIGPVNAINME
1		}	YTIDIFFAQTWYDRRLKFNSTIKVLRLNSNMVGKIWIPDTFFRN
			SKKADAHWITTPNRMLRIWNDGRVLYSLRLTIDAECQLQLHNFP
1	ł	}	MDEHSCPLEFSSYGYPREEIVYQWKRSSVEVGDTRSWRLYQFSF
			VGLRNTTEVVKTTSGDYVVMSVYFDLSRRMGYFTIQTYIPCTLI
			VVLSWVSFWINKDAVPARTSLGITTVLTMTTLSTIARKSLPKVS
	1		YVTAMDLFVSVCFIFVFSALVEYG\TLHYPVSNRKPSKDKDKKK
1			KNPAPTIDIRPRSATIQMNNATHLQERDEEYGYECLDGKDCASF
1			FCCFEDCRTGAWRHGRIHIRIAKMDSYARIFFPTAFCLFNLVYW
	1		VSYLYL
5939	66	1404	IRPGYLKEVQENSPGHRAGLEPFFDFIVSINGSRLNKDNDTLKD
			LLKANVEKPVKMLIYSSKTLELRETSVTPSNLWGGQGLLGVSIR
İ			FCSFDGANENVWHVLEVESNSPAALAGLRPHSDYIIGADTVMNE
			SEDLFSLIETHEAKPLKLYVYNTDTDNCREVIITPNSAWGGEGS
1			LGCGIGYGYLHRIPTRPFEEGKKISLPGQMAGTPITPLKDGFTE
İ			VQLSSVNPPSLSPPGTTGIEQSLTGLSISSTP\PAVSSVLSTGV
1			PTVP\LLPPQVNQSLTSVPPMESSYLHLPGLMPFTRQGLPNLPQ
1			PSTFNLPR\PTHSWPGVGLYQEFVKPGVLPPLSSMPPRNLPG\I
1			APLPLPSEFLPSFPLVPESSSAASSGELLSSLPPTSNAPSDPAT
1			TTAKADAASSLTVDVTPPTAKAPTTVEDRVGDSTPVSEKPVSAA
			VDANASESP
5940	145	717	RRSASRSASPRQSAGTAVTTGTRAGGTCLAAAHHRMRWRADGRS
			LEKLPVHMGLVITEVEQEPSFSDIASLVVWCMAVGISYISVYDH
1 1			QGIFKRNNSRLMDEILKQQQELLGLDCSKYSPEFANSNDKDDOV
] ]			LNCHLAVKVLSPEDGKADIVRAAQDFCQLVAQKQKRPTDLDVDT
			PY/AATAOWAATITI
5941	13	6147	MCLGRMGASSPRSPEPVGPPAPGLPFCCGGSLLAVVVLLALPVA
j l			WGQCNAPEW\LPFARPTNLTDEFEFPIGTYLNYECRPGYSGRPF
i			SIICLKNSVWTGAKDRCRRKSCRNPPDPVNGMVHVIKGIOFGSO
1	1		IKYSCTKGYRLIGSSSATCIISGDTVIWDNETPICDRIPCGLPP
1 1			TITNGDFISTNRENFHYGSVVTYRCNPGSGGRKVFELVGEPSIY
1 1			CTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDNRSLFSL
) [			NEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPSCSRVCQPPPD
l			VLHAERTQRDKDNFSPGQEVFYSCEPGYDLRGAASMRCTPOGDW
			SPAAPTCEVKSCDDFMGQLLNGRVLFPVNLOLGAKVDFVCDEGF
li			QLKGSSASYCVLAGMESLWNSSVPVCEOIFCPSPPVIDNGRHTG
, 1			KPLEVFPFGKAVNYTCDPHPDRGTSFDLIGESTIRCTSDPOGNG
	1	İ	VWSSPAPRCGILGHCQAPDHPLPAKLKTQTNASDFPIGTSLKYE
			CRPEYYGRPFSITCLDNLVWSSPKDVCKRKSCKTPPDPVNGMVH
	İ		VITDIQVGSRINYSCTTGHRLIGHSSAECILSGNAAHWSTKPPI
· •	1		CQRIPCGLPPTIANGDFISTNRENFHYGSVVTYRCNPGSGGRKV
]			FELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGII.
			VSDNRSLFSLNEVVEFRCQPGFVMKGPRRVKCOALNKWEPELPS
	i	İ	CSRVCQPPPDVLHAERTQRDKDNFSPGQEVFYSCBPGYDLRGAA
	i	ſ	SMRCTPQGDWSPAAPTCEVKSCDDFMGQLLNGRVLFPVNLOLGA
1	1		KVDFVCDEGFQLKGSSASYCVLAGMESLWNSSVPVCEQIFCPSP
1		ļ	PVIPNGRHTGKPLEVFPFGKAVNYTCDPHPDRGTSFDLIGESTI
	l	ľ	RCTSDPQGNGVWSSPAPRCGILGHCQAPDHFLFAKLKTOTNASD
ŀ			FPIGTSLKYECRPRYYGRPFSITCLDNLVWSSPKDVCKRKSCKT
1	ļ		PPDPVNGMVHVITDIQVGSRINYSCTTGHRLIGHSSAECILSGN
		j	TAHWSTKPPICQRIPCGLPPTIANGDFISTNRENFHYGSVVTYR
	Ĭ	1	CNLGSRGRKVFELVGEPSIYCTSNDDQVGIWSGPAPOCIIPNKC
		1	TPPNVENGILVSDNRSLFSLNEVVEFRCOPGFVMKGPRRVKCOA
1		1	LNKWEPBLPSCSRVCQPPPEILHGEHTPSHODNFSPGOEV3YSC
	1	Í	EPGYDLRGAASLHCTPQGDWSPEAPRCAVKSCDDFLGQLPHGRV
1	ł	!	LFPLNLQLGAKVSFVCDEGFRLKGSSVSHCVLVGMRSLWNNSVP
			VCEHIFCPNPPAILNGRHTGTPSGDIPYGKEISYTCDPHPDRGM

SEQ	Predicted	Predicted end	Amino agid company
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
i	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine.
ŀ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion.
	sequence		\=possible nucleotide insertion)
1			TFNLIGESTIRCTSDPHGNGVWSSPAPRCELSVRAGHCKTPEQF
ſ	1		PFASPTIPINDFEFPVGTSLNYECRPGYFGKMFSISCLENLVWS
	1		SVEDNCRRKSCGPPPEPFNGMVHINTDTQFGSTVNYSCNEGFRL
	Į.		IGSPSTTCLVSGNNVTWDKKAPICEIISCEPPPTISNGDFYSNN
	<b>[</b>	1	RTSFHNGTVVTYQCHTGPDGEQLFELVGERSIYCTSKDDQVGVW SSFPPRCISTNKCTAPEVENAIRVPGNRSFFSLTEIIRFRCQPG
1			FVMVGSHTVQCQTNGRWGPKLPHCSRVCQPPPEILHGEHTLSHQ
İ		ĺ	DNFSPGQEVFYSCEPSYDLRGAASLHCTPQGDWSPEAPRCTVKS
ĺ			CDDFLGQLPHGRVLLPLNLQLGAKVSFVCDEGFRLKGRSASHCV
		!	LAGMKALWNSSVPVCEQIFCPNPPAILNGRHTGTPLGDIPVGKE
1	I		VSYTCDPHPDRGMTFNLIGESTIRRTSEPHGNGVWSSPAPRCEL
j	i		PVGAACPHPPKIQNGHYIGGHVSLYLPGMTISYTCDPGYLLNGK
-			GFIFCTDQGIWSQLDHYCKEVNCSFPLFMNGISKELEMKKVYHY
			GDYVTLKCEDGYTLEGSPWSQCQADDRWDPPLAKCTSRTHDALT
			VGTLSGTIFFILLIIFLSWIILKHRKGNNAHENPKEVAIHLHSQ
5942	4509	688	GGSSVHPRTLQTNEENSRVLP
		355	YLYVRMRANPLAYGISHKAYQIDPPL\RKHREQ\LVIE\VGRKL
1	1		DK\AQMIRFEERTGYFSSTDLGRTASHYYIKYNTIETFNELFDA HKTEGDIFAIVSKAEEFDQIKVREEEIEELDTLLSNFCBLSTPG
1	l		GVENSYGKINILLQTYINRGEMDSPSLISDSAYVAQNAARIVRA
i .			LFEIALRKRWPTMTYRLLNLSKAIDKRLWGWASPLRQFSILPPH
			MLTRLEEKKLTVDKLKDMRKDBIGHILHHVNIGLKVKOCVHOIP
1			SVMMEAFIQPITRTVLRVTLSIYADFTNNDOVHGTVGEPWWTWV
1			EDPTNDHIYHSEYFLALKKQVISKEAOLLVFTIPIFEPLPSOVV
			IRAVSDRWLGAEAVCIINFOHLILPERHPPHTELLDLQPLPITA
			LGCKAYEALYNFSHFNPVQTQIFHTLYHTDCNVLLGAPTGSGKT
			VAAELAI FRVFNKYPTSKAVYIAPLKALVRERMDDWKVRIEEKL
1			GKKVIELTGDVTPDMKSIAKADLIVTTPEKWDGVSRSWQNRNYV QQVTILIIDEIHLLGEERGPVLEVIVSRTNFISSHTEKPVRIVG
1			LSTALANARDLADWLNIKQMGLFNFRPSVRPVPLEVHIQGFPGQ
1 1			HYCPRMASMNKPAFQAIRSHSPAKPVLIFVSSRRQTRLTALELI
] ]			AFLATEEDPKQWLNMDEREMENIIATVRDSNLKLTLAFGIGMHH
l i	l l		AGLHERDRKTVEELFVNCKVQVLIATSTLAWGVNFPAHLVIIKG
1 1	1		TEYYDGKTRRYVDFPITDVLQMMGRAGRPOFDDOGKAVILVHDI
1 1			KKDFYKKFLYEPFPVESSLLGVLSDHLNAEIAGGTITSKODALD
1 1			YITWTYFFRRLIMNPSYYNLGDVSHDSVNKFLSHLIEKSLIELE
1	1		LSYCIBIGEDNRSIEPLTYGRIASYYYLKHQTVKMFKDRLKPEC
ľ			STEELLSILSDAEEYTDLPVRHNEDHMNSELAKCLPIESNPHSF
i i	ĺ		DSPHTKAHLLLQAHLSRAMLPCPDYDTDTKTVLDQALRVCQAML DVAANQGWLVTVLNITNLIQMVIQGRWLKDSSLLTLPNIENHHL
			HLFKKWKPIMKGPHARGRTSIECLPELIHACGGKDHVFSSMVES
			ELHAAKTKQAWNFLSHLPEINVGISVKGSWDDLVEGHNELSVST
			LTADKRDDNKWIKLHADOEYVLOVSLORVHFGFHKGKPESCAVT
	1		PRFPKSKDEGWFLILGEVDKRELIALKRVGYIRNHHVASI.gpvn
		į	PEIPGRYIYTLYFMSDCYLGLDQQYD/NLSQRYTSESFCTGOHO
5943	1	2274	GL
	- 1	4414	DKPTRHKTYLSSSWAKMAAAEGPVGDGELWQTWLPNHVVFLRLR
			EGLKNQSPTEAEKPASSSLPSSPPPQLLTRNVVFGLGGELFLWD
	[		GEDSSFLVVRLRGPSGGG\EEPALSQYQRLLCINPPLFEIYQVL LSPTQHHVALIGIKGLMVLELPKRWGKNSEFEGGKSTVNCSTTP
	ĺ		VAERFFTSSTSLTLKHAAWYPSEILDPHVVLLTSDNVIRIYSLR
	١.	i	EPQTPTNVIILSEABEESLVLNKGRAYTASLGETAVAFDFGPLA
	[`		AVPKTLFGQNGKDEVVAYPLYILYENGETFLTYISLLHSPGN/T
			WKAVGSIAHAS\AAEDNYGYDACAVLCLPCVPNILVIATESGMI
j		1	YHCVVLEGEEEDDHTSEKSWDSRIDLIPSLYVFECURI.RI.AI.KI.
ł		Į	ASGEDDPPDSDFSCPVKLHRDPKCPSRYHCTHEAGVHSVGLTWT
1		1	HKLHKFLGSDEEDKDSLQELSTEOKCFVEHILCTKPLPCROPAP
Ī	[		IRGFWIVPDILGPTMICITSTYECLIWPLLSTVHPASPPLICTE
l	}	Į.	EDVEVAESPLRVLAETPDSFEKHIRSILORSVANPAFLKASEKD
•	}	-	IAPPPEECLQLLSRATQVFREQYILKQDLAKEEIQRRVKLLCDQ
·	<del></del>		KKKQLEDLSYCREERKSLREMABRLADKYEEAKEKQEDIMNRMK

SEQ	Predicted	1 5 - 3 / 5 - 3 - 3	
ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine.
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion.
<u> </u>	sequence		\=possible nucleotide insertion)
			KLLHSFHSELPVLSDSERDMKKELQLIPDQLRHLGNAIKQVTMK
	Ì		KDYQQQKMEKVLSLPKPTIILSAYQRKCIQSILKEEGEHIREMV
5944	1.02		KQINDIRNHVNF
3344	167	3428	FSIATFTDEPEVLTEPPSATTTTTIGISATWTTLAGSHGKRNNT
	i		ITTTSSKRKNRKNKITPENVQIIFDDPLPISYSQPEKVNGESKS
			SSTSESGDSDNMRISSCSDESSNSNSSRKSDNHSPAVVTTTVSS
1			KKQPSVLVTFPKEERKSVSGXASIKLSETISEGTSNSLSTCTKS
1	}		GPSPLSSPNGKLTVASPKRGQKRBEGWKEVVRRSKKVSVPSTVI
			SRVIGRGGCNINAIREFTGAHIDIDKQKDKTGDRIITIRGGTES TRQATQLINALIKDPDKEIDELIPKNRLKSSSANSKIGSSAPTT
1	i	_	TAANTSLMGIKMTTVALSSTSQTATALTVPAISSASTHKTIKNP
I		,	VN\NVRPGFPVSFP\LAYPPPOFAHALLAAQTFQQIRPPRLPMT
	·		HFGGTFPPAQSTWGPFPVRPLSPARATUSPKPHMVPRHSNQNSS
			GSQVNSAGSLTSSPTTTTSSSASTVPGTSTNGSPSSPSVRRQLF
1			VTVVKTSNATTTTVTTTASNNNTAPTNATYPMPTAKEHYPVSSD
			SSPSPPAQPGGVSRNSPLDCGSASPNKVASSSEOEAGSPPVVET
			TNTRPPNSSSSSGSSSAHSNQQQPPGSVSQEPRPPLOOSOVPPP
1			EVRMTVPPLATSSAPVAVPSTAPVTYPMPOTPMGCPOPTPKMET
1			PAIRPPPHGTTAPHKNSASVQNSSVAVLSVNHIKRPHSVPSSVQ
1 .			LPSTLSTQSACQNSVHPANKPIAPNFSAPLPFGPFSTLFENSPT
Į I			SAHAFWGGSVVSSQSTPESMLSGKSSYLPNSDPLHQSDTSKAPG
į			FRPPLQRPAPSPSGIVNMDSPYGSVTPSSTHLGNFASNISGGQM
•			YGPGAPLGGAPAAANFNRQHFSPLSLLTPCSSASNDSSAQSVSS GVRAPSPAPSSVPLGSEKPSNVSQDRKVPVPIGTERSARIRQTG
ł			TSAPSVIGSNLSTSVGHSGIWSFEGIGGNQDKVDWCNPGMGNPM
i i			IHRPMSDPGVFSQHQAMERDSTGIVTPSGTFHQHVPAGYMDFPK
1			VGGMPFSVYGNAMIPPVAPIPDGAGGPIFNGPHAADPSWNSLIK
			MVSSSTENNGPQTVWTGPWAPHMNSVHMNQLG
5945	1461	197	GVTHLFLFGKRKLRNGIAEDLKGQADFFFLLVSEAVVATGSPRA
[			WLTCLILPLPGIIFSVLPKAMSRPLLITFTPATDPSDLWKDGOO
1 !			QPQPEXPESTLDGAAARAFYEALIGDESSAPDSQRSQTEPARER
			KRKKRRIMKAPAAEAVAEGASGRHGQGRSLEAEDKMTHRILRAA
i i			QEGDLPELRRLLEPHEAGGAGGNINARDAFWWTPLMCAARAGQG
<u> </u>			AAVSYLLGRGAAWVGVCELSGRDAAQLAEEAGFPEVARMVRESH
·			GETRSPENRSPTPSLQYCENCDTHFQDSNHRTSTAHLLSLSQGP QPPNLPLGVPISSPGFKLLLRGGWEPGMGLGPRGEGRANPIPTV
i	İ		LKRDQEGLGYRSAPQPRVTHFPAWDTRAVAGRE\TPPRVATLSW
	!		REERRREE\KDRAWERDLRTYMNLEF
5946	541	1666	ILGSYSSIQPEEYS\SVVC\EVVLQDLLA\YVSPK\HSYLRDLP
İ			SEGSPQRVNSIDFV\EL\EHLQPDVLVHAVLRVVDF/TILTEAV
			YSYRGQKQKKVMLTVEQAQDQHYALVLWGPGAAW\YPQLORKKG
	i		YIWEFKYLFVQCNYTLENLELHTTPWSSCECLFDDDIRAITFKA
	į		KFQKSAPSFVKISDLATHLEDKCSGVVLIKAQISELAFPITASO
			KIALNAHSSLKSIFSSLPNIVYTGCAKCGLELETDENRIYKOCF
J			SCLPFTMKKIYYRPALMTAIDGRHDVCIRVESKLIEKILLNISA
i			DCLNRVIVPSSEITYGMVVADLFHSLLAVSAEPCVLKIQSLFVL
5947	3	1345	DENSYPLOQDFSLLDFYPDIVKHGANARL
	,	1317	RGIPDRRRRGPIGRVNMDLENKVKKMGLGHEQGFGAPCLKCKEK
ł	İ	ļ	CEGFELHFWRKICRNC\NVAKKSM/TVLLSNEEDRKVGKLFEDT
l			KYTTLIAKLKSDGIFMYKRNVMILTNPVAAKKNVSINTVTYEWA
			PPVQNQALARQYMQMLPKEKQPVAGSEGAQYRKKQLAKQLPAHD
	į	į	QDPSKCHELSPREVKEMEQFVKKYKSEALGVGDVKLPCEMDAQG PKQMNIPGGDRSTPAAVGAMEDKSAEHKRTQYSCYCCKLSMKEG
}	J		DPAIYAERAGYDKLWHPACFVCSTCHELLVDMIYFWKNBKLYCG
	Ì		RHYCDSEKPRCAGCDELIFSNEYTQAENQNWHLKHFCCFDCDSI
	į.		LAGEIYVMVNDKPVCKPCYVKNHAVVCQGCHNAIDPEVQRVTYN
			NPSWHASTECFLCSCCSKCLIGQKFMPVEGMVFCSVECKKRMS
5948	39	3370	YRERYPVSGGSVLRSALEVCWDFLSGLTEGSLLPEGFFSGPIDQ
1		1	GNHYQMRRKGRCHRGSAARHPSSPCSVKHSPTRETLTYAOAORM
- 1		1	VEIEIEGRLHRISIFDPLEIILEDDLTAQEMSECNSNKENSERP
	<u></u>		PVCLRTKRHKNNRVKKKNEALPSAHGTPASASALPEPKVRIVEY

	SEQ	Predicted	Predicted end	I having and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second a second and ----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------
	ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
		location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
		corresponding	to first	L=Leucine, M=Nethionine, N=Asparagine
	ł	to first amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine
	İ	residue of	residue of	S=Serine, T=Threonine, V=Valine
		amino acid	amino acid sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	}	sequence	aequence	Codon, /=possible nucleotide deletion,
				\=possible nucleotide insertion)
	j			SPPSAPRRPPVYYKFIEKSABELDNEVEYDMDEEDYAWLEIVNE KRKGDCVPAVSQSMFEFLMDRFEKESHCENQKQGBQQSLIDEDA
	1			VCCICMDGECQNSNVILFCDMCNLAVHQECYGVPYIPEGQWLC/
	l			RAHCLQSRARPADCVLCPNKGGAFKKTDDDRWGHV\VCALW\IP
		· .	1	E\VGFANTVFIEPIDGVRNIPPARWKLT\CNTCKEKGP\VGACT
		1		QCHKANCYTAFHVTCAOKAGLYMKMEPVKELTGGGTTRGUDWTA
		i i		YCDVHTPPGCTRRPLNIYGDVEMKNGVCRKESSVKTVPCTCKVP
	•	}		KKAKKAKKALAEPCAVLPTVCAPYIPPORINDIANOVATORKKO
-		[		FVERAHSYWLLKRLSRNGAPLLRRLQSSLQSQRSSQQRENDEEM
				KAAKEKLKYWQRLRHDLERARLLIELLRKREKLKREQVKVEQVA MELRLTPLTVILRSVLDQLQDKDPARIFAQPVSLKEVPDYLDHI
				KHPMDFATMRKRLEAQGYKNLHEFEEDFDLIIDNCMKYNARDTV
				FYRAAVRLRDQGGVVLRQARREVDSIGLEEASGMHLPERPAAAP
				RRPFSWEDVDRLLDPANRAHLGLEEOLRELLDMLDLTCAMVSSC
Į				SRSKRAKLLKKEIALLRNKLSQQHSQPLPTGPGLEGFEEDGAAL
1	i i			GPEAGEEVLPRLETLLQPRKRSRSTCGDSEVEEESDCKPLDAGT
		. 1		TNGFGGARSEQEPGGGLGRKATPRRRCASESSISSSNSPLCDSS
ł				FNAPKCGRGKPALVRRHTLEDRSELISCIENGNYAKAARIAAEV GOSSMWISTDAAASVLEPLKVVWAKCSGYPSYPALIIDPKMPRV
-				PGHHNGVTIPAPPLDVLKIGEHMQTKSDEKLFLVLFFDNKRSWQ
-		1		WLPKSKMVPLGIDETIDKLKMMEGRNSSIRKAVRIAFDRAMNHL
ŀ	5949			SRVHGEPTSDLSDID
1	2343	39	3370	YRERYPVSGGSVLRSALEVCWDFLSGLTEGSLLPEGFFSGPIDQ
۱.				GNHYQMRRKGRCHRGSAARHPSSPCSVXHSPTPETLTVAGAGOM
-				VEIBIEGRLHRISIFDPLEIILEDDLTAQEMSECNSNKENSERP
1				PVCLRTKRHKNNRVKKKNEALPSAHGTPASASALPEPKVRIVSY SPPSAPRRPPVYYKFIEKSAEELDNEVEYDMDEEDYAWLEIVNE
ſ				KRKGDCVPAVSQSMFEFLMDRFEKESHCENQKQGEQQSLIDEDA
1	ĺ			VCCICMDGECQNSNVILFCDMCNLAVHOECYGVPYIPECOWLC/
ſ		· [	·	RAHCLQSRARPADCVLCPNKGGAFKKTDDDRWGHV\VCALW\ TD
1	[:		* *	E\VGFANTVFIEPIDGVRNIPPARWKLT\CNLCKEKGR/VGACI
1	j	1		QCHKANCYTAPHVTCAQKAGLYMKMEPVKELTGGGTTFSVRKTA YCDVHTPPGCTRRPLNIYGDVEMKNGVCRKESSVKTVRSTSKVR
1				KKAKKAKALAEPCAVLPTVCAPYIPPQRLNRIANQVAIQRKKQ
1			Ì	FVERAHSYWLLKRLSRNGAPLLRRLOSSLOSORSSOOPENDREM
ı	ŀ			KAAKEKLKYWQRLRHDLERARLLIELLRKREKT KREOVKYROVA
1			[	MELRLTPLTVLLRSVLDOLODKDPAR I FAOPVSLKEVDDVLDUT
	i	•		KHPMDFATMRKRLBAQGYKNLHEFEEDFDLIIDNCMKYNARDTV
L			1	FYRAAVRLRDQGGVVLRQARREVDSIGLEEASGMHLPERPAAAP
	1		·	RRPFSWBDVDRLLDPANRAHLGLEEQLRELLDMLDLTCAMKSSG SRSKRAKLLKKBIALLRNKLSQQHSQPLPTGPGLEGFEEDGAAL
Ì	]	j		GPEAGEEVLPRLETLLQPRKRSRSTCGDSEVEEESPGKRIDDAGI.
	ł		1	TNGFGGARSEQEPGGGLGRKATPRRRCASESSISSSNSDLCDGG
ļ			1	FNAPKCGRGKPALVRRHTLEDRSELISCIENGVVAKAARTAARV
1	- 1		]	GQSSMWISTDAAASVLEPLKVVWAKCSGYPSYPALTIDPKMDDV
	- 1			PGHHNGVTIPAPPLDVLKIGEHMQTKSDEKLFLVLFFDNKRSWQ
L				WLPKSKMVPLGIDETIDKLKMMEGRNSSIRKAVRIAFDRAMNHL SRVHGEPTSDLSDID
آ	5950	1166	373	ESRS_TMSTSQPGACPCQGAASRPAILYALLSSSLKAVPR?RSR
	l	į	· · · · · · · · · · · · · · · · · · ·	CLCRQHRPVQLCAPHRTCREALDVLAKTVAFLRNI, PSFWOI, DDO
	1		1	DQRRLLQGCWGPLFLLGLAQDAVTFEVAEAPVPSILKKILLERD
	]		1	SSSGGSGQLPDRPQPSLAAVOWLOCCLESFWSI.FLSDKE\ VACT
	- 1		1	KGPILFNPDVPGLQAASHIGHLQQEAHWVLCEVLBPWCPAAQGR
Г	5951	143	5449	LTRVLLTASTLKSIPTSLLGDLPFRPIIGDVDIAGLIGDMLLLR WNVKPSLLVVQLFKFSDKEEHEQNDSISGKTGETGVEEMIATRK
	1			VEQDSKETVKLSHEDDHILEDAGSSDISSDAACTNPNKTENSLV
				GLPSCVDEVTECNLELKDTMGIADKTENTLERNKIEPLGVCEDA
	- 1	1	1:	ESNRQLESTEFNKSNLEVVDTSTFGPESNILENAICDVPDONSK
	1	1.	1	QLNAIESTKIESHETANLODDRNSOSSSVSYLESKSVKSKHTKD
	j	1	I '	VIHSKQNMTTDAPKKIVAAKYEVIHSKTKUNVKSVKPNTDVDFC
		<del></del>		QQNFHRPVKVRKKQIDKBPKIQSCNSGVKSVKNQAHSVLKKTLQ
				——————————————————————————————————————

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
αI	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lvsine.
-	corresponding	to first	L-Leucine, M-Methionine, N-Asparagine
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine
ļ	amino acid residue of	residue of	S=Serine, T=Threonine, V=Valine,
	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
j	sequence	sequence	Codon, /=possible nucleotide deletion,
	boquence		\=possible nucleotide insertion)
1		İ	DOTLVQTFKPLTHSLSDKSHAHPGCLKEPHHPAQTGHVSHSSQK
ì	1	ļ	QCHKPQQQAPAMKTNSHVKEELEHPGVEHFKEEDKLKLKKPEKN
l.			LQPRQRRSSKSFSLDEPPLFIPDNIATIRREGSDHSSSFESKYM WTPSKQCGFCKKPHGNRFMVGCGRCDDWFHGDCVGLSLSQAQQM
- {	1		GEEDKEYVCVKCCAEEDKKTEILDPDTLENQATVEFHSGDKTME
1			CEKLGLSKHTTNDRTKYIDDTVKHKVKILKRESGEGRNSSDCRD
1			NEIKKWQLAPLRKMGQPVLPRRSSEEKSEKIPKESTTVTCTGEK
ļ			ASKPGTHEKQEMKKKKV\EKGVLNVHPAASASKPSADQIRQSVR
1	į.		HSLKDILMKRLTDSNLKVPEEKAAKVATKIEKELFSFFRDTDAK
j			YKNKYRSLMFNLKDPKNNILFKKVLKGEVTPDHLIRMSPEELAS
			KELAAWRRRENRHTIEMIEKEQREVERRPITKITHKGEIEIESD
			APMKEQEAAMEIQEPAANKSLEKPEGSEK\RKEEVDSMSKDTTS
			QHRQHLFDLNCKICIGRMAPPVDDLSPKKVKVVVGVARKHSDNE
1			AESIADALSSTSNILASEPFEEEKQESPKSTFSPAPRPEMPGTV
1			BVESTFLARLNFIWKGFINMPSVAKFVTKAYPVSGSPEYLTEDL
i			PDSIQVGGRISPQTVWDYVEKIKASGTKEICVVRFTPVTEEDQI
			SYTLLFAYFSSRKRYGVAANNNKQVKDMYLIPLGATDKIPHPLV PFDGPGLBLHRPNLLLGLIIRQKLKRQHSACASTSHIAETPESA
	l i		PPIALPPDKKSKIEVSTEEAPEEENDFFNSFTTVLHKQRNKPQQ
Į.			NLQEDLPTAVEPLMEVTKQEPPKPLRFLPGVLIGWENQPTTLEL
ĺ	! ·		ANKPLPVDDILQSLLGTTGQVYDQ\AQSVMEQNTVKBIPFLNEQ
1	.		TNSKIEKTDNVEVTDGENKEIKVKVDNISESTDKSARIETSVVG
i			SSSISAGSLTSLSLRGKPPDVSTEAFLTNLSIOSKOEETVESKE
			KTLKRQLQEDQENNLQDNQTSNSSPCRSNVGKGNIDGNVSCSEN
	1		LVANTARSPQFINLKRDPRQAAGRSQPVTTSESKDGDSCRNGEK
			HMLPGLSHNKEHLTEQINVEEKLCSAEKNSCVQQSDNLKVAQNS
			PSVENIQTSQAEQAKPLQEDILMQNIETVHPFRRGSAVATSHFE
1			VGNTCPSEFPSKSITFTSRSTSPRTSTNFSPMRPQOPNLOHLKS SPPGFPFPGPPNFPPQSMFGFPPHLPPPLLPPPGFG\FA\QNPM
1	1		VPWPPVV\HLP\GQPQRMMGPLSQASRYIGPQNFYQVKDIRRPE
Ī			RRHSDPWGRQDQQQLDRPFNRGKGDRQRFYSDSHHLKRERHEKE
ŀ			WEQESERHRRRDRSQDKDRDRKSREEGHKDKERARLSHGDRGTD
1			GKASRDSRNVDKKPDKPKSEDYEKDKEREKSKHREGEKDRDRYH
			KDRDHTDRTKSKR
5952	3226	639	PPARRSARDLPRALSMEAARPSGSWNGALCRLL\LVTL\AFLIF
			ASDACKNVTLHVPSKLDAEKLVGRVNLKECFTAANLIHSSDPDF
]			QILEDGSVYTTNTILLSSEKRSFTILLSNTENQEKKKIFVFLEH
1			QTKVLKKRHTKEKVLRRAKRRWAPIPCSMLENSLGPFPLFLQQV
]			QSDTAQNYTIYYSIRGPGVDQEPRNLFYVERDTGNLYCTRPVDR
	}		EQYESFEI1AFATTPDGYTPELPLPLIIKIEDENDNYPIFTEET YTFT1FENCRVGTTVGQVCATDKDEPDTMHTRLKYSIIGQVPPS
	. 1		PTLFSMHPTTGVITTT3SQLDRELIDKYQLKIKVQDMDGQYFGL
			QTTSTCIINIDDVNDHLPTFTRTSYVTSVEENTVDVEILRVTVE
	•	ì	DKDLVNTANWRANYTILKGNENGNFKIVTDAKTNEGVLCVVKPL
1	ł	l	NYEBKQQMILQIGVVNEAPFSREASPRSAMSTATVTVNVEDODE
j Í		l	GPECNPPIQTVRMKENAEVGTTSNGYKAYDPETRSSSGIRYKKI.
	1	İ	TDPTGWVTIDENTGSIKVFRSLDREAETIKNGIYNITVLASDOG
j			GRTCTGTLGIILQDVNDNSPFIPKKTVIICKPTMSSAEIVAVDP
1 1	. 1	ŀ	DEPIHGPPFDFSLESSTSEVQRMWRLKAINDTAARLSYQNDPPF
			GSYVVPITVRDRLGMSSVTSLDVTLCDCITENDCTHRVDPRIGG
	1		GGVCLGKWAILAILLGIALFFCILFTLVCGASGTSKQPKVIPDD
]		į	LAQQNLIVSNTEAPGDDXVYSANGFTTQTVGASAQGVCGTVGSG IKNGGQETIEMVKGGHQTSESCRGAGHHHTLDSCRGGHTEVDNC
	1		RYTYSEWHSFTQPRLGEESIRGHTLIKN
5953	330	811	PLLCNPDPGWYWWVKQESEISKESQEMDARPKLDLGFKEGQTIK
		_	LCIGNITNKKGGASKPRTARGGGLSLLPPPPGGKVTIPPPSS/V
			KLPSTNHVTPPSIPKSNHGGSDADILLDLDSPAPVTTPAPTPVS
			VSNDLWGDFSTASSSVPNQAPQPSNWVQF
5954	32	2130	PPPPPPKLANMADLEAVLADVSYLMAMEKSKATPAARASKRIVL
		ľ	PEPSIRSVMQKYLAERNEITFDKIFNQKIGFLLFKDFCLNEINE
			avpovkfyeeikeyekldnbedrlcrsrqiydayimkellscsh

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P-Proline, Q-Glutamine, R-Arginine
j	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	WaTryptophan, YaTyrosine, XaUnknown, *aSton
	amino acid	sequence	Codon, /=possible nucleotide deletion.
<u> </u>	sequence		\=possible nucleotide insertion)
1			PFSKQAVEHVQSHLSKKQVTSTLFQPYIEEICESLRGDIFOKPM
			ESDKFTRFCQWKNVELNIHLTMNEFSVHRIIGRGGFGEVYGCRK
ŀ			ADTGKMYAMKCLNKKRIKMKQGETLALNERIMLSLVSTGDCPFI
i			VCMTYAFHTPDKLCFILDLMNGGDLHYHLSQHGVFSBKEMRFYA
J	<b>j</b>		TEIILGLEHMHNRFVVYRDLKPANILLDEHGHARIS\DLGLACD
ţ			FSKKKPHASVGTHGYMAPEVLQKGTAYDSSADWFSLGCMLFKLL
l		:	RGHSPFRQHKTKDKHEIDRMTLTVNVELPDTFSPELKSLLEGLL
			CRDVSKRLGCHGGGSQEVKEHSFFKGVDWQHVYLQKYPPPLIPP
1			RGEVNAADAFDIGSFDEEDTKGIKLLDCDQELYKNFPLVISERW
-			QQEVTETVYEAVNADTDKIEARKRAKNKQLGHEEDYALGKDCIM
i			HGYMLKLGNPFLTQWQRRYFYLFPNRLEWRGEGESRQNLLTMEQ ILSVEETQIKDKKCILFRIKGGKQFVLQCESDPEFVQWKKELNE
	ì		TFKEAQRLLRRAPKFLNKPRSGTVELPKPSLCHRNSNGL
5955	1726	444	KREREFRLAVCPLRYPSAYESSPGTELRECGLCRSGQBFADCRR
			PANRODVLSGWINLPVLQLTKDPLKTPGRLDHGTRTAFIHHREQ
1	1		VWKRCINIWRDVGLFGVLNEIANSEEEVFEWVKTASGWALALCR
			WASSLHGSLFPHLSLRSEDLIAEFAQVTNWSSCCLRVFAWHPHT
			NKFAVALLDDSVRVYNASSTIVPSLKHRLORNVASLAWKPLSAS
	f .		VLAVACQSCILIWTLDPTSLSTRPSSGCAQVLSHPGHTPVTSLA
1	1		WAPSGGRLLSASPVDAAIRVWDVSTETCVPLPWFRGGGVTNLLW
			SPDGSKILATTPSAVFRVWEAQMWTCERWPTLSGRCQTGCWSPD
Į	:		GSRLLFTVLGEPLIYSLSFPERCGEGKG\ALEVQSQQRLWQICL
5956	1705	139	ROOYRHOMVRRGLGERLTPWSGTPVGNVWLCL
1		437	GVGVRGARAMATVQEKAAALNLSALHSPAHRPPGFSVAQKPFGA TYVWSSIINTLQTQVEVKKRRHRLKRHNDCFVGSEAVDVIFSHL
1 .	!		IQNKYFGDVDIPRAKVVRVCQALMDYKVFEAVPTKVFGKDKKPT
	1		FEDSSCSLYRPTTIPNQDSQLGKENKLYSPARYADALFKSSDIR
1	l.		SASLEDLWENLSLKPANSPHVNISATLSPQVINEVWQEETIGRL
1	l l		LQLVDLPLLDSLLKQQEAVPKIPQPKRQSTMVNSSNYLDRGILK
1 1			AYSDSQEDEWLSAAIDCSEYLPDOMVVEISRSFPEOPDRTDLVK
1			ELLFDAIGRYYSSREPLLNHLSDVHNGIAELLVNGKTEIALEAT
			QLLLKLLDFQNREEFRRLLYFMAVAANPSEFKLQKESDNRMVVK
1			RIFSKAIVDNKNLSKGKTDLLVLFL\MDHQKDVFKIPGTL\HKI
1			VS\VK\LMAIQNGRDPNRDAGYIYCQRIDQRDYSNNTEKTTKDE LLNLLKTLDEDSKLSAKEKKK\LLGQFYKCHFDIFIEHFGD
5957	1479	451	ELQVAVAMDTLDRVVKPKTKRAKRFLEKREPKLNENIKNAMLIK
! !			GGNANATVTKVLKDVYALKKPYGVLYKKKNITRPFEDQTSLEFF
1			SKKSDCSLFMFGSHNKKRPNNLVIGRMYDYHVLDMIELGIENFV
1 1	,		SLKDIKNSKCPEGTKPMLIFAGDDFDVTEDYRRLKSLLIDFFRG
1 1			PTVSNIRLAGLEYVLHFTALNGKIYFRSYKLLLKKSGCRTPRIE
] [	}		LEEMGPSLDLVLRRTHLASDDLYKLSMKMPKALKPKKKKNISHD
1		i	TFGTTYGRIHMQKQDLSKLQTRKM\KGLKKRPAERITEDHEKKS
5958	1	3,30	KRIKKKLMELSQPLLFHCVLLKRIIKHQSIQSFL
	· • •	3138	AAALGMLLWFPACQAFNLDVEKLTVYSGPKGSYFGYAVDFHTPD
			ARTASVLVGAPKANTSQPDIVEGGAVYYCPWPAEGSAQCRQIPF DTTNNRKIRVNGTKEPIEFKSNQWFG\ATVKA\HKGKSCGPVAP
	ĺ		LLFTWRNFLKPTPEKGPVGTCYVAIQNFSAYAEFSPCGNSNADP
]			EGGGYCQAGFSLDFYKNGDLIVGGPGSFYWQGQVITASVADIIA
1 1		ľ	NYSFKDILRKLAGEKQTEVAPASYDDSYLGYSVAAGEFTGDSQQ
l I		İ	ELVAGIPRGAQNFGYVSIINSYDMTFIQNFTGEQMASYFGYTVV
1 1		Ĭ	VSDVNSDGLDDVLVGAPLFMEREFESNPREVGOIYLYLOVSSLL
i I		1	FRDPQILTGTETFGRFGSAMAHLGDLNQDGYNDIAIGVPFAGKD
1 1		Ì	QRGKVLIYNGNKDGLNTKPFPKFCOGVWASHAVPSGFGFTLRGD
	ſ	1	SDIDKNDYPDLIVGAFGTGKVAVYRARPVVTVDAQLLLHPMIIN
		[	LENKTCQVPDSMTSAACFSLRVCASVTGQSIANTIVLMAEVQLD
		1	SLKQKGAIKRTLFLDNHQAHRVFPLVIKRQKSHQCQDFIVYLRD
			ETEFRDKLSPINISLNYSLDESTFKEGLEVKPILNYYRENIVSE QAHILVDCGEDNLCVPDLKLSARPDKHOVIIGDENHLMLIINAR
	1	1	NEGEGAYEAELFVMIPEEADYVGIERNNKGFRPLSCEYKMENVT
	Ī		RMVVCDLGNPMVSGTNYSLGLRFAVPRLEKTNMSINFDLQIRSS
<u></u>			NKDNPDSNFVSLQINITAVAQVEIRGVSHPPQIVLPIHNWEPEE
*			

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A-Alanine, C-Cysteine, D-Aspartic Acid, E-
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
J	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine.
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine.
l l	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
İ	sequence	sequence	Codon, /-possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
Į			EPHKEEEVGPLVEHIYELHNIGPSTISDTILEVGWPFSARDEFL
- (	1		LYIFHIQTLGPLQCQPNPNINPQDIKPAASPEDTPELSAFLRNS TIPHLVRKRDVHVVEFHRQSPAKILNCTNIECLQISCAVGRLEG
1			GESAVLKVRSRLWAHTFLQRKNDPYALASLVSFEVKKMPYTDQP
			AKLPEGSIAIKTSVIWATPNVSFSIPLWVIILAILLGLLVLAIL
			TLALWKCGFFDRARPPQEDMTDREQLTNDKTPEA
5959	1	1166	GTSGYAAQQLPSLLKEREFHLGTLNKVFASQWLNHRQVVCGTKC
1			NTLFVVDVQTSQITKIPILKDREPGGVTQQGCGIHAIELNPSRT
ĺ			LLATGGDNPNSLAIYRLPTLDPVCVGDDGHKDWIFSIAWISDTM
1			AVSGSRDGSMGLWEVTDDVLTKSDARHNVSRVPVYAHITHKALK
İ			DIPKEDTNPDNCKVRALAFNNKNKELGAVSLDGYFHLWKAENTL
1			SKLLSTKLPYCRENVCLAYGSEWSVYAVGSQAHVSFLDPROPSY
1	ł		NVKSVCSRERGSGIRSVSFYEHIITVGTGQGSLLFYDIRAQRFL
1	[		EERLSACYGSKPRLAGENLKLTTG\KGWLNHDETWRNYFSDIDF
5960	2853	870	FPNAVYTHCYDSSGTXLFVAGGPLPSGLHGNYAGLWS
	1 2033	670	FVWSDGGPRPRRGPAVGAGAAHLSDPWAMTPGTANRATNPLNKE
i			LDWASINGFCEQLNEDFEGPPLATRLLAHKIQSPQEWEAIQALT VLETCMKSCGKRFHDEVGKFRFLNELIKVVSPKYLGSRTSEKVK
1			NKILELLYSWTVGLPEEVKIAEAYQMLKKQG\IVKSDPKLPDDT
}	İ		TFPLPPPRPKNVIFEDEEKSKMLARLLKSSHPEDLRAANKLIKE
			MVQEDQKRMEKISKRVNAIEEVNNNVKLLTEMVMSHSQGGAAAG
			SSEDL\MKEL\YQRCERMRPTLFPTGRVDTEDND\EALAEILOA
			NDNLTQVINLYKQLVRGEEVNGDATAGSIPGSTSALLDLSGLDL
			PPAGTTYPAMPTRPGEQASPEQPSASVSLLDDELMSLGLSDPTP
1 1			PSGPSLDGTGWNSFQSSDATEPPAPALAQAPSMESRPPAQTSLP
			ASSGLDDLDLLGKTLLQQSLPPESQQVRWEKQQPTPRLTLRDLQ
1 -			NXSSSCSSPSSSATSLLHTVSPEPPRPPQQPVPTELSLASITVP
1 1			LESIKPSNILPVTVYDQHGFRILFHFARDPLPGRSDVLVVVVSM LSTAPQPIRNIVFQSAVPKVMKVKLQPPSGTELPAFNPIVHPSA
1 1			ITQVLLLANPQKEKVRLRYKLTFTMGDQTYNEMGDVDQFPPPET
			WGSL WGSL
5961	198	3147	SGEPRPEPGNMATCIGEKIEDFKVGNLLGKGSFAGVYRAESIHT
,	-		GLEVAIKMIDKKAMYKAGMVQRVQNEVKIHCQLKHPSILELYNY
]	i		FEDSNYVYLVLEMCHNGEMNRYLKNRVKPFSENEARHFMHOIIT
1	ĺ		GMLYLHSHGILHRDLTLSNLLLTRNMNIKIADFGLATQLKMPHE
) )			KHYTLCGTPNYISPEIATRSAHGLESDVWSLGCMFYTLLIGRPP
1 1	İ		FDTDTVKNTLNKVVLADYEMPTFLSIEAKDLIHQLLRRNPADRL
1			SLSSVLDHPFMSRNSSTKSKDLGTVEDSIDSGHATISTAITASS STSISGSLFDKRRLLIGQPLPNKMTVFPKNKSSTDFSSSGDGNS
1 1			FYTOWGNQETSNSGRGRVIQDAEERPHSRYLRRAYSSDRSGTSN
1			SOSOAKTYTMERCHSAEMLSVSKRSGGGENEERYSPTDNNANIF
1	ľ	İ	NFFKEKTSSSSGSFERPDNNQALSMHLCPGKTPFPFADPTPQTE
1			TVQQWFGNLQINAHLRKTTEYDSISPNRDFOGHPDLOKDTSKNA
l i			WIDTKVKKNSDASDNAHSVKQQNTMKYMTALHSKPEIIQQECVF
			GSDPLSEQSKTRGMEPPWGYQNRTLRSITSPLVAHRLKPIROKT
	İ		KKAVVSILDSEEVCVELVKEYASQEYVKEVLQISSDGNTITIYY
]	ł	j	PNGG\RGFPLA\DRPPSPT\DNISR\YSF\DNLPEKYWRKYQYA
	ĺ		SRFVQLVRSKSPKITYFTRYAKCILMENSPGADFEVWFYDGVKI
			HKTEDFIQVIEKTGKSYTLKSESEVNSLKEEIKMYMDHANBGHR ICLALESIISEEERKTRSAPFFPIIIGRKPGSTSSPKALSPPPS
		1	VDSNYPTRDRASFNRMVMHSAASPTQAPILNPSMVTNEGLGLTT
	ĺ	1	TASGTDISSNSLKDCLPKSAQLLKSVFVKNVGWATQ\LTSGAVW
ļ l		Į.	VQFNDGSQLVVQAGVSSISYTSPNGQ\TTR\YGENEKLPDYIKQ
			KLQCLSSILLMFSNPTPNFH
5962	20	2447	RVCSSSASTASQAVMADAWEETRRLAADFQRAQFAEATQRLSER
		į	NCIEIVNKLIAQKQLEVVHTLDGKEYITPAOISKEMRDELHVRG
			GRVNIVDLQQVINVDLIHIBNRIGDIIKSEKHVOLVLGOLIDEN
		1	YLDRLAEEVNDKLQESGQVTISELCKTYDLPGNFLTOALTORLG
			RIISGHIDLDNRGVIFTEAFVARHKARIRGLFSAITRPTAVNSL
	1	1	ISKYGFQEQLLYSVLEELVNSGRLRGTVVGGRODKAVFVPDIYS
<u> </u>	<u>1.</u>		RTQSTWVDSFFRQNGYLEFDALSRLGIPDAVSYIKKRYKTTQLL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
aı	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F-Phenylalanine G-Glycine
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine.
İ	to first amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine.
	residue of	residue of	S=Serine, T=Threonine, V=Valine,
	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	sequence	Codon, /=possible nucleotide deletion,
			\=possible nucleotide insertion)  FLKAACVGQGLVDQVEASVEEAISSGTWVDIAPLLPTSLSVEDA
1			ALLLQQVMRAFSKQASTVVFSDTVVVSEKF\INDCTELFRELMH
	1	1	QKAEKEMKNNPVHLITEEDLKQISTLESVSTSKKDKKDERRRKA
	}	I	TEGSGSMRGGGGGNAREYKIKKVKKKGRKDDDSDDESQSSHTGK
			KKPEISFMFQDEIEDPLRKHIQDAPEEFISELAEYLIKPLNKTY
			LBVVRSVFMSSTTSASGTGRKRTIKDLQEEVSNLYNNIRLFEKG
		ŀ	MKFFADDTQAALTKHLLKSVCTDITNLIFNFLASDLMMAVDDPA
1		İ	AITSEIRKKILSKLSEETKVALTKLHNSLNEKSIEDFISCLOSA
i		(	ARACDIMVKRGDKKRERQILFQHRQALAEQLKVTEDPALILHLT
1			SVLLFQFSTHSMLHAPGRCVPQIIAFLNSKIPEDOHALLVKYOG
ı			LVVKQLVSQSKKTGQGDYPLNNELDKEQEDVASTTRKELQELSS
5963	62		SIKDLVLKSRKSSVTEE
	1	1130	PWNPQDFPGNRGLMG\QKGEIGPP\GQQGKKGAPGMP\GLMGSN
1		Ī	GSPGQPGTPGSKGSKGEPGIQGMPGASGLKGEPGATGSPGEPGY
1		,	MGLPGIQGKKGDKGNQGEKGIQGQKGENGRQGIPGQQGIQGHHG AKGERGEKGEPGVRGAIGSKGESGVDGLMGPAGPKGQPGDPGPQ
			GPPGLDGKPGREFSEQFIRQVCTDVIRAQLPVLLQSGRIRNCDH
}	l		CLSQHGSPGIPGPPGPIGPEGPRGLPGLPGRDGVPGLVGVPGRP
	[		GVRGLKGLPGRNGEKGSQGFGYPGEOGPPGPPGPEGPPGTSKEG
1			PPGDPGLPGKDGDHGKPGIQGQPGPPGICDPSLCFSVIARRDPF
5964			RKGPNY
5964	3	2147	SCRTRGRLSPLQPREAGSSRGSRARSEPPRFGGMEEACQVQTTK
			RGDPHELRNIFLQYASTEVDGERYMTPEDFVORYLGLYNDPNSN
1			PKIVQLLAGVADQTKDGLISYQEFLAFESVLCAPDSMFIVAFQL
	ļ		FDKSGNGEVTFENVKBIFGQTIIHHHIPFNWDCEFIRLHFGHNR
ł			KKHLNYTEFTQFLQELQLEHARQAFALKDKSKSGMISGLDFSDI
1			MVTIRSHMLTPFVEENLVSAAGGSISHQVSFSYFNAFNSLLNNM ELVRKIYSTLAGTRKDAEVTKEEFAQSAIRYGQATPLEIDILYQ
			LADLYNASGRUTLADIERIAPLAEGALPYNLAELQRQQSPGLGR
			PIWLQIAESAYRFTLGSVAGAVGATAVYPIDLVKTRMQNQRGSG
ļ			SVVGELMYKNSFDCFKKVLRYEGFFGLYRGLIPOLIGVAPEKAI
			KLTVNDFVRDKFTRRDGSVPLPAEVLAGGCAGGSOVIFTNPLEI
			VKIRLQVAGEITTGPRVSALNVLRDLGIFGLYKGAKACFLRDIP
	1		FSAIYFPVYAHCKLLLADENGHVGGLNLLAAGAMAG\VPAASLV
i	j		TPADVIKTRLQVAARAGQTTYSGVIDCFRKIL\REEGPSAFWKG
[			TAARVFRSSPQFG\VTLVTYELLQRGPYIDFGGLKPAGSEPTPK
	1		SRIADLPPANPDHIGGYRLATATFAGIENKFGLYLPKFKSPSVA VVQPKAAVAATO
5965	1	1498	WVTWLYRFLPTSNMAAKLRSLLPPDLRLQFWLHARLQKCFLSRG
			CGSYCAGAKASPLPGKMAMGLMCGRRELLRLLQSGRRVHSVAGP
[			SQWLGKPLTTRLLFPAAPCCCRPHYLFLAASGPRSLSTSAISFA
			EVQVQAPPVVAATPSPTAVPEVASGETADVVQTAAEQSFAELGL
	}		GSYTPVGLIQNLLEFMHVDLGLPWWGAIAACTVFARCLIFPLIV
		1	TGQREAARIHNHLPEIQKFSSRIREAKLAGDHIEYYKASSEMAL
	Ì		YQKKHGIKLYKPLILPVTQAPIFISFFIALREMANLPVPSLOTG
	į	l	GLWWFQDLTVSDPIYILPLAVTATMWAVLELGAETGVOSSDLOW
	ļ.		MRNVIRMMPLITLPITMHFPTAVFMYWLSSNLFSLVQVSCLRIP
İ			AVRTVLKI PORVVHDLDKLPPREGFLESFKKGWKNAEMTROLRE
ĺ			REQRMRNQLELAARGPLRQTFTHNPLLQPGKDNPPNIPSS\SSS SSKPKSKYPWHDTLG
5966	102	1925	
			RSKQVMARLTKRRQADTKAIQHLWAAIEIIRNQKQIANIDRITK
1	1	}	YMSRVHGMHPKETTRQLSLAVKDGLIVETLTVGCKGSKAGIEQE GYWLPGDBIDWETENHDWYCFECHLPGEVLICDLCFRVYHSKCL
ł			SDEFRLRDSSSPWQCPVCRSIKKKNTNKQEMGTYLRFIVSRMKE
			RAIDLNKKGKDNKHPMYRRLVHSAVDVPTIQEKVNEGKYRSYEE
	İ	j	PKADAQLLLHNTVIFYGADSEQADIARMLYKDTCHEL\DELQLC
	1		KNCFYLANARPDNWFCYPCIPNHELDWAKMKGFGFWPAKVMOKE
- 1	1	1	DNQVDVRFFGHHHQRAWIPSENIQDITVNIHRLHVKRSMGWKKA
		1	CDELELHQRFLREGRFWKSKNEDRGEEEAESSISSTSNEOLKVT
ŀ	į		QEPRAKKGRRNQSVEPKKEEPEPETEAVSSSQEIPTMPOPIEKV
			SVSTQTKKLSASSPRMLHRSTQTTNDGVCQSMCHDKYTKIFNDF

	SEC	Predicted	Predicted end	
i	ID		nucleotide	
	NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1		location	corresponding	Glutamic Acid, F-Phenylalanine, G-Glycine,
		corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
		to first	amino acid	P-Proline, Q-Glutamine, R-Arginine,
		amino acid	residue of	S=Serine, T=Threonine, V=Valine,
١		residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
- 1		amino acid	sequence	Codon, /=possible nucleotide deletion,
		sequence		\=possible nucleotide insertion)
- 1				KDRMKSDHKRETERVVREALEKLRSEMEEEKRQAVNKAVANMQG
- 1		İ	1	EMDRKCKQVKEKCKEEFVEEIKKLATQHKQLISQTKKKQWCYNC
Ļ				BEEAMYHCCWNTSYCSIKCQQEHWHAEHKRTCRRKR
	5967	102	1925	RSKQVMARLTKRRQADTKAIQHLWAAIEIIRNQKQIANIDRITK
				YMSRVHGMHPKETTROLSLAVKDGLIVETLTVGCVGCVAGTEOR
ı			1	GIWLPGDEIDWETENHDWYCFECHLPGEVI.ICDI.CEPVVUCVCI.
- 1				SUBFRERUSSSPWQCPVCRSIKKKNTNKOEMGTVIDETVERMVE
- [		1	l	KAIDLNKKGKDNKHPMYRRLVHSAVDVPTIOEKINEGVVDCVPC
-			1	FRADAQUILLHNTVIFYGADSEOADIARMLYKDTCHELADRIOLC
-		1		KNCFYLANARPDNWFCYPCIPNHELDWAKMKGEGEWDAVIMOVP
- 1				UNQVDVRFFGHHHQRAWIPSENIODITVNIHRIHUKPSMCWVVA
- 1				CDELELHQRFLREGRFWKSKNEDRGREEAESSISSISSISSISSI
-				QEPRAKKGRRNQSVEPKKEEPEPETEAVSSSOETPTMPODTPVV
1				SVSTQTKKLSASSPRMLHRSTQTTNDGVCQSMCHDKYTKIFNDF
		i		KDRNKSDHKRETERVVREALEKLRSEMEEEKRQAVNKAVANMQG
1		1		EMDRKCKQVKEKCKEEFVEEIKKLATQHKQLISQTKKKQWCYNC
Г	5968	81	1288	EEEAMYHCCWNTSYCSIKCQQEHWHAEHKRTCRRKR
1				VRFPRRGGAPPTVLTPGRQQGVFLGPQRPGSEPDIPARGQPHPP RPVGVSTSAQAQVQPPAMHRRRLALGLGFCLLACTSLSVLWVYL
		1		ENWLPVSYVPYYLPCPEIFNMKLHYKREKPLQPVVWSQYPQPKL
Ĺ				LEHRPTQLLTLTPWLAPIVSEGTFNPELLQHIYQPLNLTIGVTV
1				FAVGN/HFLESAEEFFMRGYRVHYYIFTDNPAAVPGVDICDUDI
				LSSIPIQGHSHWEETSMRRMETISOHIAKRAHREVDYLECLDVD
Т		1		MVFKNPWGPETLGDLVAAIHPSYYAVPROOFDVEDDDUGTAEVA
				DSEGDFYYGGAVFGGQVARVYEFTRGCHMAILADKANGIMAAWD
		1		LESHLARRISAKPSKVLSPEYLWDDRKPOPPSLKLIRFSTLDK
1	5969	1126	503	DISCLES
1			503	DVGFNIKRKRCDLDVFLESPRKPSGRRDRAPEKQRRIAANKCLC
				TGVREGEPPS/TTSQKVKEAGRDFTYLIVVLFGISITGGLFYTI FKELFSSSSPSKIYGRALEKCRSHPEVIGVFGESVKGYGEVTRR
1		1 1	i	GRRQHVRFTEYVKDGLKHTCVKFYIEGSEPGKQGTVYAQVKENP
$\vdash$	5970			GSGEYDFRYIFVEIESYPRRTILIEDNRSQDD
	59/0	316	4712	SQDNIGHRLLQKHGWKLGOGLGKSLOGRTDPTDTVVVVDVMCMC
				RMEMELDYAEDATERRRVLEVEKEDTEELROKVKDVDVEVA TA
1		1 1		KALEDLRANFYCELCDKOYOKHOEFDNHINSVOHAHKODI VDI V
				QREFARNVSSRSRKDEKKOEKALRRLHELAFORKOARCADGGCD
		l i		MFKPTTVAVDEEGGEDDKDESATNSGTGATASCGLGSEFSTDKG
İ		1		GPFTAVQITNTTGLAQAPGLASQGISFGIKNNLGTPLQKLGVSF
ĺ			ĺ	SFAKKAPVKLESIASVFKDHABEGTSEDGTKPDERSSDQGLQKV GDSDGSSNLDGKKEDEDPQDGGSLASTLSKLKRMKREEGAGATE
ı			ŀ	PEYYHYIPPAHCKVKPNFPFLLFMRASEQMDGDNTTHPKNAPES
[			l	KKGSSPKPKSCIKAAASQGAEKTVSEVSEQPKETSMTEPSEPGS
ļ		1 1	•	KAEAKKALGGDVSDOSLESHSOKVSETOMCEGNGOVDDGCANDA
ſ		1: 1		GKESQEGPKHPTGPFFPVLSKDESTALOWPSPLLTETVARDOTC
		1	- 1	ISCNPLIFUFKLSRNKDARTKGTEKPKDIGSSSKDUTOGLDDGR
				PRESERVEGERIVESSGGRMDAPASGSACSGINKORDGGGUGGE
				TEDTGRSLPSKKERSGKSHRHKKKKKKKKKKSSKHVPKHVADTERV
			1	SSKAESGEKSKKRKKRKRKKNKSSAPADSRRGDKDFDDGGCGDD
		1	· · · · · · · · · · · · · · · · · · ·	PPRRRRAQDDSQRRSLPAEEGSSGKKDEGGGGGGGGODUGGDW
			i	KGELPPSSCQRRAGTKRSSRSSHRSOPSSGDEDGDDASGUDLUG
		1	4	KSPSQYSEEEEEDSGSEHSRSRSRSGRRHSSHRSSDRSVeee
			1 .	DASSDQSCYSRQRSYSDDSYSDYSDRSRRHSKPSHDSDDSDVAG
			f :	SKHRSKRHKYSSSDDDYSLSCSOSRSRSRSRTPEPSPSPSPSPS
	- 1		] -	SSCSKSKSKRKSRSTTAHSWORSRSYSRDRSRSTPSDSODECED
	ĺ	ŀ		KRSWGHESPEERHSGRRDFIRSKIYRSQSPHYFRSGRGEGPGKK DDGRGDDSKATGPPSQNSNIGTGRGSEGDCSPEDKNSVTAKLLL
	- 1	!	15	EKIQSRKVERKPSVSEEVQATPNKAGPKLKDPPQGYFGPKLPPS
	1		ĺi	LGNKPVLPLIGKLPATRKPNKKCBESGLERGEBQEQSETEBGPP
	Į	ļ	(	SSUALFGHQFP\SEETTGPLLDPPPEESK9GRVTADHDVARIC
	[		1 2	PAHFDCYLGDPTISHNYLPDPSDGNTLESLDSSSOPGDVPSSI
			1	PIAPDLEHFPSYAPPSGDPSIESTDGAEDA\SLAPLESQPITF

SEQ	Predicted	Predicted end	I mino political
ID	beginning	nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
}	location	corresponding	H-Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L-Leucine, M-Methionine, N-Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ı	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
İ	amino acid	sequence	Codon, /=possible nucleotide deletion
	sequence	L	\=possible nucleotide insertion)
- 1			TPEEMEKYSKLQQAAQQHIQQQLLAKOVKAFPASAALAPATDAL
		j [*]	QPIHIQQPATASATSITTVQHAILOHHAAAAAAATGTHDHDHDO
1		!	PLAQVHHIPQPHLTPISLSHLTHSIIPGHPATPIASHDTUTTDA
1	1	J	SAIHPGPPTFHPVPHAALYPTLLAPRPAAAAATALHLHPLLHPI
5971			FSGQDLQHPPSHGT
33/1	53	2149	SFLYFVGVDMDNPIGNWDGRFDGVQLCSFACVESTILLHINDII
ŀ	i		PESVIQERRPPKLAFMSRGVGDKGSSSHNKPKATGSTSDDGNPN
}			RSELFYTLNGSSVDSQPQSKSKNTWYIDEVAEDPAKSLTEISTD
ŀ		'	FDRSSPPLQPPPVNSLTTENRFHSLPFSLTKMPNTNGSTGHSDI.
1			SLSAQSVMEELNTAPVQESPPLAMPPGNSHGLEVGSLAEVKEND
			PFYGVIRWIGQPPGLNEVLAGLELEDECAG\CTDGTF/REGTRY
1	İ		FTCALKKALFVKLKSCRPDSRFASLQPVSNQIERCNSLAIWEAY
1	1		LSEVVEENTPTQKWEKEGLEIMIG\KKKGIQGHYNSCYLDSTLF
ł	1		CLFAFSSVLDTVLLRPKEKNDVEYYSETQELLRTEIVNPLRIYG
			YVCATKIMKLRKILEKVEAASGFTSEEKDPEEFLNILPHHILRV
ł	l i		EPLLKIRSAGQKVQDCYFYQIFMEKNEKVGVPTIQQLLEWSFIN
i			SNLKFAEAPSCLIIQMPRFGKDFKLFKKIFPSLELNITDLLEDT PRQCRICGGLAMYECRECYDDPDISAGKIKQFCKTCNTQVHLHP
1	J		KRLNHKYNPVSLPKDLPDWDWRHGCIPCQNMELFAVLCIETSHY
1	!		VAFVKYGKDDSAWLFFDSMADRDGGQNGFNIPQVTPCPEVGEYL
L	L		KMSLEDLHSLDSRRIQGCARRLLCDAIYVPCTQSPTMSLYK
5972	440	1761	ILLAGSPSPRDQCSQRQSSGGDKELVTRGCTFSTAVVSPSAMTQ
1			EPFREELAYDRMPTLERGRQDPASYAPDAKPSDLQLSKRLPPCF
1			SHKTWVFSVLMGSCLLVTSGFSLYLGNVFPAEMDYLRCAAGSCI
		•	PSAIVSFTVSRRNANVIPNFOILFVSTFAVTTTCI.TWFCCVI.VI.
i l	!		NPSAININFNLILLLLELLMAATVIIAARSSEEDCKKKKGGMG
1 1			DSANILDEVPFPARVLKSYSVVBVIAGISAVLGGITALNVDDGV
1 !	1		SGPHLSVTFFWILVACFPSAIASHVAAECPNKCLVRVLTAISSI
1 1			TSPLLFTASGYLSFSIMRIVEMFKDYPPATKPSYDVI.I.I.I.I.I.
1 1			LLLQA/GPQHGHRHPVRALOGOCKAAGCTLGHPEPPAGAPGWCC
i i			GQEPPEGVRQGESLESRRGANGPVTPRRGNRVAAPSLAPGMETH
5973	65	· 2007	NCDCVDL ECHLORUS AND AND AND AND AND AND AND AND AND AND
1	1		NGDGKDLFGHIWAWRSNGIISNFRRSPHAGMAEDEPDAKSPKTG GRAPPGGAEAGEPTTLLQRLRGTISKAVQNKVEGILQDVQKFSD
1	1		NDKLYLYLQLPSGPTTGDKSSEPSTLSNEEYMYAYRWIRNHLEE
			HTDTCLPKQSVYDAYRKYCESLACCRPLSTANFGKIIREIFPDI
1	1		KARRLGGRGQSKYCYSGIRRKTLVSMPPLPGLDLKGSESPEMGP
1 1			EVTPAPRDELVEAACALTCDWAERILKRSFSSIVEVARFLLQQH
1 1			LISARSAHAHVLKAMGLAEEDEHAPRERSSKPKNGLENPEGGAH
			KKPERLAQPPKDLEARTGAGPLARGERKKSVVESSADGANNLOV
1 1			NALVARLPLLLPRAPRSLIPPIPVSPPILAPRISSGALVUATER
}	· ·		LSSRAGAPPAAVPIINMILPTVPALPGPGPGPGPGRAPPGGITOPP
] ]	,		GIENKEVGIGGDQGPHDKGVKRTAEVDVSEASGOADDAKAAKOD
i i	1		IEDTASDAKRKRGRPLKKSGGSGERNSTPI.KSAAAMESAOCCHT.
	1	. 1	PWETWGSGGEGNSAGGAERPGPMGFARKGAVI.AOG\ OGDGTUGY
		1	GGRGPGSQHTKEAEDKIPLVPSKVSVIKGSRSOKEAFPLAKGEV
5974	4293	2222	DTAPUGNKDLKEHVLQSSLSQEHKDPKATPP
	1275	2200	LGLQMHTTSGRIHQAMVTSLNEDNESVTVEWIENGDTKGK\BID
1		1	LESIFSLNP\DL\VPDGEIEPSP\ETPPPPASSAKVNKIVKNRR
ł		l	TV\ASIKNDPPS\RDNRVVGSARARPSQFPEQFSSAQQNGSV\S
			DISPVQAAKKEFGPPSRRKSNCVKEVEKLQEKREKRRLQQQELR
			EKRAQDVDATNPNYEIMCMIRDFRGSLDYRPLTTADPIDEHRIC
			VCVRKRPLNKKETOMKDLDVITIPSKDVVMVHEPKQKVDLTRYL ENOTEREDYAEDDSAEDEMANNETARDIVETARDIVETARDIVETARDIVETARDIVETARDIVETARDIVETARDIVETARDIVETARDIVETARDIVETARDIVETARDIVETARDIVETARDIVETARDIVETARDIVETARDIVETARDIVETARDIVETARDIVETARDI
ŀ			ENOTFRFDYAFDDSAPNEMVYRFTARPLVETIFERGMATCFAYG OTGSGKTHTMGGDFSGKNQDCSKGIYALAARDVFLMLKKPNYKK
j	1		LELQVYATFFEIYSGKVFDLLNRKTKLRVLEDGKQQVQVVGLQE
1		1	REVKCVEDVLKLIDIGNSCRTSGQTSANAHSSRSHAVFQIILRR
1	1	}	KGKLHGKFSLIDLAGNERGADTSSADRQTRLEGAEINKSLLALK
]	1	į	ECIRALGRNKPHTPFRASKLTQVLRDSFIGENSRTCMIATISPG
1	1	1	MASCENTLNTLRYANRVKELTVDPTAAGDVRPIMHHPPNOT\DD
			LETQWGVGSSPQRDDLKLLCEQNEEEVSPQLFTFHEAVSQMVEM

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
İ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ĺ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ĺ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
l	sequence	ļ	\=possible nucleotide insertion)
			EEQVVEDHRAVFQESIRWLEDEKALLEMTEEVDYDVDSYATQLE
			AILEQKIDILTELRDKVKSFRAALQEEEQASKQINPKRPRAL
5975	4293	2200	LGLOMHTTSGRIHQAMVTSLNEDNESVTVEWIENGDTKGK\EID
1		1	LESIFSLNP\DL\VPDGEIEPSP\ETPPPPASSAKVNKIVKNRR
1			TV\ASIKNDPPS\RDNRVVGSARARPSQFPEQFSSAQQNGSV\S
1	ľ		DISPVQAAKKEFGPPSRRKSNCVKEVEKLQEKREKRRLQQQELR
			EKRAQDVDATNPNYEIMCMIRDFRGSLDYRPLTTADPIDEHRIC
1		<u>'</u>	VCVRKRPLNKKETQMKDLDVITIPSKDVVMVHEPKQKVDLTRYL
1		ļ	ENQTFRFDYAFDDSAPNEMVYRFTARPLVETIFERGMATCFAYG
1	·		QTGSGKTHTMGGDFSGKNQDCSKGIYALAARDVFLMLKKPNYKK
		İ	LELQVYATFFEIYSGKVFDLJ.NRKTKLRVLEDGKQQVQVVGLQE
}	'		REVKCVEDVLKLIDIGNSCRTSGQTSANAHSSRSHAVFOIILRR
l			KGKLHGKFSLIDLAGNERGADTSSADRQTRLEGAEINKSLLALK
			ECIRALGRNKPHTPFRASKLTQVLRDSFIGENSRTCMIATISPG
			MASCENTLNTLRYANRVKELTVDPTAAGDVRPIMHHPPNOI\DD
[			LETQWGVGSSPQRDDLKLLCEQNEEEVSPQLFTFHEAVSQMVEM
			EEQVVEDHRAVFQESIRWLEDEXALLEMTEEVDYDVDSYATQLE
			AILEQKIDILTELRDKVKSFRAALQEEEQASKQINPKRPRAL
5976	20	2949	VHHLHLTRVSVVVNLDIILRIAQQMGIKTLNLVLG\LKRA\LEF
		į.	PEVSWMEVKDPNMKGAMLTNTGKYAIPTIDA\EAYAIGKKEKPP
1		:	FLPEEPSSSSEEDDPIPDELLCLICKDIMTDAVVIPCCGNSYCD
1			BCIRTALLESDEHTCPTCHQNDVSPDALIANKFLRQAVNNFKNE
			TGYTKRLRKQLPSPPPPIPPPRPLIQRNLQPLMRSPISRQQDPL
		•	MIPVTSSSTHPAPSISSLTSNQSSLAPPVSGNPSSAPAPVPDIT
			ATVSISVHSEKSDGPFRDSDNKILPAAALASEHSKGTSSIAITA
1 1		•	LMEEKGYQVPVLGTPSLLGQSLLHGQLIPTTGPVRINTARPGGG
}			RPGWEHSNKLGYLVSPPQQIRRGERSCYRSINRGRHHSERSQRT
1			CGPSLPATPVFVPVPPPPLYPPPPHTLPLPPGVPPPQFSPQFPP
}			GQP\PPAGYSVPPPGFPPAPANLSTPWVSSGVQTAHSNTIPTTQ
1			APPLSREEFYREQRRLKEEEKKKSKLDEFTNDFAKELMEYKKIQ
[			KERRRSFSRSKSPYSGSSYSRSSYTYSKSRSGSTRSRSYSRSFS
}			RSHSRSYSRSPPYPRRGRGKSRNYRSRSRSHGYHRSRSRSPPYR
l i	ĺ		RYHSRSRSPQAFRGQSPNKRNVPQGETEREYFNRYREVPPPYDM
1		•	KAYYGRSVDFRDPFEKERYREWERKYREWYEKYYKGYAAGAQPR
1 1			PSANRENFS PERFI, PLNIRNS PFTRGREDYVGGQSHRSRNIGS
1 1			NYPEKLSARDGHNQKDNTKSKEKESENAPGDGKGNKHKKHRKRR KGEESEGFLNPELLETSRKSREPTGVEENKTDSLFVLPSRDDAT
1			PVRDEPMDAESITFKSVSEKDKRERDKPKAKGDKTKRKNDGSAV
1 1			SKKENIVKPAKGPQEKVDG\DVRDLLDLNL\QLKKPKEETPKDL
	,		TILNHHLPLRRMKKSL\EPP\EKLTLNQQK\TPRNKTSQRGKSE
1 1		'	EGLFQRCQIRKANN
5977	1363	1336	FLEDRGQVLSHFQCLSLHSINHILHPGAGVAAGPATGW/REYLT
1			PVLKESKFKETGVITPEEFVAAGDHLVHHCPTWQWATGEELKVK
	İ		AYLPTGKQFLVTKNVPCYKRCKQMEYSDELEAIIEEDDGDGGWV
			DTYHNTGITGITEAVKEITLENKDNIRLQDCSALCEEEEDEDEG
]	1		EAADMEEYEESGLLETDEATLDTRKIVEACKAKTDAGGEDAILQ
(	ļ	ĺ	TRTYDLYITYDKYYQTPRLWLFGYDEQRQPLTVEHMYEDISQDH
	Ì		VKKTVTIENHPHLPPPPMCSVHPCRHAEVMKKIIETVAEGGGEL
			GVHMYLLIFLKFVQAVIPTIEYDYTRHFTM
5978	160	3213	RDGARRWGGCQSPLTWAPGFYRRFDLATSGRRLRGQTAEPAGRQ
		Į	RPRREPEAMDEQSVESIAEVFRCFICMEKLRDARLCPHCSKLCC
	Į		FSCIRRWLTEQRAQCPHCRAPLQLRELVNCRWABEVTQQLDTLQ
	· 1		LCSLTKHEENEKDKCENHHEKLSVFCWTCKKCICHQCALWGGMH
			GGHTFKPLAEIYBQHVTKVNEEVAKLRRRLMELISLVQEVERNV
			EAVRNAKDERVRBIRNAVEMMIARLDTQLKNKLITLMGQKTSLT
	J		QETELLESLLQEVEHQLRSCSKSELISKSSEILMMFQQVHRKPM
			ASFVTTPVPPDFTSELVPSYDSATFVLENFSTLRQRADPVYSPP
		ļ	LQVSGLCWRLKVYPDGNGVVRGYYLSVFLELSAGLPETSKYEYR
,		}	VEMVHQSCNDPTKNIIREFASDFEVGECWGYNRFFRLDLLANEG
			YLNPONDTVILRPOVRSPTFFQKSRDQHWYITQLEAAQTSYIQQ
			INNLKERLTIELSRTQKSRDLSPPDNHLSPQNDDALETRAKKSA

SEQ	Predicted	Predicted end	Amino acid promont contact
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine.
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown *-Ston
1	amino acid	sequence	Codon, /=possible nucleotide deletion
	sequence		\=possible nucleotide insertion)
- }	•		CSDMLLER\GPYSAS\VREAKEDEEDEEKIONEDYHERISDGDI.
!			DLDLVYEDEVNQLDGSSSSASSTATSNTEENDIDEETMSCENDY
	1		BYNNMELEEGELMEDAAAAGPAGSSHGYVGSSSRISRRTHI.CSA
i			ATSSLLDIDPLILIHLLDLKDRSSIENLWGLOPRPPASILODTA
i			SYSRKDKDQRKQQAMWRVPSDLKMLKRLKTOMAEVRCMKTDVKN
			TLSEIKSSSAASGDMQTSLFSADQAALAACGTENSGRLQDLGME
1			LLAKSSVANCYIRNSTNKKSNSPKPARSSVAGSLSLRRAVDPGE
			NSRSKGDCQTLSEGSPGSSQSGSRHSSPRALIHGSIGDILPKTE
Į.			DRQCKALDSDAVVVAVFSGLPAVEKRKMVTLGANAKGGHLEGL
ł	}		QMTDLENNSETGELQPVLPEGASAAPEEGMSSDSDIECDTENEE
	•		QEEHTSVGGFHDSFMVMTQPPDEDTHSSFPDGEQIGPEDLSFNT DENSGR
5979	212	3665	
	1	3003	LPDMTMYLWLKLLAFGFAFLDTEVFVTGQSPTPSPTDAYLNASE
1			TTTLSPSGSAVISTTTIATTPSKPTCDEKYANITVDYLYNKETK LPTAKLNVNENVECGNNTCTNNEVHNLTECKNASVSISHNSCTA
1			PDKTLILDVPPGVEKVPVHCCS\QVEQPDSTIWLKWKNIETSTC
ĺ	1		DTQNITYRPQCGNMIPDNKEIKLENLEPEHEYKCDSEILYNSHK
i	<b>j</b>		FTNASKIIKTDFGSPGEPQIIFCRSEAAHQGVITWNPPQRSFHN
1			FTLCYIKETEKDCLNLDKNLIKYDLQNLKPYTKYVLSLHAYIIA
			KVQRNGSAAMCHFTTKSAPPSOVWNMTVSMTSDNSMHVKCPPDD
1			DRNGPHERYHLEVEAGNTLVRNESHKNCDFRVKDLOVSTDVTFK
1			AYFHNGDYPGEPFILHHSTSYNSKALIAFIAFITTVTSTALLIN
1			LYKIYDLHKKRSCNLDEOOELVERDDEKOLMNVEPTHADILLER
į.			YKRKIADEGRLFLAEFQSIPRVFSKFPIKEARKPFNONKNRYND
			ILPYDYNRVELSEINGDAGSNYINASYIDGFKEPRKYTALOGDP
<b>i</b> i			DETVDDFWRMIWEOKATVIVMVTRCEEGNRNKCAEVWDGMFFGT
1			RAFGECCCKDLTKHKRCP\DYIIQKLNIVNKKEKATGREVTHIQ
			FTSWPDHGVPEDPHLLLKLRRRVNAFSNFFSGPIVVHCSAGVGR
1			TGTYIGIDAMLEGLEAENKVDVYGYVVKLRRQRCLMVQVEAQYI
	· .		LIHQALVEYNQFGETEVNLSELHPYLHNMKKRDPPSEPSPLEAE
ļ i			FORLPSYRSWRTQHIGNOE\ENKSKNRNSNVIPYDYNRVPLKHE LEMSKESEHDSDESSDDDSDSEEPSKYINASFIMSYWKP\EVMI
[	}		AAQGPLKETIGDFWQMIFQRKVKVIVMLTELKHGDQEICAQYWG
1		, [	EGKQTYGDIEVDLKDTDKSSTYTLRVFELRHSKRKDSRTVYQYQ
1 1			YTNWSVEQLPAEPKELISMIQVVKQKLPQKNSSEGNKHHKSTPL
]			LIHCRDGSQQTGIFCALLNLLESAETEEVVDIFQVVKALRKARP
j			GMVSTFEQYQFLYDVIASTYPAQNGQVKKNNHQEDKIEFDNEVD
i !		İ	KVKQDANCVNPLGAPEKLPEAKEQAEGSEPTSGTEGPEHSVNGP
5980			ASPALNQGS
]	3	2363	DAWGCKLRRLRFTYGTQTRVSLALPGQYELVHTLVAHQGNWETI
1 1			PEEDLEVQENNEDAAHDLTELEVTMHHALLOEVDVVVAPCOGLP
1		ł	PTVDVLGDLVNDFLPVITYALHKDELSERDEQELQEIRKYFSFP
		l	VFFFKVPKLGSEIIDSSTRRMESERSPLYRQLIDLGYLSSSHWN
			CGAPGQDTKAQSMLVEQSEKLRHLSTFSHQVLQTRLVDAAKALN
	İ		LVHCHCLDIFINQAFDMQRDLQITPKRLEYTRKKENELYESLMN
			IANRKQEEMKDMIVETLNTMKEELLDDATNMEFKDVIVPENGEP
1	}	ŀ	VGTREIKCCIRQIQELIISRLNQAVANKLISSVDYLRESFVGTL ERCLQSLEKSQDVSVHITSNYLKQILNAAYHVEVTPHSGSSVTR
Ì			MLWEQIKQIIQRITWVSPPAITLEWKRKVAQEAIESLSASKLAK
			SICSQFRTRLNSSHEAFAASLRQLEAGHSGRLEKTEDLWLRVRK
1			DHAPRLARLSLESRSLQDVLLHRKPKLGQELGRGQYGVVYLCDN
,		1	WGGHFPCALKSVVPPDEKHWNDLALEFHYMRSLPKHERLVDLHG
1		1	SVIDYNYGGGSSIAVLLIMERLHRDLYTGLKAGLTLETRLOTAL
			DVVEGIRFLHSQGLVHRDIKLKNVLLDKONRAKITDLGFCKPEA
1		1.	MMSGSIVGTPIHMAPELFTGKYDNSVDVYAFGILFWYICSGSVK
1	ļ	1 :	LPEAFERCASKOHLWNNVRRGARPERLPVFDEECWOLMEACWOG
5001			DPLKRPLLGIVQPMLQGIMNRLCKS\NSEOPNRGLDDST
5981	1	2519	GRKHSAAMERPWGAADGLSRWPHGLGLLLLLOLLPPSTLSODET.
-		1 1	DAPPPPAAPLPRWSGPIGVSWGLRAAAA\GGAFPRGGRWPPSAD
i		(	G\EDEECGRVRDFVAKLANNTHOHVFDDLRGSVSLSWVGDSTCV
			ILVLTTFHVPLVIMTFGQSKLYRSEDYGKNFKDITDLINNTFIR

Deginning nucleotide location corresponding to first amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid am	SEQ	Predicted	Predicted end	I Prince Co
Corresponding	ID			Amino acid segment containing signal peptide
corresponding to first amino acid for first amino acid residue of amino acid soquence should be amino acid soquence should be amino acid soquence should be amino acid soquence should be amino acid soquence should be amino acid soquence should be amino acid soquence should be amino acid soquence should be amino acid soquence should be amino acid soquence should be amino acid soquence should be amino acid soquence should be amino acid soquence should be amino acid soquence should be amino acid soquence should be amino acid soquence should be amino acid soquence should be amino acid soquence should be amino acid soquence should be amino acid should be amino acid should be amino acid should be amino acid should be amino acid should be amino acid should be amino acid should be acid should be acid should be acid should be acid should be acid should be acid should be acid should be acid should be acid should be acid should be acid should be acid should be acid should be acid should be acid should be acid should be acid should be acid should be acid should be acid should be acid should be acid should be acid should be acid should be acid should be acid should be acid should be acid should be acid should be acid should be acid should be acid should be acid should be acid should be acid should be acid should be acid should be acid should be acid should be acid should be acid should be acid should be acid should be acid should be acid should be acid should be acid should be acid should be acid should be acid should be acid should be acid should be acid should be acid should be acid should be acid should be aci	NO:	nucleotide		Glutanic Acid Panhamilalasia C Cl.
Lequine, Mangharajine, Pasgarajine, saino acid residue of residue of amino acid sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequen	1	location		Harristiding Taleglauding Walter
amino soid residue of amino acid sequence solvente provide of amino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence se	1			Labeucine. MaMethionine Nanagaragine
Fesidue of amino acid sequence sequence (amino acid sequence sequence) sequence (amino acid sequence) sequence (amino acid sequence) sequence (amino acid sequence) sequence (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (amino acid sequence) (am	1		amino acid	P=Proline, O=Glutamine, R=Arginine
amino acid sequence  sequence  sequence    Sequence	ŀ		residue of	S=Serine, T=Threonine, V=Valine
Sequence    Codon, /=possible mucleotide deletion,	1		amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown +-Stop
Sequence	1	1	sequence	Codon, /=possible nucleotide deletion
TEPGMAIGPENSCKWULTAEVSGSSRGSKIPKSSDPANNEVGTU  LPHPLTOMMYS PROSVALLALISEINGLWSKNOPGKAKERIKKA VCLAKNGSDAYLIPFTTAMGSCKADLGALELMKTSDLGKSFKTL GVKLYSFGLGGREPLSVAMANDUTTRIINSTDGGDYSKNAQLD SVGCGOFYSILAANDDWYMWUDEGGTOFGTIPTSDDGGLYVS KSLDBRILYTTTGGTFOTNYSLSCADYLTSVISLEDBNISTOMTE DOGGNATELRKPENSCCDATANKNECSLHIKASYSISQKLAWY MAPLESPRAVGIVITALGSVGALSWAWDYSTDDGGSTYTML EGPHYYTILDSGGIIVALEKSSPINVIKFSTDEGCCNOTYFFT BOPTYPTOLASPEDARSNNISINGFTSTLSGWASTUTDEND LERNCGERDYTTWIAHSTDEPDYEGGCILGYKEOPILLEKSSVC ONGGDVWYKOPSICLGSLEDPLCDFGYFREDBRKCVQDELK GHOLEFCLYGREBHLTTNOYRKIPGOKCOGGVAPUREVADLKKK CTENNISPEGORSSSISVEVILLAVGRATYVAGOVLYKKYVC GGRFLWHLYSVLQORIARSNOPTHOLASHINKSGYHDDS DEDLE  SPELS  56  2316  ATRPORGSRGCGFSTRASAPGRSNNILFTVKALVGLSKSPR FCYHERLSVAGACHMYWKGWILLTNS RKKAKRGWMEPLLANPIDLOFT LOGGECULDOSMAPTOND SKPLEGGRAVAUGHTAAASNILETPURALVGLSKSPR FCYHERLSVAGACHMYWKGWILLTNS RKKAKRGWMEPLLANPIDLOFT LOGGECULDOSMAPTOND SKPLEGGRAVAUGHTAAASNILETPURALVGLSKSPR FCYHERLSVAGACHMYWKGWILLTNS RKKAKRGWMEPLLANPIDLOFT LOGGECULDOSMAPTOND SKPLEGGRAVAUGHTAAASNILETPURALVGLSKSPR FCYHERLSVAGACHMYWKGWILLTNS RKKAKRGWMEPLLANPIDLOFT LOGGECULDOSMAPTOND SKPLEGGRAVAUGHTAAASNILETPURALVGLSKSPR TAAPPETRKTES IDVNDAVGSNIVVSTRTGGWARTLEPENHEDIN BENISDKTPAYDGLKRGGRIPPURARGGIILTCHVERALVGLSKPA TAAPPETRKTES IDVNDAVGSNIVVSTRTGGWARTLEPENHEDIN BENISDKTPAYDGLKGRGRIPPURARGGIILTCHVERALSVA AGNILGSFOGKDVAALAGGLVDAAALVALKDLINRVGLDILGTER VPFTAAGGTDLRSNIVLINTILAGGECADALAKVALDILGTEN AGRICGSTORDLYNTILTSTLAGGECAALLAKVALDILGTEN TESVTGGMKVWINTILKRILSGVAALDLGVKROVEATRANPPKVLF LIGABGGCTTROLDFANTVJASSALGARDALAKVALDILGKLWN QCLADPLVPPOLTWHOPYHTDSI SRASGINAKCVKAVTEGAQA VEENSI  5983  248  1763  ERGGGGGRRRIKASGRRAGGFP NGELKSGOGRAVPERAVARGG CONRALELHPSSKELLKAMAVSTLEGOVKALVADYKTVLQIICC CONRALELHPSSKELLKAMAVSTLEGOVKALVADYKTVLQIICC CONRALELHPSSKELLKAMAVSTLEGOVKALVADYKTVLQIICC CONRALELHPSSKELLKAMAVSTLEGOVKALVADYKTVLQIICC CONRALELHPSSKELLKAMAVSTLEGOVKALVADYKTVLQIICC CONRALELHPSSKELLKAMAVSTLEGOVKALVADYKTVLQIICC STRNMFTHILDFOLDAHTNIKSKERKELSIICHVENEKGEGOPA GEVSTCCLASSKGGKSSRPEDDFRANFYNGCELEQULFUNGTVF SFKINSPFYON	<b> </b>	sequence	<u></u>	\=possible nucleotide insertion)
DEPHILTOMYS PONSOYLLALSTENGLAVISM PSIGNAGE MEET HAN VICLAKMOSDAYLE PITTAMOG CARLA BLEMATS DIGGES KEET IT OWKTYS FELGRIFLAS WARDAYTRA HINSTOCHT SKRACH SUGGEST AND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND STAND	1		1	TEFGMAIGPENSGKVVLTAEVSGGSRGGRIFRSSDFAKNFVOTD
VCLARMOSDATIFFTYAMOSCRADIGALEMETBOLGGERYTI GVKTYSFGLOGREIPASVANADUTRETHUSTOGGUTESMAGLE SVCGEOFYSILAANDDAVENHUBERDTGFGTIFTSDBGIVTY KILDERLITTTIGGETDFINTSLEGYTISDBGIVTY KILDERLITTTIGGETDFINTSLEGYTISDBGIVTY BOGGRATHLERERSRECHATAKKNECSLHHABSTSIGKLAVY MAPLESPRAGUTUHAGSVGDAISVAVPDYTISDBGIVTYT BOGGRATHLERERSRECHATAKKNECSLHHABSTSIGKLAVY MAPLESPRAGUTUHAGSVGDAISVAVPDYTISDGSYSTMEM EXPRYTTLOSGGIVALEHSSREINVIKTSTDERGCMOTTTF RDPITYTCLASEGRASMMISIKMFTSFITSGOCGOTTURED LERNCEERDTTWLAHSTDFBDYEDGCILGYKEPFLEKKSYSTIDKOC ONGROVVTKOPSICLGLESEPFLODEYTYPENDSKOVEOPEUK GHOLBECLYGREEHLITNOYRKIPGOKCGGGNEVRENVERKYEVC GGRFLVAHLYSVLQON\ARA\KOVGVDALDTASHTINKSGYHDDS DEDLLE  5982  56  2316  ATRPPRGSSNCROFSRTASAAPGRSMMLRIFYRKALVGLSSGIRK CTENNELSPEKORSKSNSVEILLAUGHLUTVAKGVUNIKKYVC GGRFLVAHLYSVLQON\ARA\KOVGVDALDTASHTINKSGYHDDS DEDLLE EKKKAREGWEPFLAHAPHLOCICOGGGCDLOGOSMPGNDIR SRPLEGKRAVEOKNIGPLWYINTRECICCTRCIRFASELAAVUD LGTTGROMMOVGTVITEMWENSELISTVYNOGSWALDTANKOWNITHS EKKKAREGWEPFLAHAPHLOCICOGGGCDLOGOSMPGNDIR SRPLEGKRAVEOKNIGPLWYINTRECICCTRCIRFASELAAVUD LGTTGROMMOVGTVITEMWENSELISTVINGGANTAKEVAPA TARPWETRKTESIOVHDAVGSNIVVSTRTOEWMILIPRWHEDIN EEMISDKTPRAYDGLKRORLIEFWRAKEKOLLITYREPEAPLF NAGILGSROGGDVAALAGGLVARALVALKOLLINRVDSDTLCTER VPFTAAGATDLASHYLLANTLAGSVULTYTYOHLUGSPKILQDLASK AGNLOSPOGGDVAALAGGUVARALVALKOLLINRVDSDTLCTER VPFTAAGATDLASHYLLANTLAGSVULTYTYOHLUGSPKILQDLASK SKEPSFOVLKEAKKWWNILIARIASQVAALDLGYKKGVEAIKKSPEKVL LGAAGAGCTIRGDLPROCHTWORTYTTOHLUGSPKILQDLASK SKEPSFOVLKEAKKWWNILIARIASQVAALDLGYKKGVEAIKKSPEKVL LGAAGAGCTIRGDLPROCHTWORTYTHOHISGSVARAVYTYRYLAGAAV EKSPIC LGAADAVARAPTARAAHRIKKSGRRAGGEP\AGKGYAVYKTVOLGAAL VERSPIC BARGGGGRRRIKASGGRRAGGEP\AGKGYAVYKTVOLGAAV VERSPIC CALLADSVNILSRAGSRIADLAGAEKKRISIGONGONGANEKKAVATGGAA VERSPIC AKKATYVONIGKKGRSVSPLASGARONGONGANEKKANARG COLLADELVRYCHLIVISKARRYKMERISLIDENGAATHACVAKAVTUGAALAGUNA LEEKDESLUKYYPHTATARAATTURGKGGGGGOTO CONRALSLIPPSMEDLARRAYATTRAGGARATKAVTOTPELRICHSPIL SEKKONGONGONGONGONGONGONGONGONGONGONGONGONGO	1		j	LPFHPLTQMMYSPQNSDYLLALSTENGLWVSKNFGGKWEETHKA
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ONGADVYTKOPSICLCSLEDFLOPGYTPRENDSKYEQUEDELK GHOLBECLYGREBHLITHOURKTRIPGOKOGGUNPVREVKOLKKK CTSNFLSPEKONSKSNSVEIILAIVGLMLOTVVAGVILVKKYVC GGRFLVHLISVSLQOM, AERANGVDGVDALDTASHTNKGVYHDVG GGRFLVHLISVSLQOM, AERANGVDGVDALDTASHTNKGVYHDVG DEDLLE  5982 56 2316 ATREPPEGSSMCROFSETASAAPGRSNMLRI PYRKALVGLSKSPK GCVRTTATAASNLIEVFVDGGSWWEPGTTVLQACEKVGWQIGR PCYHERLSVAGNCRMCLVELEKAPKVVAACAMPUWKGGRILTINS EKSKARREGWREFLLANPELDCI CLOQGGLOOCONGMINGTOR SRFLEGKRAVEDRNIOPLUTTINTRCIQCTRCIRFASELGVDD LGTTGRGDHOWQUTYIERMFMSELGWILDYCOMANTSHYPAF TARPMETRKTESIDWIDAVGSNIVVSTTTGEWRRILPTSWHEDLSRV AGNLOSFGGKOVAAIAGGLVDARALVALKOLLNRVDSDTLCTER VPFTAGAGTURENVLANTITIAGVEEADVVLLUVTINFFFAPLF NARIKKSKLINDLKVALIGSPVDLTYTYDHLOSFKILQDISGS SHPFSQVLKEAKKPWVLIGSSALQRNOGAAILAAVSSIQKIRM TGSVTGDWKWMILKRIASGVAALLGGLWOADIAAVILKOLLNRVDSDTLCTER VPFTAGAGTURENVLANTITIAGVEEADVVLLUGTSFKILQDISGS SHPFSQVLKEAKKPWVLIGSSALQRNOGAAILAAVSSIQKIRM TGSVTGDWKWMILKRIASGVAALLGGVKGVAAVTLEGANT EKSATVANTEGRAQOTKVATPFGLAEEDKHIGNTLAGAYT EKSATVANTEGRAQOTKVATPFGLAEEDKHIRALBETIAGMTL PUDTL'QQVRINLEEVSINLVXYDDISG\ANYFQQANELSKLVN QQLLADPLVPQLTINKDPYTHOSISRASGTMAKCVKAVTEGAQA VEEPSIC  5983 248 1763 ERGGGGGRRHHRASGERRAGGED JAGLKSGGGAVYKRAVARGG RA\YSAAIALLEPAGSBIADDLSILYSNRAGYILKEGNCGSGCIQ DCNRALSHIPFSMKPLLRRAMASETLEQVGKAYVVKRAVARGG RA\YSAAIALLEPAGSBIADDLSILYSNRAGYILKEGNCGSGCIQ DCNRALSHIPFSMKPLLRRAMASETLEQVGKAYVDKRAVAGG RA\YSAAIALLEPAGSBIADDLSILYSNRAGYILKEGNCGVDKRYK DALKKYSECKIKNMECAITYTRALCYLKLOWEGKEPEGPA GEVSTGCLASBEGGKSRSPEDPEKLIJAVPASVELQAMH PAKEMISKQAGDSSSHRQQGITDEKTYRALKEGNOCVUKNYK DALKKYSECKIKNMECAITYTRALCYLKLOWEGKEPEGPA A GEVSTGCLASBEGGKSRSPEDPEKLDIAKPMAYETILGSKNN LIEKDPSLVYQULLYLSKARRYKMILTISKGXELIGLEFEDL STYNNIFILEDIOALKGYSFLASGLMRVSTGPELRLHHSFVL TGDUGRICCHLIANDKATAPTRAKSKRRKIIGTSKOMEKGEREPGBA RRYDFSIPSAAAGNSHIQTPCLTELLQGYTVEVLRQQPPDLVE PAVEYFTILREARAPASVEVPERARROLAGAERKAGVSREGGBGR RRYDFSIPSAAAGNSHIQTPCLTELLQGYTVEVLRQQPPDLVE PAVEYFTHREARRAPASVEVPERARROLAGAERKAGVSREGGBGR RRYDFSIPSAAAGNSHIQTPCLTELLQGYTVENTORSGG ELALMYNTPRAATIVATSEGSLWGLDWVFRRIVKNOGNETLICGEBUTDGW GELALDTWINDE	j	1		LEBNCEEKDYTIMI AUSTDDEDVERSON SWYSYTIDFKDI
GHDLEFCLYGREHLITMCYRKIPGROCGGUNPVREVVDLKKK CTSNRISPS KONSKISNSVP ILIAIVGLMUTVVAGVLIVKYVC GGRFLVHLYSVLQQH\AEA\NGVDGVDALDTASHTNKSGYHDDS DEDLLE  5982  56  2316  ATRPPRGSSWCRQFSRTASAAPGRSNMLRIPVRKALVGLSKSPK GCVRTTATAABNILISVFVDGGSVWSPGTTVLQACEKVGMQIR FCTHERLSVAGNCRMCLUEFKAPKVVAAGWMGVBHLINS EKSKKARRGWSPLLLANHPLDCPICQGGEDLQOGSMMGNDR SRPIGERRAVBDRNIGPLYNTIMTRCICGTRASBIAGVD LGTTGRGNDMQVGTY1EKMPMSELGGNIIDICPVGALTSKPVAF TARPHETEKTESIDVMDAVGNIVYSTTGRASBIAGVD LGTTGRGNDMQVGTY1EKMPMSELGGNIIDICPVGALTSKPVAF TARPHETEKTESIDVMDAVGNIVVSTTGRASBIAGVD LGTTGRGNDMQVGTY1EKMPMSELGGNIIDICPVGALTSKPVAF TARPHETEKTESIDVMDAVGNIVVSTTGRASBIAGVD LGTTGRGNDMQVGTY1EKMPMSELGGNIIDICPVGALTSKPVAF TARPHETEKTESIDVMDAVGNIVVSTTGRASBIAGVD LGTTGRGNDMQVGTY1EKMPMSELGGNIIDICPVGALTSKPVAF TARPHETEKTESIDVMDAVGNIVVSTTGRAFSLFAV FANGLERGNIVANTIVAGVALDLINGTNSKPVAF AKHLOSSKIVAN GAMLQSFGGKOVAALAGGUNDAVALVULVGTNFRFFADFA VPFTAGRGTDLRKOLTTITGAVEADAVALLVGTNFRFFADFA VPFTAGRGTDLRKOLTTITGAVEADAVALLVGTNFRFFADFAF VPFTAGRGTDLRKOLTTITGAVEADAVALLVGTNFRFFADFAF VPFTAGRGTDLRKOLTTITGAVEADAVALLVGTNFRFFADFAF VPFTAGRGTDLRKOLTTITGAVEADAVALLVGTNFRFFADFAF VPFTAGRGTDLRKOLTTYTOMLGDSSKILDDLSGV VPFTAGRGTDLRKOLTTYTOMLGDSKILDDLASV VPFTAGRGTDLRKOLTTYTOMLGDSKILDDLASV VPFTAGRGTDLRKOLTTYTOMLGDSKILDDLASV VREPSIC LLAGADGCTRADETTYTOMLGDSKILDDLASV VREPSIC PPTTALVALEGGAATAAA LAAVSSIAQKTRM TSSVTGDKRKVATTYTGARGAVALKCANAVARGG RGVSTAGALAAVARGG RGVSTAGALAAVARGG RGVSTAGALAAVARGG RGVSTAGALAAVARGG RGVSTAGALAAVARGG RGVSTAGALAAVARGG RGVSTAGALAAVARGG RGVSTAGALAAVARGG RGVSTAGALAAVARGG RGVSTAGALAAVARGG RGVSTAGALAAVARGG RGVSTAGALAAVARGG RGVSTAGALAAVARGG RGVSTAGALAAVARGG RGVSTAGALAAVARGG LTDLKTKAAVARGG RGVSTAGALAAVARGG RGVSTAGALAAVARGG LTDLKTKAAVARGG LTDLKTKAAVARGG LTDLKTAAVARGG LTDLKTAAVARGG LTDLKTAAVARGG RGVSTAGALAAVARGG LTDLKTKAAVARGG LTDLKTAAVARGG LTDLKTAAVARGG LTDLKTAAVARGG LTDLKTAAVARGG LTDLKTAAVARGG LTDLKTAAVARGG LTDLKTAAVARGG LTDLKTAAVARGG LTDLKTAAVARGG LTDLKTAAVARGG LTDLKTAAVARGG LTDLKTAAVARGG LTDLKTAAVARGG LTDLKTAAVARGG LTDLKTAAVARGG LTDLKTAAVARGG LTDLKTAAVARGG LTDLKTAAVARGG LTDLKTAAVARGG LTDLKTAAVARGG LTDLKTAAV		1		ONGROYVVTKOPSICLCGLEDELCDECVVDDGATECKSSVC
S982   S6   2316   ATRIPESES, SERVILLA IVELMENT VAGALLY VKYVC GERFLYHLY SYLQRU A LEAR, ANGUGUDAL DISHTINKS GYHDDS DEDLLE	i			GHDLEFCLYGREEHLTTNGVEKI DCDVCOCCUMDUDERRY
5982 56 2316 ATRPPRGSSWCROPSRTASDAPGRSMURIPVEKALVGLSKSPK GCVRETATAASNILEVYDOGSVMVBPGTTVLQAGEKSWQIPR PCYHERLSVAGNCRMCLVEIEKAPKVVACAMPVMKGWNLINS EKSKRARRGVWBFLLANNPLDCPICDQGGEDLQDQSMMFGNDR SRPLESKRAVBDINIOPLVKITHRRCQFREABSLAGVD LGTTGGGDDMQVGTVIEMFMSELSGNIIOICPVGALTSKPVAF TARPMETEKTESIDVMDAVOSNIVVSTTGERGABSLAGVD LGTTGGGDDMQVGTVIEMFMSELSGNIIOICPVGALTSKPVAF TARPMETEKTESIDVMDAVOSNIVVSTTGERABSLAGVD LGTTGGGDDMQVGTVIEMFMSELSGNIIOICPVGALTSKPVAF TARPMETEKTESIDVMDAVOSNIVVSTTGERABSLAGVD LGTTGGGDDMQVGTVIEMFMSELSGNIIOICPGABLTSKPVAF TARPMETEKTESIDVMDAVGNIVSTTVGTRAFBLAGVD LGTTGGGDKOVARIAGRUDPALVALKDLINFVGSPLICTE VPFTAGAGTDLRSNYLLNTTIAGVEGADVVLLVGTNRFFFADF NARIRKSWLENDLAVALGSPUDLTYTVDMLGDSRILGDISG SNPFSQVLKBAKKPMVVLGSSALQNDGAALLAAVSSIAQKTRM TSGVTGDWKVMNILHRIASQVAALDLGVRGVGVEATKMPPKVLF LLGADGGCITTGDDLEKNCFIIVGGHGGVGAPIAVVLLQARAYT EKSATYVNTEGRAQOTKVAVTPPGLAXEDMKIIRALBEINGMIL PVDTI.\DQVMRILEUSPRILVXPXDDISG\AMPEQAMELSKLVN QOLLADPLVPPQLITMKDFYMTDSISRASQTMARCVKAVTEGQA VEEPSIC  5983 248 1763 BARGDGGRRHRASGRRAGRGEP\AGLKSQGQRAVPKRAVARGG RQ\YSAAIALLEPAGSEIADDLSILYSNRAACYLKEGNCSGCIQ DCNRALSLHFSMKPLLKRAMAYSTLEGVGAVVDKTVLOIDC GCQLANDSVARRLSRIIMELDGINNERLISLIPAVPASVLQAWH PAKKMISKQAGDSSHRQQGITDENTYKALKBGONQCVADRNYK DALSKYSECLKINNKEGAIYTTRALCYLKLQFEEAKODCOQL QLADGNVKAPYRRALAHKGLKVYQKSLIDLINNVILLDFSIIBAK MELBEVTRILNIKKNTAPTNKEKERKISLIDGVAVECKEEPGCRPA GSVSTGCLASSKGGKSSSPEDPEKKDIRKNONAYPEGGIINAL STRKOKEACAHLAITTARDLOPMFLISHLEGIVAVECKEEPGCRPA GSVSTGCLASSKGSKSSPEDPEKDIRKPTSLILIGSIKNN LLEKDPSLVYGHLLYLEKAERRKMMILISKGQKELIEQLFEDL STYNNHFILBIOJALKRGYSEL  5984 755 1193 SSVCMACTYVSNLGKKGRSVSPLASGLMRVSTGFELLHESFVL TODWGRNICGHLVSLFTKKOTRSCTVFWQRCSCHDSGRR RRNDSIJPSAAAGNSHIQTPGLTELLQGYTVZVLRQOPPDLVS FHINLSRISERSSG RRNDSIJPSAAAGNSHIQTPGLTELLQGYTVZVLRQOPPDLVS FHISLSSISREBEDDLEVVPSRRNRVSVCAFTYNPDEEEDIDDRVI HPKTDEQRCRLQEACDLILIFKRIDDGGLSGVULDANFFRIVKAD EHVIDQGDDORFVIERSTTVILVTKNOTGSVGQYDNAGSFG ELALMYNTPRAATIVATSEGSLWGLUNDVORGSVGLONDANSFG ELALMYNTPRAATIVATSEGSLWGLUNDVORGELIGPCMDIMWP	1			CTSNFLSPEKONSKSNSVPI ILATVGIMI VTVVAGVI TVZVVVG
5982  56  2316  ATRPPRGSSWCRQFSRTASAAFGRSNMLRIFVRRALVGLSKSPK GCVRTTATAASNLIEVFURGGSVAVEPGTTVLQACEKVGMQIPR PCYHELESVAGNCRMCLVEIEKAPKVVAACAMPWKGWILINS EKSKKARBGYWEFLLANHPLDCPICOGGGCDLODGSMMGFSDR SRPLEGKRAVEDKNIGPLWRIMTRCIQCTRCIRASELAGVDD LGTTGRGKDMOVGTYIEKKMPMELSGIIDICPVGALTSRAPVAF TAAPMETRKTESIDVADAVGSNIVVSTTGEWAHILBRAMEDIN EEMISKKTRAYDGLKRAKHMESISAIIDICPVGALTSRAPVAF TAAPMETRKTESIDVADAVGSNIVVSTTGEWAHILBRAMEDIN EEMISKKTRAYDGLKRALTSPWINTERGLUTTTSWEDALSRV AGMLQSFGGKDVAALAGGLVDAEALVALKOLLINEVDSDTLCTEB VFPTAGAGTDLRSNYLLNTTLAGVERDVVLLVTSNEVBAPLF NARIKKSNLIHDLKVALIGSSVALLTYTYPHLGDSPKLLGDILSG SHPFSQVLKEAKKPMVVLGSSALDRINGAAILAAVSIAQKTRM TSGVTGDWKVANILHRIASGVAALDLGVRPGVEAIRKNIPPKLPF LIGADGGCITRGDLPKDCFITYGGHRGUWGAPLADVLLVGAAYT EKSATYVATBERAQQTKAVATYPGCLARBEMKIIRALSEIAGMTL PYDTLAQDVRNRLEEVSPNLVRYDDIEGANVFQANELSKLVN QQLLADPLVPQIDINKDFYMTDGISRASGTMAKCVKAVTEGAA  ERRGGGGRRHRASGGRAGGEP\AGLKSGOGRAVPKRAVARGG GCNYSAALALLEPAGSSIADDLGILVSNRACYLKEGNGSGCIQ DCNRALELHFFSMKPLLRRAMAVETLEQYGKAYVDYKTVLQIDC GCQLALNDSVALERILMBLOGPNWERKLSLIPAVPASVELQAMH PAKEMISKQAGDSSHRQGITDEKTFALESMOCVOMDKNYK DALSKYSECLKINNKECAITTNAALCYLKLOGVERAKOCHOQAI QLAGNGNVAHAYPRALAHKGKNYOKSLIDEKSMOCVOMDKNYK DALSKYSECLKINNKECAITTNAALCYLKLOGVERAKOCHOQAI QLAGNGNVAHAYPRALAHKGKNYOKSLIDEKSMOCVOMDKNYK MELEEVTRLINLKDKTAPFNKEEGRRKLEIGDWBEKKEPGRPA GEVSTGCLASEKGGGKSSRSPEPDEKLIDLEKSMOCVOMDKNYK MELEEVTRLINLKDKTAPFNKEEGRRKLEIGDWBEKKEPGRPA GEVSTGCLASEKGGKSSRSPEPDEKLIDLEKSMOCVOMDKNYK MELEEVTRLINLKDKTAPFNKEEGRRKLEIGUNGKEEPGRPA GEVSTGCLASEKGGKSSSPEPDEKLIPFSGFCLLCLARVG SSPKINSPFYON\QTSTORSCTVFVWQRCSLVGPPQVTVPTMY PHHSLBSISRFSG  TODWGRRI GREILDVGATKGTTSSKEWIPFSGFGCFLLACLARVG SSPKINSPFYON\QTSTORSCTVFVWQRCSLVGPPQVTVPTMY PHHSLBSISRFSGS RRPNPSIPSAAAGMSHIQIFGGTELLGQFTEVADAK GDSSEDBDLEVPPSFRNREVSCAETYNDESEEDTDPRVI HPKTDERGGRCLOEACKULLKFRNLDGGGLGDRVTFRIILVKNAKKRM BEHYIDGGDDGDNFYVIERGTYDILVTRONGTRSVGQVDNAGSGG ELALMTNFRAATIVATSGGSLGGRUFTFRIILVKNAKKRMK FESFIESVELKSLEVSERMKIVDVIGGRYLLARGCHOGOFFLIGDEMUMP GERALDTVINGRAAAAA	1			GGRFLVHLYSVLOOH\AEA\NGVDGVDALDTASHTNKSGVUDDS
ATK-PROSSWCRQFSRTASARJERSNNLRT PURKALVGLSKSPK GCVRTTATASANLIEVYLOGGSWURGKONTLAGACEKVGMQ1R FCYHERLSVAGNCRMCLVEIEKAPKVVAACAMPVWKGWNILTNS EKSKARREGVWEPILANHPLDCP1CDQGECDLDDQSMMFGWND SRFIEGKRAVEDKNIGPLVKTIMTGLQCTGCIRGASELAGVDD LGTTGRGBDMQVGTY1EKMFMSELSGNIID1CPVGAATGRYAGF TARPMETKETSIOVMDAVGSNIVVSTGWMGTURIPKAPKAF TARPMETKETSIOVMDAVGSNIVVSTGWMGTURIPKAPKAF AGMLOSFGGKOVAA1AGGUVDAEALVALKDLLNRVDSDTLCTBE VPFTAGAGTDLRSNYLLNTTLAGVEBADVALLVGTNERFEABLF NARIRKSWLINDBLKVALIGSSPUDLTTYTYDHLGDSPKILQDIAGS SHFFSQVLKERKKPMVVLGSSALQNIGSALLAAVSSIAJKKTM TSGVTGDWKVMNILHRIASGVAALDLGYKPGVERAIKAPKPVLP LIGADGGGITTRODLFROEPTIVOGHTBUGGAPIADVILPGAAYT EKSATYVMTBGRAQQTKVAVTPPGLAREDWKIIRALSETAGMTI PYDTL\DQVRRNLESVSPILVYDDIEG ANTPGQANELSKLVN QQLLADPLVPPQLTMMDFYMTDSISRASGTMAKCVKAVTEGAQA VEEPSIC  SARGGGGGRRHRASGRRAGKGEP\AGLKSQGGRAVPERAVARGG RQ\YSAATALLEPAGSETADDLSILYSNRAACYLKEGNCSGCIQ DCNRALSHIPFSMKPLLRRAMAETLEQYGKAVYDYKTVLQIDC GQLANDSVARLSHIMSLDGPWMERKLSITPAVPASVPLQAMH PAKEMISKQAGDSSSHRQQGITDEKTFKALKEGNCCVADKNYK DALGKYSEGCKIKNNKEGITTNAACYLKGPEAKUDOOML QLADGNVKAPYRRALAHKGLKNYGKSLIDLNKVILLDPSIIEAK MELBEYTRLLNIKKNTAPFNKEKERRKLEIQEWREKEEPGRPA GEVSTGCLASEKGGKSSSSPEDEELLPIARNNAYEFGQIINAL STRKKEACAHLLATTAPKDLPMFISNLEGOTPLLIQSIKNN LIEKDPSILVYQHLIYLEKARPKMMILTISKGKELIGLFUEGKEEPGRPA GEVSTGCLASEKGGKSSSSPEDEELLPIARNNAYEFGQIINAL STRKKEACAHLLATTAPKDLPMFISNLEGOTPLLIQSIKNN LIEKDPSILVYQHLIYLEKARPKMMILTISKGKELIGLPVEGKEEPGRPA GEVSTGCLASEKGGKSSSSPEDEELLPIARNNAYEFGQIINAL STRKKEACAHLLATTAPKDLPMFISNLEGOTPLLIQSIKNN LIEKDPSILVYQHLIYLEKARPKMMILTISKGKELIGLPVEGWEG SSPKINVSFYQN\OTSTGSSKVIPFSPGCFLLCULARVG SSPKINVSFYYON\OTSTGSSKVIPFSPGCFLLCULARVG SSPKINVSFYYON\OTSTGSSKVIPFSPGFCLLCULARVG SPKINVSFYYON\OTSTGSSKVIPFSPGFCLLCULARVG SPKINVSFYYON\OTSTGSSKVIPFSPGFCPLACKGDAGK PHSILSSISFSG RRPNPSIPSAAAGMSHQIPPGTSLGQVDAMPERIVKAD ENYIDGGDGOMFYVIERGTYDILVTKNONGTRVGQUDAMFERIVAD ENYIDGGDGOMFYVIERGTYDILVTKNONGTRVGQUDAMFERIVAD ENYIDGGDGOMFYVIERGTYDILFFNLOGGSVGADMFRIIVKNONGTRVG GELALVTNIVRARAATIVATSSGSLUGGDVTFRRIIVKNO				DEDLLE
GCVRTTATAASNILEVFUDGGSVAWERGTTVLUGAEKUMQUILINS FCYHERLSVAGNCRMCLUSIEKAPKUVAACAMPWAKGRNILINS EKSKKARRGUMEPLLANHPLDCPICDGGGECDLQDQSMMFGNDR SRFIEGKRAVEDKNIGPLUKTIMTRCIQCTRCIRRASEIAGUDD LGTTGRGNDMQUGTYIEKMFMSLIGSNIIDICPUGALTSKPYAF TARPMETAKTESIDVADAUGSNIUVSTRGEWMILIPRMHEDIN EEWISDKTRFAYDGLKRGALTEPMYREKSLLITTYSVEDALGRV AGMLQSFGGKDVAAIAGGLVDRAEMILIPRMHEDIN PFTAGAGTDLRNYLLINTITAGVERAUVALKOLLNRYDGDTLCTEE VFFTAGAGTDLRNYLLINTITAGVERAUVALKOLLNRYDGDTLCTEE VFPTAGAGTDLRNYLLINTITAGVERAUVALKOLLNRYDGDTLCTEE VFPTAGAGTDLRNYLLINTITAGVERAUVALKOLLNRYDGDTLCTEE VFPTAGAGTDLRNYLLINTITAGVERAUVALKOLLNRYBOLGS SHPFSQVLKEAKKPMVVLGSSALGRNDGAAILAAVSIAQKTRM TAGVTGDWKVMNILRRIASQVAALDLGYRFGVEAIRKNPPKVLP LUGADGGCITRQDLFRDCFIITYQCHRGDWGAPIADVLLOGAAYT EKSATYVATFBCRAQGTVAVYTPPCLAREDWKITRAGSTLAGGTL PYDTTL\DQVRNRLEEVSNLWYDDLEG\ANYFQQAABLSKLVN QCLLADPLVPPQLITMKDFYHTDSISRASQTMAKCVKAVTEGAQA VEEPSIC  5983 248 1763 EARGDGGRRHRASGRRAGRGEP\AGLKSQGGRAVFKRAVARGG CN\YSAAIAALEPAGSSTADDLSILYSNRACYLKSCNCSGCIQ DCNRALELHFFSNKPLLRRAMAVELGYGKAYYDYKTVLQIDC GCQLALNDSVNRLSRIIMELDGPMWEKKJSLIPAVPASVPLQAWH PAKEMISKQAGDSSSHRQQGITDEKTFTGLKEGNQCVNDKNYK DALSKYSECLKINNKECAITINRACYLKLQCYEERKQDCDQAL QLAGGNVKAFYRRALAHKGLNYOKSLIDLINKVILLDPSIIEAK MELBEVTRLINKUNKTAPFNKEERRKLEIQURKAVPLQAWH PAKEMISKQAGDSSSHRQQGITDEKTFTGLKEGNQCVNDKNYK MELBEVTRLINKUNKTAPFNKEERRKLEIQURKAVPLLQUH LIEKDPSILVQHLILVLSKAERFKMALTLISKGCKELIGUFFDL STRKNEACAHLLATARKDLMMFLSNKLEGDTFLLLIQSLKNN LIEKDPSILVQHLILVLSKAERFKMALTLISKGCKELIGUFFDL STRKNEACAHLLATARKDLMMFLSNKLEGDTFLLLLGRVU SSPKINVSFYON\OTSTORSCTVFWQRCSLVGPPQVTVFTMY PHHSLRSISRFSG FROMPSIPSAAAGNSHIQIPPGLTELLQGYTWEVLRQQPPDLVE SPKINVSFYON\OTSTORSCTVFWQRCSLVGPPQVTVPTMY PHHSLRSISRFSGS RRNPSIPSAAAGNSHIQIPPGLTELLQGYTWEVLRQQPPDLVE FAVEYTTRLEREARPASULPAATPRGGLAGCHADAK GDSSEEDBDLEVEVPSRRNREVSCAETTNPDEBEEDTDPRVI HPKTDERGCRICLAGCROILLFRNLDGGDLSQVLDAMFERIVKAD EHYIDGGDDGDNFYVIERGTYDILVTRONGRSGG ELALMTNYRARASAYAVGDKKLUNDRYRLIGCHMIMP	5982	56	2316	ATRPPRGSSWCRQFSRTASAAPGRSNMLRIPVRKALVGLSKSPK
FCYHERLSYAGNCRMCLVETERAPKVVAACAMPVMKGWILLINS EKSKKARGOVMEFILANPELDCI CDOGGECULDOGSMFGNDR SRFIEGKRAVEDKNIGPLVKTIMTRCIQCTRCIRFASEIAGVDD LGTTGRODDMQVGTYIEKMPMSELSGNIIDICPVGALTSKPYAF TARPMSTRKTESIDVMDAVGSNIVVSTRTGSVMRILPRHEDIN EEWISDKTRFAYDGLKRQRUIFBWVRNSKGLLTTTSWEDALSRV AGMLOSFGOKDVAALAGGLVDABALVALKDLLRNVEDDTLCTES VPFTAGAGTDLRSWYLLNTTIAGVERADVVLLVGTNPRYEAPLF NARIKSKHANDLKVALIGSPVDLTYTYDHLGDFNILQDIASG SHPFSQVLKEAKKPMVVLGSSALQRNDGAATLAAVSSTAQKTRM TSGVTGDWKVWNILHRIASGVAALDLGYKPGVVEAIRKNPPKVLP LUGADGGCITRQDLPDKDFIIYOGRNDGAATLAAVSTAQKTRM TSGVTGDWKVWNILHRIASGVAALDLGYKPGVVEAIRKNPPKVLP EKSATYVNTEGRAQOTKVAVTPPGLAREDWKIIRALSGIAGMTL PYDTLLOQVRNRLESVENSPNLVTYPDGLAREDWKIIRALSGIAGMTL PYDTLLOQVRNRLESVENSPNLVTYPDGLAREDWKIIRALSGIAGMTL PYDTLLOQVRNRLESVENSPNLVTYPDGLAREDWKIIRALSGIAGMTL PYDTLOQVRNRLESVENSPNLVTYPDGLAREDWKIIRALSGIAGMTL PYDTLOQVRNLESVENSPNLVTYPDGLAREDWKIIRALSGIAGMTL PYDTLOQVRNRLESVENSPNLVTYPDGLAREDWKIIRALSGIAGMTL PYDTLOQVRNRLESVENSPNLVTYPDGLAREDWKIIRALSGIAGMTL CQLLADPLVPPQLTMKDFYMTDSISRASGTMACVKAVTEGAQA VEEPSIC  5983  246  1763  EARGDGGRRHRASGRRAGRGEP\AGLKSQGQFAVPKRAVARGG RO\YSAATALLEPASSRIADDLSILYSNRAACYLKEGNCSGCIQ DCNRALEHPPSMKPLLRRAMAYSTLEQYGKAYDYKTVLQIDC GLQLANDSVNRLSRIIMELDGGNNEKEKSISIIAPVRASVPLQAWH PAKKMISRQAGDSSGIRQQGITDEKTFKALKEGNCVNDKNYK DALSKYSGCKLMINKSCATYNRNLCYLKCOPFEEKADDLOQAL QLADGNVKAFYRRALAHKGLKNYQKSLIDLNKVILLDPSIIEAK MELEVEYTELLINLOKTAAPHNLEKKERRKIBIQVENGKEEPGRPA GEVSTGCLASEKGGKSSRSPEDPEKLPIAKPRNAYEFGQIINAL STRKOKEACAHLLATTARKDLPMFLSNKLEGGTFLLLIGGIKKN LIEKDPSILVYGHLLIYKARAFKWHILISKGQKELIEQLFEDL SSPINNSFPYON\OTSTGRSCTVFVWQRCSLVGPFQVTVPTMY FHISLISSIRFSSG  5984  755  1193  SSVCMACTOTVSNIGKKQRSVSFLASGLMRVSTGPELRCHHSFVL TGDVGRRICRLIVGHFTKGDTSSKRVHPFSEGPCFLLCDLARVG SSPKINVSFPYON\OTSTGRSCTVFWQRCSLVGPFQVTVPTMY FHISLISSIRFSSS  6DSSSEEDBDLEVFPPSRFRNRVSVCAETTYRPDEBEDTDFRVI HHSLISSIRFSSS GDSSEEDBDLEVFPPSRFRNRVSVCAETTYRPDEBEDDTDFRVI HYKTDEQGRCCLQCAEAKGLILLFKNLOGLGOUDAMPERILAGCRITYCKNAKKRM PSPSFISVPLLKSEVSEKRKIVTVUGKRYKRYDCHNIVKN EHYNDGCDGDDFNTYIESGVSILLIBRSTVSNDGGNOGVSLARCKRGOFF	1	]		GCVRTTATAASNLIEVFVDGQSVMVBPGTTVLOACEKVGMOT PR
SRP.LEGKRAVEDKNIGPLVKITHRCIGCTECREASEIAGUD  LGTTGRENDMOGGTIYIEKMEMESLSGNIIDICPVGALTSKPYAF  TARPWETRKTESIDVMDAVGSNIVVSTRTGEVMRILPRHHEDIN  EEWISDKTRFAYDGLKRQRLITEMVMNEKGLLITTSWEDALSRV  AGMLQSFGGKDVAALAGGJUDAEALVALKDLLINVEDSDTLCTEE  VPFTAGAGTDLRSNYLLNTTIAGVEEADVULLUGTNPEREAPLF  NARIKRSKHINDLKVALLIGSPVDLTYDHLIGDSPKILDQIASG  SHPFSQVLKERAKKEMVVLGSSALQRNDGAAILAAVSSIAQKIRM  TSGVTGDWKVMNILHRIASQVAALDLGYKGVEVAIKANPPKVLP  LIGADGGCITRQDLPKDCTIIVQGHGDVGAPIADVLIBGARYT  EKSATYVNTEGRAQQTTVAVUTPGGLAREDWKITRALSEIAGMTL  PYDTL.DQVRNRLESEVSPHLWXYDIG.NANFQGABLSKLVN  QQLLADPLVPPQLTMKDFYMTDGISRASQTMAKCVKAVTEGAQA  VEEPSIC  5983  248  1763  EARGDGGRRHRASGRRAGRGEP\AGLKSQGGRAVPKRAVARGG  RQ\YSAAIALLEPAGSEIADDLSILYSNRAGCIKEGNCSCCIQ  DCNRALEHPPSMEPLHRAMAVSTLYGKKAVDYKTVLQIDC  GQLANDSVNKAEYTRALAHKGLKNYQKSLIDLNKVLLDEDSILGAK  MELEEVTRILINLENKTAPPNKEKERAKERISIOEVNEGKERPQRPA  GEVSTGCLASEKGKSSRSPEDPEKLPIAKPNAYERQCINNANYK  DALSKYSECLKINNKSCAITYNRALCYLKLCOPEERAKDCDQAL  QLADGNVKAFYRRALAHKGLKNYQKSLIDLNKVLLDESIIEAK  MELEEVTRILINLENKTAPPNKEKERRISIOEVNEGKEEPGRPA  GEVSTGCLASEKGGKSSRSPEDPEKLPIAKPNNAYERQCIINAL  STRKOKEACAHLLAITAPKDLPMFLSNKLEGTFFLLLIGSIKN  LIEKDPSLVYGHLLYLSAREFKWHITISKGCKELIEQHFEDL  SDTPNNHFTLEDIQALKRQYEL  5984  755  1193  SSVCMACTYVSNIGKKRQSVSPLASGLMRVSTGPELRHHSFVL  TGDVGRRICRLLVGIFTKGDTSSKRVHFPSPGPCFLLCDLARVG  SSPKINVSFFYON\CTSTGRSCTVFWQRCSLVGPPQVTVPTMY  FHISLRSISRFSSG  RRPNPSIPSIPSAAAGMSHIQIPPGLTELLQGYTVEURQQPPDLVE  PAVEYFTRIREARAPASULANTRUSCHEPPERPGPRAVDAK  GDSSSEEDBDLEVFVPSRFNRVSVCATTYNEDEEEDTDFRVI  HYKTDEGRCRLLFAKARTTVRRGGARRDLAGAERKAGVSERGDSGR  RRPNPSIPSIPSAAAGMSHIQIPPGTELLLQGYTVEURQQPPDLVE  PAVEYFTRIREARAPASULANTRUSCLGHPPPBEPGPRAVDAK  GDSSSEEDBDLEVFVPSRFNRVSVCATTYNEDEEEDTDFRVI  HYKTDEGRCRCALLGAGUSKERVSPLAGGLMCVSCATTYNEDEEEDTDFRVI  HYKTDEGRCRCALLGAGUSKERVSPLAGGLMCVTFRCIITVONAKKRKM  PESFIESVPLLKSEEVSERMKINDVIGKEVTRACKRGOTFG  ELALMYNTPRAAATIVATSBGSUMGLDRVTFRCIITVONAKKRKM  PESFIESVPLLKSEEVSERMKINDVIGKEVTRACKRGOTFG	i			PCYHERLSVAGNCRMCLVEIEKAPKVVAACAMPVMKGWNII.TNS
LGTTGRGNDQUGTTIERMFNELGGNILDICPUGALITREPATA TARPMETRITES IDUMDAUGNUSTRICBURGILPRHHEDIN EEWISCKTRPAYDGLKRQRLTEPMVRNEKGLLTYTSMEDALSRV AGMLQSTQGKDVAATAGGLVDAEALVALKOLINRVSDSTLCTEE VPFTAGAGTDLRSNYLLINTTAGEADVALKORINPRFRAPLF NARIRKSMIHNDLKVALIGSPUDLTYTYDHLGDSPKILGDING SHPFSQVLKEAKKMPVILGSSALQRNGGAAILAAVSSIAQKIRM TSGVTGDWKVMNILHRIASQVAALDLGYKRGVEAIRKMPPKVLF LLGADGGCITRQDLDKDCFIIYQGHEGDVAPAILAAVSSIAQKIRM TSGVTGDWKVMNILHRIASQVAALDLGYKRGVEAIRKMPPKVLF LLGADGGCITRQDLDKDCFIIYQGHEGDVAPAILAGIRAMTL PYDTIL\DQVRRLEEVSSHLVRYDDLEG\ANYFQQANELSKLVN QOLLADPLVPPQLIMKDFYHTDGISRAGGTMAKCVKAVTEGAQA VEEPSIC  ERARGTGGRRHHRASGRRAGGEP\AGLKSQGGAVPKRAVARG GO\YSAAITALLEPAGSSHIADQLSILYSNRAACYLKEGNCSGCIQ DCNRALELHPSMKPLLRRAMAYETLBQYGKAYVDYKTVLQIDC GLQLANDSVNRLSRIINMEGAIYTNRALCYLKLQFEEAKODCDQAL QLALGNVKAFYRRALAHKGLKNYQKSLIDLKKVILLDFSIIEAK MELEEVTRLINLKOKTAPPNKEKERKIELIGEVBEGKEFGRPA GEVSTGCLASEKGGKSSRSPEDPEKLPIAKPNNAYEFGQIINAL STRKDKEACAHLLAITAPRDLEPHSKLEGTFILLIQSLKNN LIEKDPSLVYQHLLYLSKARRFKMMLTLISKGQKELIEQDFEDL SDTPNNHFTLEDIQALKRQYEL  SSVENGACTYVSNLGKKGRSVSFLASGLMRVSTGFELRLHHSFVL TGDVGRRICGLLVGLETKGGTSSKRVHFFSEGCFFLLCDLARVG SSPRINVSPFYQN\QTSTORSCTVFVWQRCSLVGPPQVTVFTMY FHISLRSISRFSG  1193 SSVCMACTYVSNLGKKGRSVSFLASGLMRVSTGFELRLHHSFVL TGDVGRRICGLLVGLETKGGTSSKRVHFFSEGCFFLLCDLARVG SSPRINVSPFYQN\QTSTORSCTVFVWQRCSLVGPPQVTVFTMY FHISLRSISRFSG  1408 RRVARFGTAEPBAKARRTVKRGRARRDLAGAERKAGVSERGDGGR RRVDFSISPAAAGMSHIQIPPELTELLQGYTVEVLRQQPPDLVE PAVEYFTRLREARAPASVLPAATPRQSLGHPPEPGPDRVADAK GDSSEEDEBLEVPVSRRNRVSVCAETTNDFEEEDTDPRVI HPXTDEQGCGCLOEACGTLILFKRIDOGEGLSQVLDAMFERIVKAD EHVIDGGDDGDMFYVIERGTVDILVTKDNGTRSVGQYDNRGSFG ELALMYNTPRAATIVATSEGSLWGLDRVTTRRIIVKNNAKKKM PESFIESVPLLKSLEVSERMILVDVOGEKTYRS\COERTITYGE K\ADSFYIISGEVSILLTSSERMINDOGROELLRCHKGGYF GEALLVMNTPRAATIVATSEGSLWGLDRVTFRRIIVKNNAKKKM PESFIESVPLLKSLEVSERMILVDVOGEKTYRS\COERTITYGE K\ADSFYIISGEVSILLTSSERMINDOGROELLARCHKGGYF	İ	1		EKSKKAREGVMEFLLANHPLDCPICDQGGECDLQDQSMMFGNDR
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SSPKINVSPFYQN\QTSTQRSCTVFVWQRCSLVGPFQVTVPTMY FHHSLRSISRFSSG RRVARPGTAEPBAKARTVRRGRARRDLAGAERKAGVSERGDSGR RRPNPSIPSAAAGMSHIQIPPGLTELLQGYTVEVLRQQPPDLVE FAVEYFTRLREARAPASVLPAATPRQSLGHPPPEPGPDRVADAK GDSESEEDEDLEVPVPSRFNRRVSVCAETYNPDEEEEDTDPRVI HPKTDEQRCRLQEACKDILLFKNLDQEQLSQVLDAMFERIVKAD EHVIDQGDDGDNFYVIERGTYDILVTKDNQTRSVGQYDNRGSFG ELALMYNTPRAATIVATSEGSLWGLDRVTFRRIIVKNNAKKRKM FESFIESVPLLKSLEVSERMKIVDVIGBKIYKR/DGBRIITQGE K\ADSFYIISSGEVSILIRSRTKSNKDGGNQEVELARCHKGQYF GGLALVTNKPRAASAYAYGDVKCLVMDVOAFERLIGPCMDIMKPR		)	ł	TGDVGRRICRLLVGLFTKGDTSSKRVHPFSPGPCFLLCDLAPUG
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RRVARPGTAEPAKARRTVRGRARRDLAGAERKAGVSERGDSGR RRPNPSIPSAAAAGMSHIQIPPGLTELLQGYTVEVLRQQPPDLVE FAVEYFTRLREARAPASVLPAATPRQSLGHPPPEPG PDRVADAK GDSESEEDEDLEVPVPSRFNRRVSVCAETYNPDEEEEDTDPRVI HPKTDEQRCRLQEACKDILLFKNLDQEQLSQVLDAMFERIVKAD EHVIDQGDDGDNFYVIERGTYDILVTKDNQTRSVGQYDNRGSFG ELALMYNTPRAATIVATSEGSLWGLDRVTFRRIIVKNNAKKRKM PESFIESVPLLKSLEVSERMKIVDVIGBKIYRR/DGERIITQGE K\ADSFYIISGEVSILIRSRTKSNKDGGNQEVEIARCHKGYF GGLALVTNKPRAASAYAYGDVKCLVMDVOAFERLIGPCMDIMKP	5985	22	1409	FHHSLRSISRFSSG
FAVEYFTRIREARAPASVLPAATPRQSIGHPPPEPGPDRVADAK GDSESEEDEDLEVPVPSRFNRRVSVCAETYNPDEEEEDTDPRVI HPKTDEQRCRIQEACKDILLFKNLDQEQLSQVLDAMFERIVKAD EHVIDQGDDGDNFYVIERGTYDILVTKDNQTRSVGQYDNRGSFG ELALMYNTPRAATIVATSEGSLWGLDRVTFRRIIVKNNAKKRKM FESFIESVPLLKSLEVSERMKIVDVIGBKIYKR/DGERIITQGE K\ADSFYIISSGEVSILIRSRTKSNKDGGNQEVEIARCHKGQYF GELALVTNKPRAASAYAVGDVKCLVMDVOAFERLIGPCMDIMKP	1		1408	RKVARPGTAEPAKARRTVRRGRARRDLAGAERKAGVSERGDSGR
GDSESEEDEDLEVPVPSRFNRRVSVCAETYNPDEEEEDTDPRVI HPKTDEQRCRLQEACKDILLFKNLDQEQLSQVLDAMFERIVKAD EHVIDQGDDGDNFYVIERGTYDILVTKDNQTRSVGQYDNRGSFG ELALMYNTPRAATIVATSEGSLWGLDRVTFRRIIVKNNAKKRKM FESFIESVPLLKSLEVSERMKIVDVIGBKIYKR/DGERIITQGE K\ADSFYIIESGEVSILIRSRTKSNKDGGNQEVEIARCHKGQYF GELALVTNKPRAASAYAVGDVKCLVMDVOAFERLIGPCMDIMKP	1	į		PAVEVETEL PEARA DAGIN PARE EN
HPKTDEQRCRLQEACKDILLFKNLDQEQLSQVLDAMFERIVKAD EHVIDQGDDGDNFYVIERGTYDILVTKDNQTRSVGQYDNRGSFG ELALMYNTPRAATIVATSEGSLWGLDRVTFRRIIVKNNAKKRKM FESFIESVPLLKSLEVSERMKIVDVIGBKIYKR/DGERIITQGE K\ADSFYIISSGEVSILIRSRTKSNKDGGNQEVEIARCHKGQYF GELALVTNKPRAASAYAVGDVKCLVMDVOAFERLIGPCMDIMKP	1		1	GDSESEDEDLEVEVENDED ENTERVENCE TO THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY
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FESFIESVPLLKSLEVSERMKIVDVIGEKIYKR/DGERIITQGE K\ADSFYIIESGEVSILIRSRTKSNKDGGNQEVEIARCHKGQYF GELALVTNKPRAASAYAVGDVKCLVMDVOAFERLIGPCMDIMKP	Í		1	ELALMYNTPRAATIVATSEGSLWGI.DRVTFDDITUKNNAVODUL
K\ADSFYIIESGEVSILIRSRTKSNKDGGNQEVEIARCHKGQYF GELALVTNKPRAASAYAVGDVKCLVMDVOAFERLIGPCMDIMKP			i i	FESFIESVPLLKSLEVSERMKIVDVIGBKIYKR/DGERITTOGE
GELALVTNKPRAASAYAVGDVKCLVMDVOAFERLIGPCMDIMKP				K\ADSFYIIESGEVSILIRSRTKSNKDGGNOEVEIARCHKGOVE
NISHYEEQLVKMFGSSVDLGNLGQ	1		[ (	GELALVTNKPRAASAYAVGDVKCLVMDVOAFERLIGPCMDIMKP
		<u>-</u>	1	NISHYEEQLVKMFGSSVDLGNLGQ

SEC	Predicted	Predicted end	
ID			Amino acid segment containing signal peptide
NO:		nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
I NO:	location	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	1	corresponding	H=H1stidine, I=Isoleucine, K=Lvsine.
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	1	\=possible nucleotide insertion)
5986	1806	484	DAWKSTSLTFHWKLWGRHRGRRRGLAHPKNHLSPQQGGATPQVP
1	1	100	SPCCPED CRECORDED COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR
		}	SPCCRFDSPRGPPPPRLGLLGALMAEDGVRGSPPVPSGPPMEED
1			GLRWTPKSPLDPDSGLLSCTLPNGFGGQSGPEGERSLAPPDASI
İ	İ		LISNVCSIGDHVAQELFQGSDLGMAEEAERPGEK\AGQHSPLRE
1			EHVTCVQSILDEFLQT\YGSLIPLSTDEVVEKLEDIFQQEFSTP
-	Į.		SRKGLVLQLIQSYQRMPGNAMVRGFRVAYKRHVLTMDDLGTLYG
			QNWLNDQVMNMYGDLVMDTVPEK\VHFPNSFFY\DKLRTKGVDG
}	1	ļ	VKRWTKNVDIFNKELLLIPIHLEVHWSLISVDVRRRTITYFDSQ
İ	i	1	RTLNRRCPKHIAKYLQAEAVKKDRLDFHQGWKGYFKMNVARQNN
	i	i	DSDCGAFVLQYCKHLALSQPFSFTQQDMPKLRRQIYKBLCHCKL
	i		TV TV
5987	1806	484	1 * '
1		704	DAWKSTSLTFHWKLWGRHRGRRRGLAHPKNHLSPQQGGATPQVP
1	1		SPCCRFDSPRGPPPPRLGLLGALMAEDGVRGSPPVPSGPPMEED
ı		I	GLRWTPKSPLDPDSGLLSCTLPNGFGGOSGPEGERSLAPPDASI
1	1	1	LISNVCSIGDHVAQELFQGSDLGMAEEAERPGEK\AGOHSPTRE
1			EHVTCVQSILDEFLQT\YGSLIPLSTDEVVEKLEDIFOOEFSTP
			SRKGLVLQLIQSYQRMPGNAMVRGFRVAYKRHVLTMDDLGTLVG
1			CNWLNDQVMNMYGDLVMDTVPEK\VHFFNSFFY\DKLRTKGYDG
	1		VKRWTKNVDIPNKELLLIPIHLEVHWSLISVDVRRRTITYFDSQ
1			RTLNRRCPKHIAKYLQAEAVKKDRLDFHQGWKGYFKMNVARQNN
			DSDCGAFVLQYCKHLALSQPFSFTQQDMPKLRRQIYKELCHCKL
1	1		TV TV
5988	1292	410	1 **
		410	FKKYFLSFLGLLESSHSRDRIHNLVLMFLLATHNLVWWFTCRFQ
	1		RLDCIYLNAGIMPNPQLNIKALLFGLFS\AEGLLTQGDKITADG
			LQEVFETDVFGHFILIRELEPLLCHSDNPSQLIWTSSRNARKSN
1			FSLEDFQHSKGKEPYSSSKYATDLLSVALNRNFNQQGLYSNVAC
1	1		PGTALTNLTYGILPPFIWTLLMPAILLLRFFANAFTLTPYNGTE
1	]		ALVWLFHQKPESLNPLIKYLSATTGFGRNYIMTOKMDLDEDTAE
5000			KFYQKLLELEKHIRVTIQKTDNQARLSGSCL
5989	194	2610	AMDFPQHSQHVLEQLNQQRQLGLLCDCTFVVDGVHFKAHKAVI.A
	1 1		ACSEYFKMLFVDQKDVVHLDISNAAGLGQVLEFMYTAKLSLSPE
			NVDDVL\AVATFLQMQDIITACHALKSLAEPATSPGGNAEALAT
İ	l J		EGGDKRAKEEKVATSTLSRLEQAGRSTPIGPSRDLKEERGGQAQ
	i		SAASGAEQTEKADAPREPPPVELKPDPTSGMAAEAEAALSESS
			EQEMEVEPARKGEEEQKEQEEQEEEGAGPAEVKEEGSQLENGEA
j			PEENENEESAGTDSGQELGSEARGLRSGTYGDRTESKAYGSVIH
i ·	1		KCEDCGKEFTHTGNFKRHIRIHTGEKPFSCRECSKAFSDPAACK
			AUDITORIA KATETATGERPFSCRECSKAFSDPAACK
	1		AHEKTHSPLKPYGCEECGKSYRLISLLNLRKKRHSGEARYRCED
1	1		CGKLFTTSGNLKRHQLVHSGEKPYQCDYCGRSFSDPTSKMRHLE
]			THDTDKEHKCPHCDKKFNQVGNLKAHLKIHIADGPLKCRECGKQ
			FTTSGNLKRHLRIHSGEKPYVCIHCQRQFADPGALQRHVRIHTG
	1		EKPCQCVMCGKAFTQASSLIAHVROHTGEKPYVCERCGKRFVOS
[	<b>.</b>		SQLANHIRHHONIRPHKCSVCSKAFVNVGDLSKHIIIHTGRKDY
1	1		LCDKCGRGFNRVDNLRSHVKTVHQGKAGIKILEPEEGSEVSVVT
!	1		VDDMVTLATEALAATAVTQLTVVPVGAAVTADETEVLKAEISKA
1			VKQVQEEDPNTHILYACDSCGDKFLDANSLAQHVRIHTAQALVM
f	1		FQTDADFYQQYGFGGTWPAGQVLQAGELVFRPRDGAEGQPALAE
			TSPTAPECPPPAE
5990	2	4700	FGPGPDSGGGARGSGWGSRSQAPYGTLGAVSGGEQVLLHEEAGD
	]		SCENSISDICUSTORING SASSAN IGTLEAVSGEROVILHERAGD
			SGFVSLSRLGPSLRDKDLEMEELMLQDETLLGTMQSYMDASLIS
			LIEDFGSLGEVEMSLPDPSWDFSPPSFLETSSPKLPSWRPPRSR
			PRWGQSPPPQQRSDGEEEEEVASFSGQILAGELDNCVSSIPDFP
			MHLACPEEEDKATAAEMAVPAAGDESISSLSELVRAMHPYCLPN
			LTHLASLEDELQEQPDDLTLPEGCVVLEIVGOAATAGDDLEIPV
	}		VVRQVSPGPRPVLLDDSLETSSALQLLMPTLESETEAAVPKVTI.
	1	1	CSEKEGLSLNSEEKLDSACLLKPREVVEPVVPKEPONPPANAAP
		1	GSQRARKGRKKKSKEQPAACVEGYARRLRSSSRGOSTVGTEVTS
	1	ł	QVDNLQKQPQEELQKESGPLQGKGKPRAWARAWAAALENSSPKN
	1		LERSAGQSSPAKEGPLDLYPKLADTIQTNPIPTHLSLVDSAQAS
	1		PMPVDSVEADPTAVGPVLAGPVPVDPGLVDLASTSSELVEPLPA
		į	EPVLINPVLADSAAVDPAVVPISDNLPPVDAVPSGPAPVDLALV

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
}	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
İ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
- [	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion.
	sequence		\=possible nucleotide insertion)
ł			DPVPNDLTPVDPVLVKSRPTDPRRGAVSSALGGSAPOLLVESES
			LDPPKTIIPEVKEVVDSLKIESGTSATTHEARPRPLSLSEYRRR
			RQQRQAETEERSPQPPTGKWPSLPETPTGLADIPCLVIPPAPAK
			KTALQRSPETPLBICLVPVGPSPASPSPEPPVSKPVASSPTEQV
ł			PSQEMPLLARPSPPVQSVSPAVPTPPSMSAALPFPAGGLGMPPS
			LPPPPLQPPSLPLSMGPVLPDPFTHYAPLPSWPCYPHVSPSGYP
			CLPPPPTVPLVSGTPGAYAVPPTCSVPWAPPPAPVSPYSSTCTY
			GPLGWGPGPQHAPFWSTVPPPPLPPASIGRAVPQPKMESRGTPA
1			GPPENVLPLSMAPPLSLGLPGHGAPQTEPTKVEVKPVPASPHPK
	1		HKVSALVQSPQMKALACVSAEGVTVEEPASERLKPETQETRPRE KPPLPATKAVPTPRQSTVPKLPAVHPARLRKLSFLPTPRTQGSE
			DVVQAFISEIGIEASDLSSLLEQFEKSEAKKECPPPAPADSLAV
· I	1		GNSGGVDIPQEKRPLDRLQAPELANVAGLTPPATPPHQLWKPLA
			AVSLLAKAKSPKSTAQEGTLKPEGVTEAKHPAAVRLQEGVHGPS
	ļ		RVHVGSGDHDYC\VRSRTPPKK\MPALLIPEVGSRWNVKRHQDI
1,	) j		TIKPVLSLGPAAPPPPCIAASREPLDHRTSSEQADPSAPCLAPS
4			SLLSPEASPCRNDMNTRTPPEPSAKQRSMRCYRKACRSASPSSQ
1.			GWQGRRGRNSRSVSSGSNRTSEASSSSSSSSSSSSRSRSRSLSPP
1			HKRWRRSSCSSSGRSRRCSSSSSSSSSSSSSSSSSSSRSRSRS
1			PSPRRRSDRRRRYSSYRSHDHYQRQRVLQKERAIEERRVVFIGK
	]	:	IPGRMTRSELKQRFSVFGEIEECTIHFRVQGDNYGFVTYRYAEE
1	1		AFAAIESGHKLRQADEQFFDLCFGGRRQFCKRSYSDLDSNREDF
5991	334	1379	DPAPVKSKFDSLDFDTLLKQAQKNLRR RLSSHFSQCSPSIYC\TKFDKQGNVTSFERKKTELYQELGLQAR
		2373	DLRFQHVMSITVRNNRIIMRMEYLKAVITPECLLILDYRNLNLK
			QWLFRELPSQLSGEGQLVTYPLPFEFRAIEALLQYWINTLQGKL
			SILOPLILETLDALGDPKHSSVDRSKLHILLONGKSLSELETDI
]			KIPKESILEILDEEELLEELCVSKWSDPQVFEKSSAGIDHAEEM
		· .	ELLLENYYRLADDLSNAARELRVLIDDSQSIIFINLDSHRNVMM
i i		İ	RLNLQLTMGTFSLSLFGLMGVAFGMNLESSLEEDHRIFWLTTGT
5992	2	609	MFMGSGLIWRRLLSFLGR/LARSSIASYGMKDMVHGGIVEGL
","	•	609	AGPDFRLVCGVSGSGFPGGRQGQATEWRPLRPWNGAMEKLRRVL
1 1			SGODDEEQGLTAQDSQINL/SEVLDASSLSFNTRLKWFAICFVC GVFFSILGTGLLWLPGGIKLFAVFYTLGNLAALASTCFLMGPVK
1			QLKKMFEATRLLATIVMLLCFIFTLCAALWWHKKGLAVLFCILQ
			FLSMTWYSLSYIPYARDAVIKCCSSLLS
5993 .	1650	594	AEGLGSWAVWAGLGWAGRHMEAGGATGALGVGCKLPSAFCFPGS
1 1	!	ľ	SVAMDMFQKVEKIGEGTYGVVYKAKNRETGQLVALKKIRLDLEM
j l	1		EGVPSTATREISLLKELKHPNIVRLLDVVHNERKLYLVFEFLSO
ļ [		1	DLKKYMDSTPGSELPLHLIKSYLFQLLQGVSFCHSHRVIHRDLK
} !	1		PONLLINELGAIKLADFGLARAFGVPLRTYTHEVVTLWYRAPEI
	· 1.		LLATRFYTTAVDIWSIGCIFAEMVTRKALFPGDS\EIDQ\LFRI
	ľ	İ	FRMLGTPSEDTWPGVTQLPDYKGSFPKWTRKGLEEIVPNLEPEG
	1		RDLLMQLLQYDPSQRITAKTALAHPYFSSPEPSPAARQYVLQRF RH
5994	394	1934	AGEVQLHVWIRGMRIQPQ/KAAAIIDLDPDFEPQSRPRSCTWPL
	:		PRPEIANQPSKPPEVEPDLGEKVHTEGRSEPILLPSRLPEPAGG
!!!			PQPGILGAVTGPRKGGSRRNAWGNQSYAELISQAIESAPEKRLT
			LAQIYEWMVRTVPYFKDKGDSNSSAGWKNSIRHNLSLHSKFIKV
			HNBATGKSSWWMLNPEGGKSGKAPRRRAASMDSSSKLLRGRSKA
	ŀ	l l	PKKKPSGLPAPPEGATPTSPVGHFAKWSGSPCSRNREEADMWTT
		į.	FRPRSSSNASSVSTRLSPLRPESEVLAEEIPASVSSYAGGVPPT
		į.	LNEGLELLDGLNLTSSHSLLSRSGLSGFSLOHPGVTGPLHTYSS
		l	SLPSPAEGPLSAGEGCFSSSQALEALLTSDTPPPPPADVLMTQVD
	•	į	PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLEAPGPSSLVPTL
		1	SMIAPPPVMASAPIPKALGTPVLTPPTEAASQDRMPQDLDLDMY
5995	2		MENLECDMDNI ISDLMDEGEGLDFNFEPDP RPPGPGPASGAWLCTRARGSAAFVPPLPRPPSRGARRRRLPGR
	-		GVAALRRGPGSAPGLPRGRAERSAAGSGRGPSREERGAAAAAAA
			AEMMEELHSL\DP\RRQELLEARF\TGLGVSKGPLNSESSNQSL
		1;	CSVGSLSDKEVETPEKKQNDQRNRKRKAEPYETSQGKGTPRGHK

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
l l	location	corresponding	H-Histidine, I-Isoleucine, K-Lysine,
j	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ŀ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
I	amino acid	sequence	Codon, /=possible nucleotide deletion,
}	sequence		\=possible nucleotide insertion)
		<del></del>	ISDYFERRVEQPLYGLDGSAAKEATEEQSALPTLMSVMLAKPRL
Ì	1 .	1	DTEQLAQRGAGLCFTFVSAQQNSPSSTGSGNTEHSCSSQKQISI
i			QHRQT\QSDLTIEKISALENSKNSDLEKKEGRIDDLLRANCDLR
İ	1	1	RQI\DEQQKMLEKYK\ERLNRCFDNEPRNFLIEKSKQEKMACRD
1			KSMQDRLRLGHFTTVRHGASFTEQWTDGYAFQNLIKQQERINSQ
			REEIERQRKMLAKRKPPAMGQAPPATNEQKQRKSKTNGAENETL
			TLAEYHEQEEIFKLRLGHLKKEEAEIQAELERLERVRNLHIREL
1			KRIHNEDNSQFKDHPTLNDRYLLLHLLGRGGFSEVYKAPDLTEQ
			RYVAVKIHQLNKNWRDEKKENYHKHACREYRIHKELDHPRIVKL
ŀ	1		YDVESI.DTDSECTUI PYCECNDI DEVI KOMA MORANI I
1			YDYFSLDTDSFCTVLEYCEGNDLDFYLKQHKLMSEKEARSIIMQ
	1		IVNALKYLNEIKPPIIHYDLKPGNILLVNGTACGEIKITDFGLS
	1		KIMDDDSYNSVDGMELTSQGAGTYWYLPPECFVVGKEPPKISNK
·			VDVWSVGVIFYQCLYGRKPFGHNQSQQDILQENTILKATEVQFP PKPVVTPEAKAFIRRCLAYRKBDRIDVQQLACDPYLLPHIRKSV
ľ	<b>)</b> .		STSSPAGAAIASTSGASNNSSSN
5996	1612	981	
1			DQQACIJGIMLTLEFGILEFDPSWIGSWTQR/SWVSWRSRPGCE
ł	Í	•	LFSIVVFGSIVNEGYLNSASEGEEFCIYNRNPNACSYGVAVGVL AFLTCLLYLALDVYFFQISSVKDRKK\AVLSGHPVVSGEPHPAA
	ľ		FWAFLWFTGDSCYL\ANQWQVSKPKDNPLNEGTDASPGRPSPFS
	<u> </u>		FFSIFTWSLTAALAVRRFKDLSFQEEYSTLFP\ASAQP
5997	1612	981	DQQACLIGLMLTLEFGILEFDPSWIGSWTQR/SWVSWRSRPGCE
			LFSIVVFGSIVNEGYLNSASEGEEFCIYNRNPNACSYGVAVGVL
			AFLTCLLYLALDVYFPQISSVKDRKK\AVLSGHPVVSGEPHPAA
Ì			FWAPLWFTGDSCYL\ANQWQVSKPKDNPLNEGTDASPGRPSPFS
			FFSIFTWSLTAALAVRRFKDLSFQEEYSTLFP\ASAQP
5998	1612	981	DQQACLIGIMLTLEFGILEFDPSWIGSWTQR/SWVSWRSRPGCE
1	<u> </u>	, , ,	LFSIVVFGSIVNEGYLNSASEGEEFCIYNRNPNACSYGVAVGVL
			AFLTCLLYLALDVYFPQISSVKDRKK\AVLSGHPVVSGEPHPAA
1 "		•	FWAFLWFTGDSCYL\ANQWQVSKPKDNPLNEGTDASPGRPSPFS
1 .			FFSIFTWSLTAALAVRRFKDLSFQEEYSTLPP\ASAQP
5999	2	1790	RPPMEKARRGGDGVPRGPVLHIVVVGFHHKKGCQVEFSYPPLIP
			GDGHDSHTLPEEWKYLPFLALPDGAHNYQEDTVFFHLPPRNGNG
1			ATVFGISCYR\QIEAKALKVRQADITRETVQKSVCVLSKLPLYG
1		4	LLQAKLQLI'THAYFEEKDFSQISILKELYEHMNSSLGGASLEGS
		i	QVYLGLSPRDLVLHFRHKGLILFKLILLEKKVLFYISPVNKLVG
1	1		ALMTVLSLPPGMIEHGLSDCSQYRPRKSMSEDGGLQESNPCADD
1	ļ. I		FVSASTADVSHTNLGTIRKVMAGNHGEDAAMKTEEPLFQVEDSS
1 '	1		KGQEPNDTNQYLKPPSRPSPDSSESDWETLDPSVLEDPNLKERE
	i i		QLGSDQTNLFPKDSVPSESLPITVQPQANTGQVVLIPGLISGLE
			EDQYGMPLAIFTKGYLCLPYMALQQHHLLSDVTVRGFVAGATNI
[ :	1		LFRQQKHLSDAIVEVEEALIQIHDPELRKLLNPTTADLRFADYL
			VRHVTENRUDVFLDGTGWEGGDEWIRAOFAVVTHALLAATLOLU
j l			LFRIVNVAKKIGNVMVTT\SRNVVQTGK\AVGQSVGGAFS\SAK
<u> </u>			TA\MSSWLSTFTTSTSQSLTEPPDEKP
6000	101	1561	TEPCRTAENCTATMSENNKNSLESSLRQLKCHFTWNLMEGENSL
	•	,	DDFEDKVFYRTEFQNREFKATMCNLLAYLKHLKGQNEAALECLR
1			KAEELIQQEHADQAEIRSLVTWGNYAWVYYHMGRLSDVQIYVDK
	1		VKHVCEKFSSPYRIESPELDCEEGWTRLKCGGNQNERAKVCFEK
			ALEKKPKNPEFTSGLAIASYRLDNWPPSQNAIDPLRQAIRLNPD
	1		NQYLKVLLALKLHKMREEGEEGEGEK\LVEEALEKAPG\VTDV
	. [		LRSAA/KFYRGKDEPDKAIELLKKALEYIP/NNAYLHCQIGCCY
		1	RAKVFQVMNLRENGMYGKRKLLELIGHAVAHLKKADEANDNLFR
ĺ			VCSILASLHALADQYEDAEYYFQKEFSKELTPVAKQLLHLRYGN
	ļ	İ	FQLYQMKCEDKAIHHFIEGVKINQKSREKEKMKDKLQKIAKMRL
	İ	į	SKNGADSEALHVLAFLQELNEKMQQADEDSERGLESGSLIPSAS
			SWNGB
6001	176	1038	AFAHSPSRGHRETHIHTPRHTPRCTMAESHLQSSLITASQFFEI
		ļ	WLHFDADGSGYLEGKELQNLIQELQQARKKAGLELSPEMKTFVD
			QYGQRDDGKIGIVELAHVLPTEENFLLLFRCOOLKSCE\EFMKT
			WRKYDTDHSGFIETEELKNFLKDLLEKANKTVDDTKLAEYTDLM

Deginning   nucleotide   location   corresponding to first   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino a		SEQ	Predicted	Predicted end	hmino acid company
No: nucleotide location corresponding to first amino acid residue of amino acid residue of amino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence		ID	beginning		Amino acid segment containing signal peptide
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Sequence		i			w=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
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HLSTVLGINKPHGAEATUPTILINUPNSAKUNATSGCAAIRFII RRTHVPRILIPLITISTICSKSVPVRRSPEPLDLLLQBWQCHMSLE RRAAVLVETIKKGHDADAEARVERRTYMGLRNHFPGEAETLY NSLEPSYGKSLQTTLKSKSGVASLPQSDRSSSSSCESLNRPPSS KKSTANPETVAGRVSAGSKASSLPGSLGRSKSIDTONAAAGAK AHHAAGQSVRSGRIGAGALMAGSYASLEDTSBKLDGTASEDGRV RAKLSAPLAGMRNAKADSGRSRFRYWSYGSQFGRGSS PGRUIT TTALSTVSSGVQRULVNSASAQKRSKIPRSQGCSREASPSRIKSY ARSSRIPPBSVSQGCSREASFESSERTSFSFFFSFFSFOFLASRHSRS TGALYAPBVYGASGPGYGISQSSRLSSSVAARVLUTGGDVERA VADALLLGDIRTKKKRARRTYSSVGHDDANSDASSACSERS YSSRNGSJPTYMROT\EDV\AEVLINCASSNWSERKEGLIGUGN LLKNQRTLSRVELKRICEIFTMFADPHGKRVFSMHEFILODFI QVHKDDLDDHIFVLITQLLKKMGADLLGSVGAKVOKALDVTESS FPRDLQFRILMRFTVDQTQTSSLKVKVALLKYITTAKOMDEGD FINSSETRLAVSRVTWATTEFKSSDVAKAAGSVLISLFFELHOPFI FPHLLGALPRTFQGGATKLLINHFRRTVGRTQSSMSPLTRFTP RSPANNSSPLTSFTNTSGONTLSPRAPDVTRMSSDIVSSLRG VTEAJONPSFRSGEMNRPLKRDSKUDDSMCGGPG\MSDPRA GGDATDSSTAL\DNKASLLHSMPTHSPRSDKVDTRSNSDIVSSLRG VTEAJONPSFRSGEMNRPLKRDSKUDDSMCGGPG\MSDPRA GGDATDSSTAL\DNKASLLHSMPTHSPRSRVDYFNYSDSIS FFNKSALKEMFDDDADGPPDLSLDHSKLLEHISHINDER VESRRIALYSELMKLITQESSFSVWBEHFKTILLLLETLGDKEPT IRRALKLKLELIRHQPAFFRYNASLTVELSHLDHEVVAN SAEEAASV\LATSI\SPEQCIKVLCPITQTADVPINLAAIKMOT KVIERVSKETINLLDEETHRPOLTGGYBKSSVRACVYCLVAV HAVIGDELKPHLSQLTGSKMKLINLYIKRAQTGSGGADPTTDVS GGS GGS GGS GKLRAFRGMRRLICKRICDYKSFDDEESVDGNFPSSAASAFKVP ARKTSGNPANSARKRGSRGGPKVGAGASKEGGGADVEDDPIKA FTDVSIGITYSSRELEETHRALTELLSDMDFRAMALKKIR SLLVAGAAQYDCFFPHLRLLDGALKISAKDLBSQVVERACITTVA HLSTVLGNKEDHGABATVTPTPHVINVANTSGCALTFFII RHTHVPRILIPLTTSNCTSKSVPVRRRSFEPLDLLLQENQTHSLE RHAAVLUETIKKGHDABATVTPTPHVINVANTSGCALTFFII RHTHVPRILIPLTISNCTSKSVPVRRRSFEPLDLLQENQTHSLE RHAAVLUETIKKGHDABATVARSAVSLENGSSGGBRUTT TTALSTVSSGVVSGGGCSREASPSSSGSGSRGSGGRGVLT TTALSTVSSGVVSGGGCGREASPSSTGSGGRRVLT TTALSTVSSGVVSGGGGGRGGSSGFGSGGFRLYFFS KRSTANPSTVAGRVSAGSSKASSLGGGRSSGGFRLYFFSS KASTANPSTVAGRVSAGSGSRATSJGGSRCGGRAVERSCGFRLY TALSTVSSGVGGGGGCREASPSRSGGFRLYFT TALSTVSSGVGGGGGRAFTSTSTMVSQSOPGGSRSGGFRLYF TALSTVSSGVGGGGGGRAFTSTSTMVSQSOPGGSRSGGFRLYFT TALSTVSSGVGGGGGGRAFTSTSTMVSQSOPGGRSGGGFRLYFT TALSTVSSGVGGGGGGGFTFTAMPADHORDANATHTSS	-				FIDVPSIQIYSSRELEETLNKIREILSDDKHDWDQRANALKKIR
RHATAVPELIPLITENCTSKSPVPARSFEFLDLLLGEWOTHSLE RHAAVLVETIKKGHADABARVERAFTUMIRNHFPGERETLY NSLEPSYOKSIGITIKSGSVASILPQSDRSSSSQESLNRPPSS KWSTANPESYVAGRVSGSKASSLPGSLGRKSSIDIVONAAAGAK AHHAAGQSVRGRIGAGALMAGSYASLEDTISKKLDTASEDGRV RAKUSAPLAGMGNAKADSKRSRTKWYGQOPGERGSPGSDFORVLT TTALSTVSSGVQVLVUNSASAQKRSKIPRSGGCGREASPERGSPGRUT TTALSTVSSGVQVLVUNSASAQKRSKIPRSGGCGREASPERGSPGRUT TTALSTVSSGVQVLVUNSASAQKRSKIPRSGGCGREASPERGSV ARSSIPPRSVSGCGREASPESSRDTSPVRSFOPLASRHHSRS TGALVAPREVGASGGOPGOTSGOSRLSSPAMFULNTOSDVCEA VADALLLGDIRTKKKPARRRYESYGMHSDDDANSDASSACSERS YSSRNGSIPTYMROT\EDVLANGASSWNSERKGGLIGGON LLKNGRTLSRVELKRLCSIFTRMFADPHGKRVFSMFLETUDFI QVHKDLQDWIFVILTOLLKKKMGADLLGSVQAKVOKALDVTRES FPRULGFILLMFTVDGOTTOTPSLKVXVALKVISTTAKAMDEG FINSSETELAVSRVTWTTEPKSSDVRKAAGSVLISLFELNTPE FSHLLGABLWYFOGGATKLLINHLBRTGGSMGSPLTRPTP RSFANWSSPLTSPTNTSQNTLSPSAFDVDTENMSSDIVSSLAG VTEALQNFSFRSGEDMNEPLKRDSKUDGOSMCGGG\MSDPRA GGDATDSSQTAL\DNKASLHISMPTISSFRVDPSYNYNSDSIS FFNKSALKEAMFDDDADOFPDDLSLDHSDLVABLLKRISNINER VEERKIALVSLMINLIGESFSVUNDEHFLLLLLLETLGDKEPT IRALALKVLREILRHQPARFKNYABLTVMKTLEAHKOPHKEVVR SABEAASVLATSI\SPEQCIKVLCPIIQTADVPIILAAIKMOT KVIERVSKETLALLEPEMBGLIGGVONSESSVRACVFCLVAV HAVIGDELKPHLSQLTGSKWLLINLYIKRAQTGSGGAPTTDVS GGS GKRAFFGMRRLICKRICDYKSFDDESVVORRPSSAASAFKVP AKTSGMPANSARKFGSAGGRVKGGAGAVERDOTTAV HENTYLCHKPDIGGABTIVTYLPNIVPNSAKVMATSGCAAIRFII RHTHVPRLIPLITISNCTSKSVPVRRRSFEFIDLLLQRMQTHSLE FINALVALFIKKGIHDADARBARVRAKTYGGAMFENTY NSLEPSVOKSLOTTILKSGGSVASLPGSLORSHSDIDVNAAGGAK AHHAAGGVVSGRGLGAGALMAGSYASLEDTSDKLDGTASEDGRV RAKLSAPLAGMONAKADSRGSSTKMVSQSQPOSSSSGGFRLYDFS TALSTVSGGVVGLVINSASAGAKSKIFFISGGCGREAPBERTLY NSLEPSVOGGCSREAPBESSRDTSPVRSFOPLARHENS TGALYAPEVVGAGGGGVGIGGSSRLSSSSRGGFRLYDFS TALSTVSGGVVGLVINSASAGAKSKIFFISGGCGREAPBERTLY NSLEPSVGGCGREAPFERSTAMVSQSQPORSASGFRLY TALSTVSGGVVGLVGTARGASSNASSERSGGLGCAN LLKNGRTLSGGVALRURGFTFTMADDHORKFVFSMFLETLYDFI QVHKDDLQDWLFVLITGLLKKNGADARSSNASERSREGLIGGON LLKNGRTUSGVVLANGAGSSRNTESSKREGLIGGON LLKNGRTUSGVVLANGRASSNINGENSREGLIGGON LLKNGRTUSGVVLANGREFTTERMADHORED FYNDLGFTILRRFTUDOTTSELKKVALUSTELSKUNDED					SDLVAGAAQYDCFFQHLRLLDGALKLSAKDLRSQVVREACITVA
RHAAVLVETIKKGHDADAEARVERRETYMGLRHIFFGERETLY NSLEPSYGKSLQTYLKSSGSVASLPGSLQCRSSDIDVINAAAGAK AHLAAGGSVASGTAGGALANGSVASLEDTSDKLDGTASEDGRV AHLAAGGSVASGTAGGALANGSVASLEDTSDKLDGTASEDGRV ARKLSAPLAGMANKADSRGRSTKWVSGOFGSRGS FORUT TTALSTVSSGVQRVLVNSASAQRSKIPSGGGGSGSGSGSGSGTRUT TTALSTVSSGVQRVLVNSASAQRSKIPSGGGGSGSGSGSGSGTRUT TTALSTVSSGVQRVLVNSASAQRSKIPSGVGGRGSGSGSGSGTRUT TTALSTVSSGVQRVLVNSASAQRSKIPSGVGGRASPSRLGV ARSSLIPARSVVGGGSRSHSSSVSAMRVLNTGGDVEA VADALLGDISTKKKPARRETSSYGNTDDVABAGAKSERS TGALYAPSVYGASGFGYGISGSSKISSSVSAMRVLNTGGDVEA VADALLGDISTKKVERREGE IFTEMRADPUDDABGASGSRGS YSSRNGSIPTYMRGT\EDV\ABVUNRCASSNNSERKGLLGLQN LLKNGRTISTVELKRUCE IFTEMRADPUDDABGASGSRGS YSSRNGSIPTWRGT\EDV\ABVUNRCASSNNSERKGLLGLQN LLKNGRTISTVELKRUCE IFTEMRADPUDABGASGRGSF FFINLGALPKTFGDGATKLLHNHIRRTGGTGSBMGPLTRTP RSPAMMSPLTSPTNTSGOTTSPASPTDYTENMSDIVSSLRG FFINLGALPKTFGDGATKLLHNHIRRTGGTGGSMGPLTRTPT RSPAMMSPLTSPTNTSGOTTSPASPTDYTENMSDIVSSLRG GGADTDSSGTALDNKRAGLHISMPTESFRSTVPIPYNYSDSIS FFINKSALKEAMFDDDADOPPDLSLDHSDLVABLLKRISHNINER VEEKKIALYELMKLTGESS YVENDEHFKTILLLLETLGDKEPT IRALAKVLREILRHQGRSS YVENDEHFKTILLLLETLGDKEPT IRALAKVLREILRHQGRSS YVENDEHFKTILLLLETLGDKEPT IRALAKVLREILRHGTESSSTVRACVYCLVAV HAVIGDELKPHLSQLTGSKMKLLNLYIKRAQTGSGADPTDVS GGS GG GGATDSSGTALDNKRAGLHSBOTTSSSTVRACVYCLVAV HAVIGDELKPHLSQLTGSKMKLLNLYIKRAQTGSGADPTTDVS GGS GG GKARFFGMRRLICKRICDYKSFDDESVDRIPSSAASAFKVP APKTSGNPANSARKPGSAGGPKVGAGASKEGGADPTDVS GGS GKARFFGMRRLICKRICDYKSFDDESVDRIPSSAASAFKVP APKTSGNPANSARKPGSAGGPKVGAGASKEGGADPTDVS GGS RKALSPETURITYTINGTSKSVPVRRFSSEPLDLLQENQTHSLE RHAMLVELTIKKGIHDADABARVEARKTYMGLRNIPFGEAETLY NSLEPSYQKSLQTYLKSGSVASLPGSDRSSSSGSGSNUTT TTALSTVSSGVVGNUNGAAGKRSGRSRTMVSQSQOPGSRSGSFGRVLT TTALSTVSSGVVGNUNGAAGAKSKTJRKHFGSAEGRUT TALSTVSGSVVGNGGAGARKGGGRSGFGRPAPSSRLPFS KNSTANSTYAGRVSAGSSKASSLPGSLGRSSSGFGRRAPFSRLPV ARSRIPRBSVSQCGREAPSSSRDTSPVRFQGCSREAPSGRLV TALSTVSGSVVGNGGAGARKAGGARASVASLEDFIKJORGSGFGRVLT TTALSTVSSGVVGNGGAGARKAGSGASRTMVSGSOPGRAPS TAALYAPSTVAGRVAGASSKASSLPGSLAGSSDANSGSGFRLV TAALSTVAGRVAGASGRSRTMVSGSOPGRSSPDFRLVV ARSRIPRBSVSGCGREAPSSGRAFLSSVSARVALTRISTSVDERA				i '	HLSTVLGNKFDHGAEAIVPTLFNLVPNSAKVMATSGCAAIRFII
NSLEPSYORS.LOTYLKSSGSVASLPQSINGERSDIDVNAAGAK KASTANPETVAGREVAGSSKASLPGSLQGSRGSIDMEPPSS KASTANPETVAGREVAGSSKASLPGSLQGSRGSIDGREVE HAKASAPLAGMINAKADSRGSRTKKWSQQGPGSRGSGSGRULT TTALSTVSSGVQRVLVMSASAQKRSKIPRGQGSREASPSRLSV ARSSRIPRSVSQCGSREASRESSDTSPVRSQPLASKHHSRS TGALYAPEVYGASGPGYGIGQSSRESSVEAMPUNTGDVEEA VADALLLGDIRTKKKPARRYBSYGHSDASNDASSACSERS YSSRNGSIPTYMROT/BDV\AEVIGNSGASNWSERKEGLIGLON LLKNQRTLSRVELKRLCEIFTRMFADPHGKRVFSWHIETLUDFI QVHKDLQDWLFVILITQLIKKKMADLLGSVQAKVQKALDVTRES FPNDLQFWILMFFVUDTOTPSLKVKVAILKYIETLAKKMDPGD FINSSTRIAVSRVITWTTEPRSSDVRRAAGSVLISLFBLNTPE FPNLLGALPXRFQGGARKLHHNILKNOTGOSSMSSPLTRETP RSPANNSSPLTSPTNTGQNTLGFSAFDVDTENNMSEDIYSSLRG VTRAIQNFSFRSQEDMNEPLKRDSKKDDGDSMCGGFGVMSDPRR GGDATDSSQTAL\DNRASLLHSWFTHTSSPRSDYNFXSDSIS FPNKSALMEANFDDDADGPPDLSLDISDLVABLKKRISNHINER VERKIALYELMKLTGESFSVWBHFKYTLLLLETGMEPT IRALALKVLREILRHQPARFNYABLTVMKTLBAKDPHKSVVR SABEARSVLATSI\SPECIKLUPLITQTADYPINLAKKMYT KVIERVSKETLNLLLPEINFGLIQGYDNSESVERACVFCLVAV HAVIGDELKPHLSQLTGSMMLLKLIYIKRAGYGSGADPTTDVS GG GKURAFRGMRRLICKRICDYKSFDDEBSVUBGNFSSAASAFKVP APKTSGNPANSARKFGSAGGPKVGAGSKKSGGAAVEDDFPIKA FTDVSSIOIYSSRELBETINKIRBILDDKHDWDQRANALKKIR SLLVAGAQYDCFFQHLRLDGAKLKSAKDGSVVBACATRFII RHTHYPALIPLITSNCTSKSVPVRRSFFFFLDLLIQBWOTHSLE RHAAULVEITKKGIHADABARVERMTGGRANFSGAAGRK KSTANBSTVAGRVSAGSKSSLPGSLQGRSGSGSGSCGNULT TTALSTVSGQVQRLVNASSAGVRSKIPRGGGGRSGSSGSCGVULT TTALSTVSGQVQRLVNASSAGVRSKIPRSGGGSRGSSGSFGRULT TTALSTVSGQVQRLVNASSAGVRSKIPRSGGGSRGSSGSFGRULT TTALSTVSGQVQRLVNASSAGVRSKIPRSGGGSRGSSGSFGRULT TTALSTVSGQVQRLVNASSAGVRSKIPRSGGGSRGSSFGRULT TTALSTVSGQVQRLVNASSAGVRSKIPRSGGGSRGSSFGRULT TTALSTVSGQVQRLVNASSAGVRSKIPRSGGGSRGSSFGRULT TTALSTVSGQVQRLVNASSAGVRSKIPRSGGGSRGSSFGRULT TTALSTVSGQVQRUNANSASAGRSKIPRSGGGSRGSSFGRULT TTALSTVSGQVQRUNANSASGRGSRTMRSPSRGGGRRESPRISV ARSSRIPPSVGGGGSREARFSSRTTSPVRSPGGGRRESPRISV ARSSRIPPSVGGGGSREARFSSRTTSPVRSPGGGRRESPRISV ARSSRIPPSVGGGGSRGSRSRRSKRSKRSKYSMRVUNTGSDVEBA VADALLLGDIRTKKKPARRYFSYGMISDDDANDASSACSERS YSSRNGSIPTYMRGT\CDDVASVLNRCASSNNSSERREGLLGLQN LLNQRTLKRYLKRICLEITINFALDAPHGKRVFSMIFLTUDPI QVHNDLQDWLDVLLTQLLKKGGDLLGSV	- [	•	'	· E	RHTHVPRLIPLITSNCTSKSVPVRRRSFEFLDLLLQEWQTHSLE
AMHARGSVRSGRIGAGALMGSYSBEDTDKLADTASEDGRY RAKUSAPLAGMONAKADSRGRSTKWVSQSQPGSRSSPGRVLT TTALSTVSGVQRVLVNSASAQKRSKIPRQGGSRBASPSBLSV ARSSRIPRPSVSQGCSRBASRESSRDTSPVRSQGGSRBASPSBLSV ARSSRIPRPSVSQGCSRBASRESSRDTSPVRSQGGSRBASPSBLSV ARSSRIPRPSVSQGCSRBASRESSRDTSPVRSQGGSRBASPSBLSV ARSSRIPRPSVSQGCSRBASRESSRDTSPVRSQGGSRBASPSBLSV ARSSRIPRPSVSQGCSRBASRESSRDTSPVRSQGGSRBASPSBLSV ARALLGIRTKKAPRRYESSYGMSDDDANSDASACSERS YSSRNGSIPTWROT\DVADVUMRCASSNWSERKEGLLGLQN LLKNQRVLSRVELKELGIFTRMFADPHGKRVFSMFLETLUDFI QVHKDDLQDWIFVILITQLLKKWAALLGSVVGAKVQKALDVTRES FPNDLQFWILMFFTVQTCTOTPSLKVKVALLKYIETLAKQMDPGD FINSSTELAUSRVITWTTEPKSSYRAGVSLISTPLEMTPE FTMLGALPKYFQDGATKLLHHHLBNTCHCOGSMGSPLTRFTP RSPANNSSPLTSPFTNTSQNTLSPSAFDYDTENNNSEDIYSSLGG VTEAIQNPSFRSQEDNNFPLKRDGKKUDGSMGGGF\MSDPRA GGDATDSSQTAL\DNRASILHSMTTHSSPRSRBYMPYNYSDSIS FPNKSALKEANFDDADAOFPDDLSLDHSDLVABLUKRISNINGR VEERKIALYSELMKLTQESFSVWDEHFKTILLLLETIGDKEPT IRALAKKULREILENDGAFKNYAELTVMKTLEAHKDPHKEVVR SABEAASV\LATSI\SPEQCIKVLPIQTADYPINLAAIKMOT KVIERVSKETINLLDEINPGLIGGYDNSSSSVRACCYFCLVAV HAVIGDEKKPHLSQLTGSFMKLLNLYIKRAQTIGSGADPTTDVS GQS  6004  140  4098  GKURAFRGMRRLICKRICDYKSFDDEESVDGNFSSASAFKVP APKTSGNPANSARKPGSAGGFXVGAGASKEGGAGAVEDDFIKA FTDVPSIQISSRELEETINKIRSILSDKHWDQRANALKKTR SLLVAGAQVQCFFCHLRLIGGALKISAKDLBSQVVREACHTVA HLSTYLCNKFDHGABEATVPTLFNLVDNSAKVMATSGCAAIRFII RHTHPHLIPLITSNCTSKSVPVRRRSFEFDLAGRRHIDGRANALKKTR SLLVAGAQVQCFFCHLRLIGGALKISAKDLBSQVVREACHTVA NSLEPSYQKSLGTYLKSSGSVASSLPOSDRSSSSGSINRPFSS KNSTANPSTVAGRVSAGSSKASSLPGGRSRSDGTMVLT TTALSTVSSGVQRUVNNSASQKRSKTPRGQGGSRGSFGRUV RAKLSAPLAGMCNAKADGRGRSTKTMVSQSQPGSRGSFRLSV ARSSRIPRPSVGGCSREAFSSRTSFVRSFDLASRHHSRS TGALYAPEVYQASGGVGSTGAGASKRSTRSPLSVSRRHSRS TGALYAPEVYQASGGVGSIGSGSRSSFRSSRFSFRLSV ARSSRIPRPSVGGGCSREAFSSRTSFVRSFDLASRHHSRS TGALYAPEVYQASGGVGSIGSGSRSSTSFRANSFRKGLIGGQN LLNQRTLSRVBLKRLCHVARVLRRCASSLWSSRKERGLIGGQN LLNQRTLSRVBLKRLCHVARVLRRCASLUSVSSKKETUDDFSPSRR VSSRNGSIPTYMRTV\LDUKKGADLLGSSVQKKUDKALDVTRES FPNDLQFTLIMPFTVDGTOTPSLKKVARADPLO			1		RHAAVLVETIKKGIHDADAEARVEARKTYMGLRNHFPGEAETLY
AMHARGSVRSGRIGAGALMGSYSBEDTDKLADTASEDGRY RAKUSAPLAGMONAKADSRGRSTKWVSQSQPGSRSSPGRVLT TTALSTVSGVQRVLVNSASAQKRSKIPRQGGSRBASPSBLSV ARSSRIPRPSVSQGCSRBASRESSRDTSPVRSQGGSRBASPSBLSV ARSSRIPRPSVSQGCSRBASRESSRDTSPVRSQGGSRBASPSBLSV ARSSRIPRPSVSQGCSRBASRESSRDTSPVRSQGGSRBASPSBLSV ARSSRIPRPSVSQGCSRBASRESSRDTSPVRSQGGSRBASPSBLSV ARSSRIPRPSVSQGCSRBASRESSRDTSPVRSQGGSRBASPSBLSV ARALLGIRTKKAPRRYESSYGMSDDDANSDASACSERS YSSRNGSIPTWROT\DVADVUMRCASSNWSERKEGLLGLQN LLKNQRVLSRVELKELGIFTRMFADPHGKRVFSMFLETLUDFI QVHKDDLQDWIFVILITQLLKKWAALLGSVVGAKVQKALDVTRES FPNDLQFWILMFFTVQTCTOTPSLKVKVALLKYIETLAKQMDPGD FINSSTELAUSRVITWTTEPKSSYRAGVSLISTPLEMTPE FTMLGALPKYFQDGATKLLHHHLBNTCHCOGSMGSPLTRFTP RSPANNSSPLTSPFTNTSQNTLSPSAFDYDTENNNSEDIYSSLGG VTEAIQNPSFRSQEDNNFPLKRDGKKUDGSMGGGF\MSDPRA GGDATDSSQTAL\DNRASILHSMTTHSSPRSRBYMPYNYSDSIS FPNKSALKEANFDDADAOFPDDLSLDHSDLVABLUKRISNINGR VEERKIALYSELMKLTQESFSVWDEHFKTILLLLETIGDKEPT IRALAKKULREILENDGAFKNYAELTVMKTLEAHKDPHKEVVR SABEAASV\LATSI\SPEQCIKVLPIQTADYPINLAAIKMOT KVIERVSKETINLLDEINPGLIGGYDNSSSSVRACCYFCLVAV HAVIGDEKKPHLSQLTGSFMKLLNLYIKRAQTIGSGADPTTDVS GQS  6004  140  4098  GKURAFRGMRRLICKRICDYKSFDDEESVDGNFSSASAFKVP APKTSGNPANSARKPGSAGGFXVGAGASKEGGAGAVEDDFIKA FTDVPSIQISSRELEETINKIRSILSDKHWDQRANALKKTR SLLVAGAQVQCFFCHLRLIGGALKISAKDLBSQVVREACHTVA HLSTYLCNKFDHGABEATVPTLFNLVDNSAKVMATSGCAAIRFII RHTHPHLIPLITSNCTSKSVPVRRRSFEFDLAGRRHIDGRANALKKTR SLLVAGAQVQCFFCHLRLIGGALKISAKDLBSQVVREACHTVA NSLEPSYQKSLGTYLKSSGSVASSLPOSDRSSSSGSINRPFSS KNSTANPSTVAGRVSAGSSKASSLPGGRSRSDGTMVLT TTALSTVSSGVQRUVNNSASQKRSKTPRGQGGSRGSFGRUV RAKLSAPLAGMCNAKADGRGRSTKTMVSQSQPGSRGSFRLSV ARSSRIPRPSVGGCSREAFSSRTSFVRSFDLASRHHSRS TGALYAPEVYQASGGVGSTGAGASKRSTRSPLSVSRRHSRS TGALYAPEVYQASGGVGSIGSGSRSSFRSSRFSFRLSV ARSSRIPRPSVGGGCSREAFSSRTSFVRSFDLASRHHSRS TGALYAPEVYQASGGVGSIGSGSRSSTSFRANSFRKGLIGGQN LLNQRTLSRVBLKRLCHVARVLRRCASSLWSSRKERGLIGGQN LLNQRTLSRVBLKRLCHVARVLRRCASLUSVSSKKETUDDFSPSRR VSSRNGSIPTYMRTV\LDUKKGADLLGSSVQKKUDKALDVTRES FPNDLQFTLIMPFTVDGTOTPSLKKVARADPLO	1				NSLEPSYQKSLQTYLKSSGSVASLPQSDRSSSSSQESLNRPFSS
AHHAAGGSVRSGRLGAGALMAGSYASLEDTSKLOTTASEDGRV RAKUSAPLAGMONAKADSGRGSRTKWSGGSQGSGRUT TTALSTVSSGVQRVLVNSASAQKRSKIPRSGGCSREASPSRLGV ARSSRIPERPSVSQGCSREASPESRRTSPVRSGPLTASKHHSRS TGALYAPEVYGASGFGTGIGSSRLSSVSAMRVINTGSDVERA VADALLLGDIRTKKKPARRRYESYGMHSDDDANSDASSACSERS YSSRNGSIPTYMRGT, EDV\AEVINCASSAMSERREGLIGLGU, LLKNQRTLSRVELKRLCEIFTRMFADPHGKRVSSMYERREGELIGLGU, CVHKDLGDUBLFVLITOLLKKWSAJGNSGREGELIGLGU, CVHKDLGDWLFVLITOLLKKWSAJGVKYALDVTRES FPRDLGFRILMSFTVOQTQTPSLKVVAILKYTETLAKQMDPGD FINSSETLAVSRVITWTTEPRSSDVRKAAQSVLISLEFLNTDE FFRLIGALPKTFQGGATKLHHHLINTGTOSSMSGPLITRPTP RSPANNSSPLISPTNTTGQNTLSPSAFDYDTENNNSDTLYSSLRG VTRAIQNFSFRSGEDNMEDLKRGBKOGDSMGGGFG/MSDPRA GGDATDSSQTAL\DNKASLLHSMPTHSSPRRDTNPYNYSDSIS PFNKSALKEAMFDDDADGPPDLSLDGISDLVARBLKRISNHINER VESRKIALYELMKLTQESSFSVWBHYKTILLLLETIGKEPT IRALALKVLREILENGPAFFKNYAELTVMKTLEDKEPT IRALALKVLREILENGPAFFKNYAELTVMKTLEDKEPT IRALALKVLREILENGPAFFKNYAELTVMKTLEDKEPT VEURKIALLVLESILENGGARSKEGGGAVGFCLVAV HAUGGBEKPHLSQLTGSKMKLLNLYIKRAGTGSGGADPTTDVS GQS  6004  140  4098 GKLRAFRGMRRLICKRICDYKSFDDESVDGNRPSSAASAFKVP APKTEGNPANSARKFGSAGGFKVAGAGSKKGGGAQAVDEDDPIKA FTDVSIGIYSSRELEETINKIREILSDDKHDWDQRANALKKIR SLLVAGAQAVDCFFGHELLDGAKLSAKDLRSQVVRRACITVA HLSTVLCNKFDHGABAIVPTLFNLVPNSKVWARTSGCAATRFII RHTHYPALIPLITSNCTSKSVPVRRSFFFFLDLLIQENQTHSLE RHAAVLUSTIKKGHIADABARVERATMGLRNHFGGRATFYI NSLEPSYQKSLDTYLKSSGSVASLPQSRSSSSOSSINRPFSS KNSTANFSTVAGRVSAGSSKASSLPGGRSSGSGSGSRGCRUTT TALSTVSSGVQRLUVNASSAQKRSKIRRGGGGRSGSGSFGCULT TTALSTVSSGVQRLUVNASSAQKRSKIRRGGGGRSGSGSFGLGVLT TTALSTVSSGVQRLUVNASSAQKRSKIRRGGGGRSGSGSFGRUTT TTALSTVSSGVQRLUVNASSAQKRSKIRRGGGGRSGSGSFGRUTT TTALSTVSSGVQRLUVNASSAQKRSKIRRGGGGRSGSGSFGRUTT TTALSTVSSGVQRUVNASSAQKRSKIRRGGGGRSGSGSFGRUTT TTALSTVSSGVQRUVNASSAQKRSKIRRGGGGRSGSGSFGRUTT TTALSTVSSGVQRUVNASSAQKRSKIRRSGGGRSGSGSFGRUTT TTALSTVSSGVQRUVNASSAQKRSKIRRSGGGRSGRSGRFGLGLGLGU LLNQRTLSRVPLKRICEITINFRGTAGRSSRKSKRSSLPGLGGRSGRSFGLGLGLGU LLNQRTLSRVPLKRICEITINFRGTADDABRANSRKRGRRGLIGLGU LLNQRTLSRVPLKRICEITINFRGTAGDABRANGSRKSKRGLIGLIGU LLNQRTLSRVPLKRICEITINFRGTAGDABRANGSRKRGLIGLIGU LLNQRTLSRVPLKRICEITINFRGTAGDA	- 1			,	KWSTANPSTVAGRVSAGSSKASSLPGSLORSRSDIDVNAAAGAK
RAKUSAPLAGMGNAKADSRGERTKMVGSOPGERSGESPENT TTALSTVSSGVORVLVNSSAGVREKTPRSGCERSASPRIGV ARSSIPPRBVSGCGREASRESRDTSPVRSFQPLASRHISRS TGALYAPEVYGASGGTVGISGSRLSSVSARVLINTGSDVEEA VADALLIGDIRTKKKPARRYESYGHHSDDANSDASACSERS YSSRNGSIPTWRQT\EDV\AEVUNRCASSMSERKEGLIGLON LLKNGWTLSRVELKRLGEIPTRMFADPHGKRYSMFENELTLUDFI QVMKDDLODWLFVLLTQLIXKMGADLLGSVQAKVQKALDVTRES FPNDLQFNILMRFTVDQTQTPSLKVKVALIKYIETLAKQMDFGD FINSSETRLAVSRVITTWTTEPKSSDVRKAQSVLISJEELNTPE FTMLLGALPKTFQDGATKLHNHLRHTGNGTGGSMGSPLTRPTP RSPANMSSPLTSPTNTSONTLSPDYDTEMMNSEDIYSSLRG VTEAIQNPSFRSQEDMNEPLKRDSKKDDGDSMCGGPG\MSDPRR GGDATDSQTAL\DNKASLLHSNFTHSSFRSDIVNFNYSDSIS FFNKSALKEAMFDDADOFFPDLSLDHSDLVABLLKRISNINGR VEBRKIALYELMKLTQEESFSVWDEHFKTILLLLETLGDKEPT IRALALKVLREILENGARFKNASLTVWKTLEAKKDPHKEVVR SABEAASV\LATSI\SPEQCIKVLCPIIQTADYPINLAAIKMOT KVIERVSKTINLLEHPENGLIQGYDNESSVKKACVFCLVAV HAVIGDELKPHLSGLTGSKNKLINJIKRAGTGSGGADPTTDVS GGS GKLRAFRGMRRLICKRICDYKSFDDEESVDGNRFSSAASAFKVP APKTSGNDANSARKPGSAGGPKVGAGASKEGGAGAVDEDDFIKA FTDVPSIQITYSSRELEETLINKIREILSDKHDWQRANALKKIR SLLVAGAAQYDCFFQHIRLIDGALKISAKDLRSGVVREACITYA HLSTVLGNKFDHGAEAIVPTLFNLVPNSAKVMATSGCAARFFII RHTHVPRILPLITINGTSKSVPVRRRSFEPFLDLLQENQTHSLE RHAAVLVETIKKGIHDADAERVEARKTYMGLKNHFFGSAETLY NSLEPSYGKSGKSGSKSLEGSLGRSSSSSSESINRPFSS KNSTANSPTVAGRVSAGSSKASSLPGSLGRSRSSSGSEINRPFSS KNSTANSPTVAGRVSAGSSKASSLPGSLGRSRSSSGSEINRPFSS KNSTANSPTVAGRVSAGSSKASSLPGSLGRSRSSSGSGRVLT TTALSTVSSCVGRVLVNSNSAQKRSKTPRSQGGSRSSSFSRVLSV ARSGRIPRSVSGGCSREASRESSRCTSPVRSPGPLASRHHSRS TGALYAPEVYGASGGVALDSRCSSLTSSVSAMRVLNTGSDVERA VADALLLGDIRTKKKPARRYESYGMHSDDDANSDASSACSERS YSSRNGSIPTRVSVGGCSREASRESSRCTSPVRSPGPLASRHHSRS TGALYAPEVYGAGGSTCTEDVATTSDVERA VADALLLGDIRTKKKPARRYESYGMHSDDDANSDASSACSERS YSSRNGSIPTRVSQGCGREASRESSRCTSPVRSPGPLASRHHSRS TGALYAPEVYGAGGSTCLTTVANTGDVERA VADALLLGDIRTKKRPARRYESYGMHSDDDANSDASSACSERS YSSRNGSIPTRWGT\EDV\ABVULNCASSNNSERKEGLLGLQN LLNQRTLSRVELKRLCEIFTRMFDDHGRVESWHELTLUDFI QVHKDDLQDWLFVLLTQLLKKMGADLLGSVQAKVQKALDVYTRES FPNDLEQFNILMFTTDOTOTTSELVALLKYALLKYTETLARMOMDGD	١				AHHAAGQSVRSGRLGAGALNAGSYASLEDTSDKLDGTASEDGPV
TTALISTUSSGVQRVLVNBASAQKRSKIPRSQGCSRRASPSILSV  ARSSRIPRBSVSQGCSRRASQKSSRDFSVRARVLNTGSDVERA  VADALLLGDIRTKKKPARRRYESYGMISDDANSDASSACSERS  YSSRNGSIPTYMRQT\BUV\ABUVLNRCASSNNSERKEGLLGLON  LLKNQRTLSRVELKRLCEIFTRMFADPHGKRVFSMFLETLUDFI  QVHKDDLODNLFVLLTOLLKKMGADLLGSVQAKVQKALDVTRES  FPNDLQFNILMRFTVDQTQTPSLKVKVALLKYLETLAKQMDFGD  FINSSETRLAVSRVITTWTEPKSSDVKKAAQSVLISLFELMTPE  FINLLGALDKYFTQDGATTLLHNHLRNTGKNTGSSMGSDLTRFTP  RSPANMSSBLTSPTNTSGNTLSPSAFDYDTENMNSEDIYSSLRG  VTEAIQNPSFRSQEDMNEPLKRDSKLDGDGDNCGGFG\MSDPRA  GGDATDSSQTAL\DNKASLLHSFTSSFRSRDYNYNYSDSIS  FFNKSALKEAMFDDDADOFPDDLSDHSDLVBLLKKILSHINER  VEERKLALYEEMKLTQEESFSVDEMFKYILLLLETLGDKEPT  IRALALKVLREILEHQDARFKNYAELTVMKTLEAKKDPHEVVR  SAEEAASVLATSI\SPEQCIKVLCPIIQTADYPINLAAIKMQT  KVIERVSKETLNLLIPEIMBGLGVSNESSVKRACVFCLVAV  HAVIGDELKPHLSQLTGSKMKLLNLYIKRAQTGSGGADPTTDVS  GG  GKLRAFRGMRRLICKRICDYKSFDDEESVDGNRFSSAASAFKVP  APKTSGNPANSARKPGSAGGPKVGGGASKEGGAGAVDEDDFIKA  FTDVPSIQIYSSRELEETLINKTEILDDKADWDGDANALKKIR  SLLVAGAAQVDCFFQHLRLLDGALKLSAKDLRSQVVREACITVA  HLSTVLGNKFDHGAEAIVPTLFNLVPNSAKVMATSGCAAIRFFII  RHTHVPRLIPLITSNCTSKSVPVRESFEPLDLLLGMOTHSLE  RHAAVLUETIKKGIHDADAEARVERRKTYMGLRHFFGEAETLY  NSLEPSYQKSLQTYLKSSGSVASLPGSDRSSSSSGSLSRNFFSS  KWSTANPSTVAGRVSAGSSKASSJEGSLGRSRSDIDVNAAGAK  AHHAAGGSVRSGRLGAGALNAGSVASLEDTSDKLDGTASEGRV  TTALSTVSSGVQRVLVNSASQKRSKIFRSQCGSRSASPSKLSV  ARKSSPLAMBSVSGGCGREASRESSSNLTSPVRSGPFLASRHHSRS  TGALYAPEVYGASGPVGTGGSSKLSSVSSMKVLNTGSDVERA  VADALLLGDIRTKKKPARRYESYGMISDDANSGASKCSERS  YSSNGGIPTYMROT\EDV\ABVINGASSRNESERNESICHLOUPS  LLKNQRTLSRVSGLERELSELTLKERDSHRSDERRESERSERSPSLLSV  VADALLLGDIRTKKKPARRYESYGMISDDANSGRSCSERS  YSSNGGIPTYMROT\EDV\ABVINGASSRNESERKEILLOUPS  LLKNQRTLSRVSLKKRLEISFTLMRFBAPHGKRVFSWFLETLUDFI  QVHKDDLQDNLFVLLTQLLKKMGADLLGSVQAKVQKALDVYRES  FPNBLGDRVILMFTTDOTOTTSELVALLKYLLKYLLKYLLKYLARMMDGD	- 1				RAKLSAPLAGMGNAKADSRGRSRTKMVSOSOPGSRSGSPGRVT.T
ARSSTPRSVSQGGSRASSESSTVSFQPLASRHISRS TGALVAPEVYGASGENGYISGSSRLSSVSAMRVINTOSDVERA VADALLIGDIRTKKKPARRRYESYGMHSDDANSDASSACSERS YSSRNGSIFTYMRQT\EDV\AEVUNRCASSMSERKEGLIGLON LLKNQKTLSRVELKRLGEIFTRMFADPHGKRVFSMFLETLUDFI OVHKDDLODWLFVLLTOLLKKMGADLLGSVQAKVQKALDVTRES FFNDLQFNILMRFTVDQTQTDTPSLKVKVALLKYIETLAKQMDFGD FINSSETRLAVSRVITTWTTEPSKSDVKKAQSVLISJELNTPE FYMLLQALPKTFQDGATKLLHNHLRNTCKNGTQSMGSPLTRPTP RSPANMSSPLTSPTTNTSQNTLSPASPDYDTENMNSEDIYSSLRG VTEAIQNFSFRSQEDMMEPLKRDSKKDDGDSNCGGFG\MSDPRA GGDATDSSQTAL\DNKASLLHSMFTHSSFRSDVRPYNYSDSIS PFNKSALKEAMFDDADOFPDLSLDHSDLVABLLKRISHNINER VEERKIALYELMKLTQEESFSVWDEHFKTILLLLETLGDKEPT IRALALVIREILEHQPARFKNYAELTVMKTLEAHKOPHKEVVR SAEEAASV\LATSI'SPECIKUTJITATAVHATATKHOT KVIERVSKETLINLLPBIMGLIQGYDNSESSVRKACVFCLVAV HAVIGDELKPHLSQLTGSKMLLNIYIKRAGTGSGGADPTDVS GQS GQS GGS GKURAFRGMRRLICKRICDYKSFDDEESVDGNRFSSASAFKVP APKTSGNPANSARKFGSAGGPKVGAGSAKEGGAGAVDEDDFIKA FTDVPSIQIYSSRELEETLNKIREILSDDKHDWDQRANALKKIR SLLVAGAAQVDCFFQHLRLLDGALKISAKDLRGVVREACITYA HLSTTULGNKFDHGEAIVPTLFUNPASKVMATSGCAAIRFII RHTHVPRLIPLITSNCTSKSVPVRRRSFEPLDLLLQEMQTHSLE RHAAVLLETIKKSIHDADAERAVEARKTYMGLRHFFGEAETLY NSLEPSYGKSLGTYLKSGGNSASDSRSSSSGSLANDFSS KNSTANPSTVAGRVSAGSSKASSLPGSLQRSKSDIDVNAAGGK AHHAAGQSVRSGRLGAGALAGSVASLEDTSDKLDGTASEGGR VARKISAPLAGMGMAKADBRGSRTTMVSQSQPGSRSGSFGRVLT TTALSTVSGVQRVLVNASAGAKKSKTPRSQCGREASPSRLSV ARSGRIFPSRVSQCSREASRESSRDTSSVSGSGSFGRVLT TTALSTVSGVQRVLVNASAGAKKSKTPRSQCGREASPSRLSV ARSGRIFPSRVSQGCSREASRESSRDTSRFQPLASRHHSRS TGALVAPEVYGASGPGYGISGSSSLSSSVSAMKUNTGSDVERA VADALLLGDIRTKKKPARRYESYGMISDDDANSDASSACSERS YSSNGSIPTYMRQT\EDVARSVERKESLLGLQN LLKNQRTLSRVELKRLCEIFTRMPADPHGKRVFSMFLETLUDPI QVHKDULQDNILMRFTVDQVTGSLKAMLLKYETLIAKOMDGD PPNDLQFNILMRFTVDQVTGSLKAMLLKYBELKRLDCSUVRE					TTALSTVSSGVQRVLVNSASAOKRSKIPRSOGCSREASPSDLSV
TGALYAPEVYGASGPGYGISQSRIBSSUSAMRVLINTGSDVERA VADALLLIGDIRTKKKPARRRYBSYGMHSDDDANSDASSACSERS YSSRNGSIPTYMROT\BDV\AEVLNRCASSWSERKGGLIGLON LLKNORTLSRVELKKELGIFTMMFADDPIGKRVFSMFLETLVDFI OVHKDDLODWLFVLLTOLLKKMSADLLGSVOGAVOKALDVTRES FPNDLOFNILMRFTVDOTOTPSLKVKVALLKYISTLAKOMDPGD FINSSERTLAVSRVITWTTEPKSSDVKKAQSVLISLFELNTTEP FTMLLGALPXTFOOGATKLLHNHLRNTCNGTGSSMGSPLTRFTP RSPAMSSPLTSFTNTSONTLSPSAFDVDTENMSEDIYSSLGG VTEALONFSFRGEOMNEPLASKKDDGDSMGGPG\MSDPRA GGDATDSSQTAL\DNKASLLHSMPTHSSPRSRDYNPYNYSDSIS PFNKSALKEAMFDDDAOFPDDLSLDIBDLVABLLKKI.SHHNER VEERKIALYELMKLTQEESFSVWDEHFKTILLLILLILTETLGBKETT IRALALKVLREILBRQPARFKNYABLTTWKTLEAHKDPHKEVVR SAEEAASVLLATSI\SPECIKVLOPIIGTADYPINLAAIKMQT KVIERVSKETLNLLPEIMPGLIGGYDNSSSSVRKACVFCLVAV HAVIGDELKPHLSQLTGSKMKLINLYIKRAQTGSGGADVTDVS GGS GGS GKURAFRGMRRLICKRICDYKSFDDEESVDGNRFSSAASAFKVP APKTSGNPANSARKPGSAGGPKVGAGASKEGGAGAVDEDDFIKA FTDVSSIGIYSSRELBETLMRIRSILSDDKHDMOQRANALKKIR SLLVAGAAQYDCFFCHLRLLDGALKLSAKDLRSQVVREACITVA HLSTVLGNKFDHGAEAIVPTLFNLVPNSAKVMATSGCAAIRFII RHTHVPRLIPLITSNCTSKSVPVRRSFFEDLLLQENGTHSLE RHAAVLVETIKKGIHDADAEARVEARKTYMGLRNHFPGEAETLY NSLSPSYQKSLOTYLKSSGSVASLPOSDSRSSSGSELNFFSS KWSTANPSTVAGRVSAGSSKASSLPOSLQRSKSDIDVNAAAGAK AHHAAGGSVRSGRLGAGALMAGSYASLEDTSNKLDGTASEDGRV RAKLSAPLAGMGRAKADSRGGRSTKMVSOGOPGSRSGSGFRVLT TTALSTVSSGVORVLVMSASAQKRSKIPRSQCSREASPSRLSV ARSSRIPPSVSQGCSREASRESSRDTSPKSPGPLASRHHISRS GALYAPEVYGASGPOYGISGSSRISSSVSAKVLNTGSDVEBA VADALLLGDIRTKKKPARRYESYGMISDDANSDASSACSERS YSSRNGSIPPYMRGT\BOVARSSINDSERKBGLLGLON LLKNQRTLSRVELKRLCEIFTEMFADPHGKRKYNLNTGSDVEBA VADALLLGDIRTKKKPARRYESYGMISDDANSDASSACSERS YSSRNGSIPPYMRGT\BOVARSVSNSSERKBGLLGLON LLKNQRTLSRVELKRLCEIFTEMFADPHGKRKYFSNFLETLVDPFI QVHKDDLQDNILMRFTVDOTOTDSLKKKVGADLUSVALLDVTRES FPNBLOGDNILMRFTVDOTOTDSLKKKVGALLUSVETLADMMGCD	-			,	ARSSRIPRPSVSQGCSREASRESSRDTSPVRSFQDIASPHUSES
VADALLIGIRTKKKPARRYBSYGMHSDDANSDASSACSERS YSSRGSIFTYMROTIEDVLANGCASSNWSERKEGLIGUN LLKNQRTLSRVELKRLCEIFTRMFADPHGRKVFSMFLETLVDFI QVIKDDLQDWLFVLLTQLLKKMSADLLGSVQAKVQKALDVTRES FFNDLQFNILMRTVUDCTDTPSLKVKVAILKYIFTLAKQMDPGD FINSSETRLAVSRVTTWTTEPKSSDVRKAAQSVLISLFELNTPE FFNLIGALPKTFQDGATKLLHNHLRNTINGTQSSMGSPLTRPTP RSPANMSSPLTSPTNTSQNTLSPSAFDVDTENMISEDIYSSLZG VTEAIQNFSFRSQEMNRPLKRDSKXDGDGMCGGPG\MSDPRA GGDATDSQTAL\DNKASLLHSMFTHSSPRSRDYNTYNSDSIZ VTEAIQNFSFRSQEMNRPLKRDSKXDGDGMCGGPG\MSDPRA GGDATDSQTAL\DNKASLLHSMFTHSSPRSRDYNTYNSDSIZ FFNKSALKEAMFDDDADOLPDDLSLDHSDLVABLLKRISHNER VESRKIALYELMKLTQEBSFSVWDHFKTLLLLLETLGDKEFT IRALAKKLREILENQPARFKNYASLTVMKTLEAHKDPHKEVVR SAEEAASV\LATSI\SPEQCIKVLCPIIQTADYPINLAAIKMGT KVIERVSKSTLNLLIPEIMPGLIGGYDNSESSVRKACVFCLVAV HAVIGDELKPHLSQLTGSKMKLLNLYIKRAQTGSGGADPTTDVS GQS GKLAFRGMRRLICKRICDYKSFDDEESVDGNRPSSAASAFKVP APKTSGNPANSARKPGSAGGPKVGAGASKEGGGAQVDEDDFIKA FTDVSSIGIYSSRELEETLNKIREILSDDKHDWDQRANALKKIR SLLVAGAAQVDCFFQHLRLDGALKLSAKDLRSQVVREACITVA HLSTVLGNKFPHGAEAIVPFILNVNSAKVMATSGCAAIRFII RHTHYPRLIPLITSNCTSKSVPVRRRSFEPLDLLLQEWQTHSLE RHAAVLVETIKKSGSVASLPPGSDRSSSSSGESINNFFSS KMSTANPSTVAGRVSAGSSKASSLPGSLGRSRSDGSINNFFSS KMSTANPSTVAGRVSAGSSKASSLPGSLGRSRSDGSINNFFSS KMSTANPSTVAGRVSAGSSKASSLPGSLGRSRSDGSNAFFSS KMSTANPSTVAGRVSAGSSKASSLPGSLGRSRSDGSNAFHISRS RAKLSAFLAGMGNAKADBSGGSSTKMVSGQSGSGSGGFGRVLT TTALSTVSSGVQRVLVNSASAQKRSKIPRSQGCSREASPSRLSV ARSGIPPPSVSQGCSREASRESSTDTSPVRSFQPLASRHHISRS GRAPPPSVSQGCSREASRESSTDTSPVRSFQPLASRHHISRS GRAPPPSVSQGCSREASRESSTDTSPVRSFQPLASRHHISRS GRAPPPSVSQGCSREASRESSTNSVRSKRKBILLGLQN VADALLLGDIRTKKKPARRYFSYGMHSDDDANSDASSACSERS YSSRNGSIPPYMGTOTOPSLKWKGADLLGSVQAKVQKALDVRES FFNKLSGVIRVLTULTQLKKWGADLLGSVQAKVQKALDVRES FFNKDLGPNILMRFTVDQTOTOPSLKWKADLLGSVQAKVQKALDVRES FPNKDLGPNILMRFTVDQTOTOPSLKWKADLLGSVQAKVQKALDVRES	-			1	TGALYAPEVYGASGPGYGISOSSRLSSSVSAMRVINTGSDVERA
YSSRNGJFTYMROT\BDV\AEVINRCASSNWSERKEGLIGLON LLKNORTLSRVELKRLCEIFTRMFADPHGKRVFSMFLETLVDDT QVHKDDLQDWLFVLLTQLLKKMGADLIGSVQAKVQKALDVTRES FPNDLGFNILMRTTVDQTQTPSLKKVAILKYIETLAKQMDPGD FINSSETRLAVSRVTWTTFPKSSDVRKAQSVLISLFELNTPE FFMLGALPKTFQDGATKLLHNHLRNTGNCTGSSMGSPLTRPTP RSSANMSSPLTSFTNTSQNTLSFSAPYDTENNNSDIYSLRG VTEALQNFSFRSQEDNMEPLKRDSKKDDGDSMCGGPG\MSDPRA GGDATDSSQTAL\DNKASLLHSMFTHSSRSBDYNPYNNSDSIS FFNKSALKEAMFDDDADQFFDDLSLDHSDLVABLLKFLSNHNER VEERKIALVELMKLTQEESFSVWDEHFKTLLLLLETLGDKEPT IRALAKVLREILRHQPARFKNYAELTVMKTLEAHCDPHKEVVR SAEEAASVLATSI\SPECCIKVLCPIGTADYPINLAAIKMOT KVIERVSKSTLNLLDEINDGLIQGYDNESSUSKACVECLVAV HAVIGDELKPHLSQLTGSKMKLLNLYIKRAQTGSGGADPTTDVS GQS GKIRAFEGMRRLICKRICDYKSFDDEESVDGNRFSSAASAFKVP APKTSGNPANSARKPGSAGGPKVGAGASKEGGAGAVDEDDFIKA FTDVESIQIYSSRELEETLNLTEILSDDKHDWDQRANALKKIR SLLVAGAAQYDCFFFOHLRICALKLSAKDLRSQVVREACITVA HLSTVLGNKFDHGAEAIVPTLFNLVPNSAKVMATSGCAAIRFII RHTHVPRIPLITISNCTSKSVPVRRRSFEFDLLLIQENQTHSLE RHAAVLVSTIKKGHDADAEARVEARKYTMGIRNHFPGEAETLY NSLEPSYQKSLQTYLKSGSVASLPQSDRSSSSSQESLNRFFSS KWSTANTSTVAGRVSAGSSKASSLPGSLORGRSDIDWAAAGAK AHHAAGGSVRSGRIGJAGALNAGSVASLEDTSDKLDGTASEDGRV RAKLSAPLAGMGNAKADSRGRSRTKMVSQSQPGSRSGPGRVLT TTALSTVSGGVQRVLVNSASAQKSSKIPSGGCGRRASPGRLSV ARSGIPPRSVQGCSSERSSRSDTDSVRSTQFLASRHISRS TGALYAPEVYGASGPYGISQSSRLSSSVSAMRVINTSDVERA VADALLLDIRTKKKPARRYESTGMISDDANDASSACSERS SYSSNGSIPTHTMGT\ZDLVAJAVLANGCASSSMSERKBGLLGQN LLKMORTLSRVELKRLCEIFTRMFADPHGKRVFSMFLETLVDFI QVKNDDLQMLFVLLTQLLKKMGADLIGSVQAKVQKALDVTRES FPNDLQFNILMRFTVDOTOTPSLKVKVALLKYIETLAKMDDFG	-		•		VADALLIGDIRTKKKPARRRYESYGMHSDDDANSDASSACSERS
LLKNORTLSRVELKRICEITTRFRAPHGIRRVFSMFLETLUDET  OVHRDDLODNE FYLITCLIKKMGADLIGSVOAKVOKALDVTRES FPNDLQFNILMRFTVDQTQTPSLKVKVALLKYTETLAKOMDPGD FINSSETRLAVSRVITWTTEPKSSDVKKAAQSVLISLFBLNTEP FINLIGALPKTFOQGATKLINHLRIKTIGNTQSSMGSPLTRPTP RSPANMSSPLTSPTNTSQNTLSPSAFDYDTENNNSBDIYSSLRG VTEALONFSFRSQEDMNEPLKRDSKUDGDSMGGGFG\MSDPPA GGDATDSSQTAL\DINKSLLISMPTHSSPRSNDYNPYNYSDSIS PFNKSALKEAMFDDDADQPPDDLSLDHSDLVABLLKELSNHNER VEERKIALYELMKLTQEESFSWDBEHFKTILLLLIETLGDKEBT IRALAKKUREILRHQPARFKMYABELTVMKTLEAHKDPHKEVVR SABEAASV\LATSI\SPEQCIKVLCPIIQTADYPINLAAIKMQT KVIERVSKETLNLLLPEIMPGLIQGYDNSESSVRKCVFCLVAV HAVIGDEKKPHSQLTGSKMKLINLYIKRAQTGSGGADPTTDVS GQS GKLRAFRGMRRLICKRICDYKSFDDESSVDGNRFSSASAFKVP AFKTSGNPANSARKFGSAGGFXVGAGASKEGGAGAVUEDDFIKA FTDVPSIQIYSSRBLEETLNKTREILSDKHDWDQRANALKKIR SLLVAGAAQYDCFFQHLRILDGAKKLSAKDLRSQVVRBACITVA HLSTVLGNKFDHGABAIVPTIFNLVPNSAKWATSGCAAIRFII RHTHYPRIIPLITSNCTSKSVPVRRSFEFIDLLLQENOTHSLE BHAAVLVSTIKKGIHDADAEARVEARKTYMGLRNHFFGEAETLLY NSLEPSYQKSLQTTYLKSSGSVASIDGSDRSSSSGSGIANFFIS KWSTANPSTVAGRVSAGSSKASSLPGSLQRSRSDIDWAAAGAK AHHAAGGSVRSGRUGAGALNAGSYASLEDTSDKLDGTASEDGRV RAKLSAPLAGMGNAKADSRGRSRTKMVSQSQFGRSGSPGRVLT TTALSTVSGGVQRVLVNSASAQKRSKIPRSGGCSREASPSRLSV ARSGIPPFSVQGCSREASPSSRDTSPVRSFQPLASRHHSRS TGALYAPEVYGASGPGVIGSGSSRLSSVSAMRVLNNTSDVERA VADALLLDIRTKKKPARRRESSGMISDDANSDASACSERS SYSSRGSIPTFMRQT\GDVAJAVLNRCASSNMSERKEGLLQN LLKNORTLSRVELKRLCEIFTRMFADPHGRRVFSMFLETLVDFI QVHKDDLODULFVILTQLLKKMGADLIGSVQAKVQKALDVTRES PPNDLQDVILMRFTVDCTOTPSLKVKVAILKYIETLAKOMDED	-1			ł	YSSRNGSIPTYMROT\BDV\AEVLNRCASSNWSERKEGILGLON
QVRKDDLQDWLFYLLTQLLKKMGADLIGSVQAKUQKALDVTRES FPNDLQFNILMRFTVDQTQTPSLKVKVAILKYIETLAKQMDPGD FINSSETRLAVSRVITWTTEPKSSDVRKAAQSVLISLFELNTPE FTMLIGALPKTFQDGATKLLHNHLRTGNGTQSSMGSPLTRPTP RSPANNSSPLTSFNTTSQNTLSPSAPDYDTENMNSEDIYSSLZG VTEAIQNFSFRSQEMNEPLKRDSKKDDGDSMGGGFG\MSDPRA GGDATDSSQTAL\DNKASLLHSMFTHSSPRSRDYNPYNYSDSIS PFNKSALKEAMFDDDADQFPDDLSLDHSDLVABLLKELSNHERE VEERKIALVELKKLTQEESFSVWDEHFKTILLLLETLGDKEFT IRALALKVLREILRHQPARFKNYAELTVMKTLEAHKDPHKEVVR SAEEAASV\LATSI\SPEQCIKVLCPIIQTADYPINLAAIKNQT KVIERVSKETLMLLDEINFGLIQGYDNSESSVRKACVECUAV HAVIGDELKPHLSQLTGSKMKLLNLYIKRAQTGSGGADPTTDVS GQS GS GKLRAFRGMRRLICKRICDYKSFDDEESVDGNRFSSAASAFKVP APKTSGNPANSARKPGSAGGPKVGRGAGSKEGGAGAVDEDDFIKA FTDVPSIQIYSSRELEETLNKIREILSDKHDWDQRANALKKIR SLLVAGAAQYDCFFCHLELLDGALKLSAKDLRSQVVREACTIVA HLSTVLGNKFDHGRSAIVPTLFNLVPNSAKWAATSGCAAIRFII RHTHVPRLIPLITSNCTSKSVPVRRSFEPFDLLLLGENQTISLE RHAAVLVETIKKGHDADAEARVEARKTMGRNHFPGEAETLY NSLEPSYQKSLQTYLKSGSVASLPQSDRSSSSSQESLNRPFSS KWSTANPSTVAGRVSAGSSKASSLPGSLQRERSDIDWAAAGAK AHHAAGGSVRSGRIGAGALNAGSVASLEDTSKLLGGTASEGGRY RAKLSAPLAGMGNAKADSRGRSRTKMVSQSQPGSRSGSPGRVLT TTALSTVSSGVQRULVNSASAQKRSKIPRSGCGREASPSRLSV ARSSRIPRPSVSQCSREBSSRSDTSPVRSFQPLASRHISRS TGALYAPEVYGASGPGSIGSSRSTSVSSSPKRSDLSDVRA VADALLLGDIRTKKKRPARRYESSGMTSPVRSFQPLASRHISRS TGALYAPEVYGASGPGSIGSSGSRSSSVSSSRSRSSRSRSRSRSRSCHGLIGLQN LLKNGRTLSRVELKRLCEIFTRMFADPHGKRVFSMFLETLVDFI QVHKDDLQNVLRWITGTLOVLKKMGADLGSVQAKVQKALDVTRES PPNDLQDVILMRFTLYDDOTOPSLKVKVAILKYIETLAKMBDCD	- [				LLKNORTLSRVELKRLCEIFTRMFADPHGKRVFSMFLETLVDET
FPNDLQFNILMRFTVDQTQTBSLKVKVAILKVIETLAKQMDPGD FINSSETRLAVSRVITWTTEPKSSDVRKAAQSVLISLFELNTPE FTMLLGALPKTFQDGATKLLHNHLRNTCNGTQSSMGSPLTRPTPP RSPANMSSPLTSPTNTSQNTLSPSAFDVDTENMNSEDIYSSLRG VTEAIQNFSFRSQEDMNEPJKRDSKKDDGDSMCGFG\MSDPRA GGDATDSSQTAL\DNKASLLHSMFTHSSPRSRDYMPYNYSDSIS PFNKSALKEAMFDDDADQFPDDLSLDHSDLVABLLKELSNHNER VEEKKALYELMKLTQEESTSVWBEHFKTILLLLETLGDKEFT IRALAKVLREILHQPARFKNYAELTWKKTLEAKKDPHKEVVR SAEEAASV\LATSI\SPEQCIKVLCPIIQTADYPINLAAIKNQT KVIERVSKETLHLLLEEIMPGLIGGYDNSESSVRKACVFCLVAV HAVIGDELKPHLSQLTGSKMKLLNLYIKRAQTGSGGADPTTDVS GQS GKLRAFEGMRRLICKRICDYKSFDDESSVDGNRPSSASAFKVP APKTSGNPANSAKKPGSAGGPKVGAGASKEGGAGAVDEDDFIKA FTDVPSIQIYSSRELEETLNKIREILSDDKHDWDQRANALKKIR SLLVAGAAQYDCFFGHLRLLDGALKLSAKDLRSQVVREACITVA HLSTVLGNKFDHGAEAIVPTLVDNSAKVMATSGCAAIRFII RHTHYPRLIPLTTSNCTSKSVPVRRSFFFIDLLLQENQTHSLE RHAAVLVETIKKGIHDADAEARVEARKTYMGLRNHFPGEAETLY NSLEPSYQKSLQTTYLKSSGSVASLPQSDRSSSSSGSSINRPFSS KWSTANPSTVAGRVSAGSSKASSLPQSDRSSSSGSSGSPGRULT TTALSTVSGSVQRVLVNSASQKRSKIPRSQCGSREASPSRLSV ARKSAPLAGMGNAKADSRGSRTKMVSQSQPGSRGSGSGRCVLT TTALSTVSGSVQRVLVNSASQKRSKIPRSQGCSREASPSRLSV ARKSRIPPSVSQCGSREASRSSSDTSVKRSQCCSREASPSRLSV ARSRIPPSVSQCGSREASRSSSDTSVRSGCPGRAVHTGSDVERA VADALLLGDIRTKKKPARRRYESYGMHSDDDANSDASSACSERS YSSRNGSIPTTMRGT\EDV\ABVULNCASSNMSERKEGLLGLQN LLMQRTLSRVELKRLCEIFTRMFADPHGKRVFSMFLETLVDPI QVHKDDLQDWLFVLUTQLLKKRGADLLGSVGAVGKALDVTRES FPNDLQPNILMRFTYDOTOTPSLKVKVQKALDVTRES	ı			i .	QVHKDDLQDWLFVLLTOLLKKMGADILGSVOAKVOKAT.DVTPBE
FINSSTRILVSRVITWTTEPKSSDVRKAAQSVLISLFBLINTEP FTMLIGALPKIFQDGATKLINHLENTCHGTQSSMGSPLITRFTP RSPANWSSPLTSPTNTSQNTLSPSAFDVDTEMMSEDIYSSLAG VTEAIQNFSFRSQEDMMEPLKRDSKKDDGDSMCGGFG\MSDPRA GGDATDSQTAL\DNKASLLHSMPTHSSPRSRDYNFYNYSDSIS PFNKSALKEAMFDDDADQFPDDLSLDHSDLVABLIKKEISHNHER VESRKIALVSLMKLTQBESFSVWDEHFKTILLLLETLGDKEPT IRALALKVLREILRHQPARFKNYAELTYMKTILEAKKDPHKEVVR SAEEAASV\LATSI\SpeQCIKVLCPIIQTADYPINLAAIKMQT KVIERVSKETLNLLLPBIMPGLIQGYDNSESSVRKACVFCLVAV HAVIGDELKPHLSQLTGSKNKLLNLYIKRAQTGSGGADPTTDVS GQS GKLRAFRGMRRLICKRICDYKSFDDEESVDGNRFSSAASAFKVP APKTSGNPANSARKFGSAGGPKVAGASKEGGAGAVDEDDPIKA FTDVPSIQIYSSRELESTLMKIRBILSDDKHDWDQRANALKKIR SLLVAGAAQYDCFFQHLRLLDGALKLSAKDLRSQVVREACITVA HLSTVLGNKFDHGAEAIVPTIFMLVDNSAKVMATSGCAAIRFII RHTHYPRLIPLITSNCTSKSVPVRRRSFEPIDLLLQENQTHSLE RHAAVLVETIKKGIHDADAEARVEARKTYMGLRNHFFGEAETLY NSLEPSYQKSLQTYLKSSGSVASLPQSDRSSSSGSSGESNRFSS KMSTANPETVAGRVSAGSSKASSLPGSLQRSRSDIDVNNAAAGAK AHHAAGGSVRSGRILGAGALNAGSYASLEDTSDKLDGTASEDGRV TALSTVSGVVRSGRILGAGALNAGSYASLEDTSDKLDGTASEDGRV TTALSTVSGVQRVLVNNSASQKRSRTSPKRSGCSPGRVLT TTALSTVSGVQRVLVNNSASQKRSRTSPKNSQCGGRGSGSPGRVLT TTALSTVSGVQRVLVNNSASQKRSRTSPKNSGCGSREASPSRLSV ARSSIPPBSVQGCGREASRESSRDTSPVRSGCGDLASRHISRS TGALYAPBVYQASGGGYGISQSRLSSSVSAMRVLNTGSDVERA VADALLLGDIRTKKKPARRRYESYGMHSDDDANSDASSACSERS TGALYAPBVYQASGGGYGISQSRLSSSNYSERKGGLLGLQN LLNNGRTLSRVELKRLCEIFTRMFADPHGKRVFSMFLETLVDFI LLNNGRTLSRVELKRLCEIFTRMFADPHGKRVFSMFLETLVDFI PNDLQPNILMRFTYDDOTOTSELKVKVQKALDVTRES FPNDLQPNILMRFTYDDOTOTSELKVKVQKALDVTRES	-				FPNDLQFNILMRFTVDOTOTPSLKVKVAILKVIETLAKOMDROD
FTMLGALPKTFQDGATKLIHNHLRTTGNGTQSSMGSPLTRPTP RSPAMWSSPLTSPTNTSQNTLSPSAFDYDTEMMSEDLYSBLRG VTEAIQNFSFRSQEDMNEPLKRDSKKDDGDSMCGGPG_MSDPRA GGDATDSSQTAL\DNKASLIHSMFTHSSPRSRDYNPYNYSDSIS PFNKSALKEAMFDDADOFPDDLSLDHSDLVBELLKRISNHNER VEERKLALYELMKLTQESFSWDEHFKTLILLIETLGDKEPT IRALALKVLREILRHQPARFKNYAELTVMKTLEAHKOPHKEVVR SAEEASV\LATSI\SPEQCIKVLCPIIQTADYPINLAAIKMQT KVIERVSKETINLILPEIMPGLIQGYDNSESSVRKACVFCLVAV HAVIGDELKPHLSQLTGSKMKLLNLYIKRAQTGSGGADPTTDVS GQS  GKLRAFRGMRRLICKRICDYKSFDDESSVDGNFSSAASAFKVP APKTSGNPANSARKPGSAGGPKVGAGASKEGGAGAVDEDDPIKA FTDVPSIQIYSSRELEETLNKIREILSDXHDWDQRANALKKIR SLLVAGAAQYDCFFQHLRLLDGALKLSAKDLRSQVVREACITVA HLSTVLGNFPHGAEATVPTLFNLVPNSAKVMATSGCAAIRFII RHTHVPRLIPLITSNCTSKSVPVRRRSFEFLDLLLQEMQTHSLE RHAAVLVETIKKGIHDADAEARVERKTYMGLRNHFPGEAETLY NSLEPSYQKSLQTYLKSSGSVASLPQSDRSSSSSSSENRPFSS KWSTANPSTVAGRVSAGSSKASSLPGSLQRSKSDIDVNAAAGAK AHHAAGQSVRSGRLGAGALNAGSYASLEDTSDKLDGTASEDGRV RAKLSAPLAGMGNAKADSGGRSRTKMVSQSQPGSRSGSPGRVLT TTALSTVSSGVQRVLVNSASAQKRSKIPRSQGGSREASPSRLSV ARSSRIPRPSVSQGCSREASRESSRDTSPVRSFQPLASRHHSRS TGALYAPBVYGASGPGYGISGSRLSSSVSAMRVLNTGSDVERA VADALLLGDIRTKKKPARRYESYGMHSDDDANSDASSACSERS TGALYAPBVYGASGPGYGISGSRLSSSVSAMRVLNTGSDVERA VADALLLGDIRTKKKPARRYESYGMHSDDDANSDASSACSERS TSANGSIPTTMGCT-GEDV\AEVLINGCASSMNSERKEGLLGLON LLKNGRTLSRVELKRLCEIFTRMFADPHGKRVFSMFLETLVDPI QVKHDDLQDWLFVLLTQLLKKMCADLLGSVQAKVQKALDVTRES FPNDLQRVILNRFTVDOTOTPSLKVKVALLKYLETJAKMMDED	-1				FINSSETRLAVSRVITWTTEDKSCOVDKAAOCVLTCLEELAWDE
RSPANMSSPLTSPTNTSQNTLSPSAFDYDTENNMSEDLYSSLRG VTEALQNFSFRSQEDMNEPLKRDSKKDDGDSMCGGPC\MSDPRA GGDATDSSQTAL\DNKASLLHSMFTHSSPRSRDYNYPNYSDSIS PFMKSALKEAMFDDDADQPPDDLSLDHSDLVAELLKRISNINNER VEERKIALYELMKLTQEESFSVWDEHFKTILLLLETLGDKEPT IRALAKUREELRHQPARFKNYAELTVMKTLEAHKDPHKEVVR SAEEAASV\LATSI\SPECCIKVLCPIIQTADYPINLAAIKMQT KVIERVSKETLNLLLPEIMPGLIQGYDNSESSVRKACVFCLVAV HAVIGDELKPHLSQLTGSKMKLLNLYIKRAQTGSGGADPTTDVS GQS GQS GKLRAFRGMRRLICKRICDYKSFDDEBSVDGNRFSSAASAFKVP APKTSGNPANSARKPGSAGGPKVGAGASKEGGAGAVDEDDFIKA FTDVPSIQIYSSRELEETLNKIREILSDDKHDWQRANALKKIR SLLVAGAAQYDCFFQHLRLLDGLKLSAKDLRSQVVREACITVA HLSTVLGNKFDHGAEAIVPTLPNLVPNSAKVMATSGCAAIRFII RHTHVPRLIPLITSNCTSKSVPVRRRSFEPLDLLLQEWQTHSLE RHAAVLVETIKKGIHDADAEARVEARKTYMGLRNHFPGEAETLY NSLEPSYQKSLQTYLKKSGSVASLPQSDRSSSSQOESLNRFFSS KWSTANPSTVAGRVSAGSSKASSLPGSLQRSRSDIDVNAAAGAK AHHAAGQSVRSGRLGAGALNAGSYASLEDTSDKLDGTASEDGRV RAKLSAPLAGMGNAKADSRGRSTKMVSQSPGSRGSPGRVLT TTALSTVSSGVQRVLVNSASAQKRSKIPRSGGCSREASFSRLSV ARSGRIPRPSVSQGCSREASRESSRDTSPVRSFQPLASRHHSRS TGALYAPEVSQACGSREASRESSRDTSPVRSFQPLASRHHSRS TGALYAPEVSQACGSREASRESSRDTSPVRSFQPLASRHHSRS TGALYAPEVSQACGSREASRESSRDTSPVRSFQPLASRHHSRS TGALYAPEVSQAGSPGYGISGSSRLSSVSAMRVLINTGSDVERA VADALLLGDIRTKKKPARRRYESYGMHSDDDANSDASSACSERS YSSRNGSIPTYMRQT\EDV\ABVLINRCASSNMSERKBGLLGLQN LLKNQRTLSRVSLKRLCEIFTRMFADPHGKRVFSMFLETLVDPI QVHKDDLQDWLFVLLTQLLKKMGADLLGSVQAKVQKALDVTRES FPNDLQFFILMRFTVDOTOTPSLKVKVALLKYIETLAKOMBED	1	· .		•	FTMLLGALPKTFODGATKILLUNUL PNTCNGTOGGMGGDY GODDON
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ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	ccrresponding	to first	L=Leucine, M=Methionine, N-Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
] .	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ı	amino acid	sequence	Codon, /=possible nucleotide deletion
	sequence		\=possible nucleotide insertion)
			FTMLLGALPKTFQDGATKLLHNHLRNTGNGTOSSNGSPLTRPTP
ļ			RSPANWSSPLTSPTNTSONTLSPSAFDYDTENMNSEDIVSSLRG
i			VTEAIQNFSFRSQEDMNEPLKRDSKKDDGDSMCGGPG\MSDPRA
ŀ			GGDATDSSQTAL\DNKASLLHSMPTHSSPRSRDYNPYNYSDSTS
ı			PFNKSALKEAMFDDDADQFPDDLSLDHSDLVAELLKELSNHNER
1			VEERKIALYELMKLTQEESFSVWDEHFKTILLLLLETLGDKEPT
			IRALALKVLREILRHQPARFKNYAELTVMKTJEAHKDPHKEVVR
1			SAEEAASV\LATSI\SPEQCIKVLCPIIQTADYPINLAAIKMQT
ĺ	<b>j</b> .		KVIERVSKETLNLLLPEIMPGLIQGYDNSESSVRKACVFCLVAV
1			HAVIGDELKPHLSQLTGSKMKLLNLYIKRAQTGSGGADPTTDVS GOS
6005	133	5955	RSSGRRQEQLGQFPGRERKGMASGLGSPSPCSAGSEEEDMDALL
ł	l		NNSLPPPHPENEEDPBEDLSETETPKLKKKKKPKKPRDPKIPKS
ļ			XRQKKERMLLCRQLGDSSGEGPEFVEEBEEVALRSDSEGSDYTP
		• '	GKKKKKLGPKKEKKSKSKRKEEEEEDDDDDDDDSKEPKSSAQLL
1 .			BDWGMEDIDHVFSEEDYRTLTNYKAFSOFVRPLIAAKNPKIAVS
		×	KMMMVLGAKWREFSTNNPFKGSSGASVAAAAAAAVAVVESMVTA
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i	ł · · · · · · · · · · · · · · · · · · ·		PKKVAPLKIKLGGFGSKRKRSSSEDDDLDVESDFDDASINSYSV
1			SDGSTSRSSRSRKKLRTTKKKKKGEEEVTAVDGYETDHQDYCEV
			CQQGGEILCDTCPRAYHMVCLDPDMEKAPEGKWSCPHCEKEGI
			QWEAKEDNSEGEEILBEVGGDLEEEDDHHMEFCRVCKDGGELLC
1			CDTCPSSYHIHCLNPPLPEIPNGEWLCPRCTCPALKGKVQKILI WKWGQPPSPTPVPRPPDADPNTPSPKPLEGRPERQFFVKWQGMS
			YWHCSWVSELQLELHC\QVMFRNYQRKNDMDEPPSGDFGGDEEK
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į l			HVHYLIKWRDLPYDQASWESEDVEIQDYDLFKQSYWNHRELMRG
1	ľ		EEGRPGKKLKKVKLRKLERPPETPTVDPTVKYERQPEYLDATGG
			TLHPYQMEGLNWLRFSWAQGTDTILADEMGLGKTVOTAVFI,VSI.
			YKEGHSKGPFLVSAPLSTIIN\WEREFEMWAPDMYV\VTYUGDK
		*	DSRAIIRENEFS\FEDNAIRGGKKASRMKKEASVKFHVLLTSYE
1			LITIDMAILGSIDWACLIVDEAHRLKNNOSKFFRVLNGYSLOHK
.] [	•		LLLTGTPLQNNLEELFHLLNFLTPERFHNLEGFLEEFADIAKED
1			QIKKLHDMLG\PHMLRRLKADVFKNMPSKTELIV\RVELSPM\Q
			KKYYK\YILHSKFLKALN\ARGGGNQVSLLNVVMDLKKCCNHPY
l j			LFPVAAMEAPKMPNGMYDGSALIRASGKLLLLQKMLKNLKEGGH RVLIFSQMTKMLDLLEDFLEHEGYKYERIDGGITGNMRQEAIDR
			FNAPGAQQFCFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQ
	· .		AFSRAHRIGONKKVMIYRFVTRASVEERITOVAKKKMMLTHLVV
[			RPGLGSKTGSMSKQELDDILKFGTERLFKDEATDGGGDNKEGED
I I	1		SSVIHYDDKAIERLLDRNQDETEDTBLQGMNBYLSSFKVAQYVV
1 }	1		REEBMGEEEEVEREIIKOEESVDPDVWEKIJRHHVEGOOPDIAR
f l			NLGKGKRIRKQVNYNDGSQEDRDWQDDOSDNOSDYSVASEEGDE
1 1	• ]	i	DFDERSEAPRRPSRKGLRNDKDKPLPPLLARVGGNIEVLGFNAR
1			QRKAFLNAIMRYGMPPQDAFTTQWLVRDLRGKSEKEFKAYVSLF
}	· · · · · · · · · · · · · · · · · · ·		MRHLCEPGADGAETFADGVPREGLSRQHVLTRIGVMSLIRKKVO
ļ .	ľ		EFEHVNGRWSMPELAEVEENKKMSQPGSPSPKTPTPSTPGDTQP
l í			NTPAPVPPAEDGIKIEENSLKEEESIEGEKEVKSTAPETAIECT
			QAPAPASEDEKVVVEPPEGEEKVEKAEVKERTEEPMETEPKGKG
	1		AADVEKVEEKSAIDLTPIVVEDKEEKKEEEEKKEVMLQNGETPK
	•	i	DLNDEKQKKNIKQRFMFNIADGGFTELHSLWQNEERAATVTKKT YEIWHRRHDYWLLAGIINHGYARWQDIQNDPRYAILNEPFKGEM
1	J		NRGNFLEIKNKFLARRFKLLEQALVIEEQLRRAAYLNMSEDPSH
		i	PSMALNTRFAEVECLAESHQHLSKESMAGNKPANAVLHKVLKQL
	<u> </u>		EELLSDMKADVTRLPATIARIPPVAVRLQMSERNILSRLANRAP
			EPTPQQVAQQQ
6006	1	965	DNDFLRNTVHRHEPPVTAEPIRLLAENEDVVVVDKPSSIPVHPC
Ì			GRFRHNTVIFILGKEHQLKELHPLHRLDRLTSGVLMFAKTAAVS
		i i	ERIHEQVRDRQLEKEYVCRVEGEFPTEEVTCKEPILVVSYKVGV
}		[]	CRVDPRGKPCETVFQRLSYNGQSSVVRCRPLTGRTHQIRVHLQF
	<del></del>	<del></del>	LGHPILNDPIYNSVAWGPSRGRGGYIPKTNEELLRDLVAEHQAK

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location		Glutamic Acid, F=Phenylalanine, G=Glycine,
1	corresponding	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
i	to first	to first	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine,
- 1	residue of	residue of	S=Serine, T=Threonine, V=Valine,
		amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ļ	amino acid	sequence	Codon, /-possible nucleotide deletion,
ļ	sequence	<u> </u>	\=possible nucleotide insertion)
Ī	1		QSLDVLDLCEGDLSPGLTDSTAPSSELGKDDLEELAAAA\QKME
1			EVAEAAPQELDTIALASEKAVETDVMNQ\RQT\TLCRVPAGATG
			SLAPRPCDVPTCPTL
6007	3	2351	HELGQVEYVFTDKTGTLTENEMQFRECSINGMKYQEINGRLVPE
)			GPTPDSSEGNLSYLSSLSHLNNLSHLTTSSSFRTSPENETELIK
		1	EHDLFPKAVSLCHTVQINNVQTDCTGDGPWQSNLAPSOLEYYAS
}			SPDEKALVEAAARIGIVFIGNSEETMEVKTLGKLERYKLLHILE
ł			FDSDRRRMSVIVQAPSGEKLLFAKGAESSILPKCIGGEIEKTRI
· ·			HVDEFALKGLRTLCIAYRKFTSKEYEEIDKRIFEARTALQQR\E
			EKLAAVFQFIEKDLILLGATAVEDRLQDKVRETIEALRMAGIKV
ŀ		}	WVLTGDKHETAVSVSLSCGHFHRTMNILELINQKSDSECAEQLR
	ł		QLARRITEDHVIQHGLVVDGTSLSLALREHEKLFMEVCRNCSAV
1			LCCRMAPLQKAKVIRLIKISPEKPITLAVGDGANDVSMIQEAHV
	ł		GIGIMGKEGRQAARNSDYAIARFKFLSKLLFVHGHFYYIRIATL
		İ	VQYFFYKNVCFITPQFLYQFYCLFSQQTLYDSVYLTLY\NICFT
1			SLPILIYSLLEQHVDPHVLQNKPTLYRDISKNRLLSIKTFLYWT
	}		ILGFSHAFIFFFGSYLLIGKDTSLLGNGQMFGNWTFGTLVFTVM
			VITVTVXMALETHFWTWINHLVTWGSIIFYFVFSLFYGGILWPF
İ		•	LGSQNMYFVFIQLLSSGSAWFAIILMVVTCLFLDIIKKVFDRHL
		· ·	HPTSTEKAQLTETNAGIKCLDSMCCFPEGEAACASVGRMLERVI
L	<u> </u>	4.4	GRCSPTHISRSWSASDPFYTNDRSILTLSTMDSSTC
6008	4554	1089	AGVRRAGARRGPGRALPAGATAVPPPSARRRRRCPAPEHAGPAR
			ASRPSQETMFQLPVNNLGSLRKARKTVKKILSDIGLEYCKEHIE
			DFKQFEPNDFYLKNTTWEDVGLWDPSLTKNQDYRTKPFCCSACP
1			FSSKFFSAYKSHFRNVHSEDFENRILLNCPYCTFNADKKTLETH
			IKIFHAPNASAPSSSLSTFKDKNKNDGLKPKQADSVEQAVYYCK
1	j		KCTYRDPLYEIVRKHIYREHFQHVAAPYIAKAGEKSLNGAVPLG
1			SNAREESSIHCKRCLFMPKSYEALVQHVIEDHERIGYQVTAMIG
			HTNVVVPRSKPLMLIAPKPQDKKSMGLPPRIGSLASGNV\RSLP
			SQQMVNRLSIPKPNLNSTGVNMMSSVHLQQNNYGVKSVGQGYSV
1			GQSMRLGLGGNAPVSIPQQSQSVKQLLPSGNGRSYGLGSEQRSQ
		•	APARYSLQSANASSLSSGQLKSPSLSQSQASRVLGQSSSKPAAA
f f	•		ATGPPPGNTSSTQKWKICTICNELFPENVYSVHFEKEHKABKVP
1 1			AVANYIMKIHNFTSKCLYCNRYLPTDTLLNHMLIHGLSCPYCRS
1 1			TFNDVEKMAAHMRMVHIDEEMGPKTDSTLSFDLTLQQGSHTNIH
	•		LLVTTYNLRDAPAESVAYHAQNNPPVPPKPQPKVQEKADIPVKS
1			SPQAAVPYKKDVGKTLCPLCFSILKGPISDALAHHLRERHQVIQ
1 1			TVHPVEKKLTYKCIHCLGVYTSNMTASTITLHLVHCRGVGKTQN
1			GQDKTNAPSRLNQSPSLAPVKRTYEQMEFPLLKKRKLDDDSDSP
1 1	. !		SPFEEKPEEPVVLALDPKGH\EDDSYEARKSFLTKYFT\KQPYP
į J	1		TRREIEKLAASLWV\WK\SDIASHFSNKRKKCVRDCEKYKPGVL
1 1			LGFNMKELNKVKHEMDFDAEGLFENHDEKDSRVNASKTADKKLN
1 1	!		LGKEDDSSSDSFENLEEESNESGSPFDPVFEVEPKISNDNPERH
	į:		VLKVIPEDASESEEKLDOKEDGSKYETIHLTEEPTKLMHNASDS
1 1			EVDQDDVVEWKDGASPSESGPGSQQVSDFEDNTCEMKPGTWSDE
1 1	ļ		SSQSEDARSSKPAAKKKATMQGDREQLKWKNSSYGKVEGFWSKD
1 1			QSQWKNASENDERLSNPQIEWQNSTIDSEDGEQFDNMTDGVAEP
<u> </u>			MHGSLAGVKLSSQQA
6009	4272	1534	CHGLQHLTPFRELNLSLQG*EPH*AA*QAVRSEEKSIC*GSPSC
			HLVLGVLVPVARQSSHSAGPAQSAFR+TGTGSGTPKAAEQSGYW
j ·			EAYTLGHQHWNMPPIQRPPLVMKGRRIMCGKCEKG*VSDSVTGG
ļ. ļ			RAVAGEQASQRRTVFTAGGGECLGAKSVRASVFTGNQPGVMGLL
j l			NGKRGGCFESGYLFGFIVIGKIQSLEAKVPLPVNGQTGERASPG
	ŀ	1	NCRIHIVDAVC*SEHH*DHFLAAAFLENSTIIS*VAPGSWQDHA
1.	ł		VLQKEVQASVRCRGFESVDTAPAGFWAHSPPGLQGEPTTTSVSL
	i i	ļ	FVLAPQDGEGVPFVEGQLVTVLGLVVPQSIRHTFVHHTQLFLHP
	İ		I*KLGALDVAFLHLLTLVCSSFNVAYG*GKNGGTTLHQLFAEVN
	1	l	AVTRGSAVQRRPSITISSIHVDTKIQQELHDVMVAGADGVVQWG
	į	<b>!</b>	DPFVVGLAGIFHLIDDPLHQIELSFQRRV*EQCQGVKPDSQPVP
1	l	ł	RPLRVGLLQVGPLVRGGGRRVAGRGKRCWRDLLFPWRWGLSHRT
		1	RDLLRGGDRGHVVVIVLCRLGSLVGGLGTDBLLWFGGR*LIIIG
			TITIE TO THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE P

Deginning   location   corresponding to first   min acid   cation   corresponding to first   amino acid   cation   corresponding to first   amino acid   cation   corresponding to first   amino acid   cation   corresponding to first   amino acid   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation   cation	SEO	Predicted	Predicted end	Amino acid segment containing signal peptide				
No:   nucleotide   corresponding to first   corresponding to first   mino acid   creation corresponding to first   mino acid   residue of   saino acid   residue of   saino acid   residue of   saino acid   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   se	_		1	(A=Alapine C-Cycleine D-Accepte A-12 F				
corresponding to first smino acid residue of residue of residue of residue of amino acid sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence	NO:			Glutamic Acid. F=Phenylalaning G-Clusing				
LeLeucine, Membethionine, N-Asparagine, periodic distinct amino acid residue of residue of anino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence	1	1		Hallistidine Talsoleucine Valueine				
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residue of amino acid sequence and no acid sequence with the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the proce			1	Secondary M. M. Maranine, Rearginine,				
amino acid sequence    Codon, /-possible nuclectide deletion,    -possible nuclectide deletion,    -possible nuclectide deletion,    -possible nuclectide deletion,    -possible nuclectide deletion,    -possible nuclectide deletion,    -possible nuclectide deletion,    -possible nuclectide deletion,    -possible nuclectide deletion,    -possible nuclectide deletion,    -possible nuclectide deletion,    -possible nuclectide deletion,    -possible nuclectide deletion,    -possible nuclectide deletion,    -possible nuclectide deletion,    -possible nuclectide deletion,    -possible nuclectide deletion,    -possible nuclectide deletion,    -possible nuclectide deletion,    -possible nuclectide deletion,    -possible nuclectide deletion,    -possible nuclectide deletion,    -possible nuclectide deletion,    -possible nuclectide deletion,    -possible nuclectide deletion,    -possible nuclectide deletion,    -possible nuclectide deletion,    -possible nuclectide deletion,    -possible nuclectide deletion,    -possible nuclectide deletion,    -possible nuclectide deletion,    -possible nuclectide deletion,    -possible nuclectide deletion,    -possible nuclectide deletion,    -possible nuclectide deletion,    -possible nuclectide deletion,    -possible nuclectide deletion,    -possible nuclectide deletion,    -possible nuclectide deletion,    -possible nuclectide deletion,    -possible nuclectide deletion,    -possible nuclectide deletion,    -possible nuclectide deletion,    -possible nuclectide deletion,    -possible nuclectide deletion,    -possible nuclectide deletion,    -possible nuclectide deletion,    -possible nuclectide deletion,    -possible nuclectide deletion,    -possible nuclectide deletion,    -possible nuclectide deletion,    -possible			1	Seserine, Ternreonine, Vevaline,				
Sequence   \possible mucleotide insertion	1	1	ľ	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop				
1**RORLSGEWGGGIGSELFOYSIGIOVSIVHIGGOBEVIGA AGIJVERGALHANGOVSPALVOQLIDVERGALIGOSTORAPOOD GRVGQLPASGIGVCITUVAQORMHDGRALIGGARPOOLAHGAAI COVGGALILKAASQYPKAGGT NUKAGASO YPKKERGRWG*TR R*NGLTIHCH*LI*GAVCCKLVILRMGGLLSVIGVVT*IHGL GSFPGALIP*PIPISGEPFRIGGTOR*FRLAVPSWKCHSRRGVTVRG TWRYGNPLINLL*GANLGGAACGGOQGGPLSTWQACTOPQQAAF LPFCGACRPRYGGRERTWCDIANGCLAUTED AGAMATGDLPAGTCAGTWOCIANGCLAUTED AGAMATGDLPAGTCAGTWOCIANGCLAUTED AGAMATGDLPAGTCAGTWCDIANGCAGACGGOQGPLSTWQACTOPQQAAF LPFCGACRPRYGTGRAFGCVGTAS KALGALTERAAQAAJVGFTP PMSQAGGGLVDPIOFARANGAIQMACQNLVDPGSSPSQVLSAA AGIGNAKTGDLPAGTCAGSTWOCIANGCHAVEPOSAGSVULSEAA TIVAKHITSALCHACHASSKTANFVAKHPVOSAKSVANSTANL VKTIKALGOPSENNIKCRIATSKTANFVAKHPVOSAKSVANSTANL VKTIKALGOPSENNIKCRIATSKTANFVAKHPVOSAKSVANSTANL VKTIKALGOPSENNIKCRIATSKTANFVAKHPVOSAKSVANSTANL VKTIKALGOPSENNIKCRIATSKTANFVAKHPVOSAKSVANSTANL VKTIKALGOPSENNIKCRIATSKTANFVAKHPVOSAKSVANSTANL VKTIKALGOPSENNIKCRIATSKTANFVAKHPVOSAKSVANSTANL VKTIKALGOPSENNIKCRIATSKTANFVAKHPVOSAKSVANSTANL VKTIKALGOPSENNIKCRIATSKTANFVAKHPVOSAKSVANSTANL VKTIKALGOPSENNIKCRIATSKAPLICAGCLTSVVOSAGSICHICH INATAGGRAALATVATOMINIKALSVALTSCOLTINGAGNITSD PMSVALAGHSHVASHSTANTALAUTAGEMIKTSKAPAGTCHTAAQLIMK EAVDDIMVTINRAASSVGLIVGAWDALAEMSKLDGOTPERKS TRUDYTVVLIKNALAVAGGEMIKTSVANSTANGAMTOOLAE EAVDDIMVTINRAASSVGLIVGAWAATSTORACHTAAQLOMK EAVDDIMVTINRAASSVGLIVGAWAATSTORACHAVAAANSCOCOL TAATAVSGIITAADLOTTIMPATAGTIANSKAPTADHERNILKTA KALVEDTILLSVANSTANDAGAAATSALCAANATSALVAAAANSCOCOL TAATAVSGIITAADLOTTIMPATAGTIANATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	]	ì	sequence	Codon, /=possible nucleotide deletion,				
AGLVERGALIHATGGOVEALVOQLIDVGFRGAIGLCGGALFGOAL GRVGOLPAGGIOUT TWAQRAMINGGELGGAEWPOALHGGAAI COVGGAILIKALSOYFIKGG FRUNCARGO FPUKERGRINGOVER RYGUTTUROTH THE GAVCCRIVITURGGILEVURGGUTF THELL GSFPGALMF PPTSGERPIGICOWEFILAVESWICKRERREVEWG THRYGMPLIALLI-GAVCCRIVITURGGILEVURGGTFOQAAF FRYGMENDLIALLI-GAVCCRIVITURGGILEVURGGTFOQAAF THRYGMPLIALLI-GAVCCRIVITURGGILEVURGGTFOQAAF LPFFGGACRAFTQACTAWACHGAACAGOGPETSTAGACTGFOQAAF LPFFGGACRAFTQACTAWACHGAACAGOGPETSTAGACTGFOQAAF LPFFGGACRAFTQACTAWACHGAACAGAGAACAGAGAACAGAACAGAACAGAACAG	ļ	sequence		\=possible nucleotide insertion				
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AGISONAKTOOLPASFECVGITASKALCSLITPAAQAAYLUGIFD PHSQAGGGGUVDPIQFARANACIMACONLITPASSPESPOULSAA TIVAKHISALCHAGRIASSKTANFVAKRHFVQSAKEVANSTANL VKTIKALDODFSENNINKCRITATAPLIEZBUFARSHEFEVS IPAGISSEGSQAEPILVSAKPHLESSSYLIRTARSLAINFKOP PWSVLAGHSVIVSSIKSLITSIRDARPQGECOYSIOLING IRDIEQASLAAVSQSLARTDDISVEALGEGLITSVOOSIGHLIDP PWSVLAGHSVIVSSIKSLITSIRDARPQGECOYSIOLINGC IRDIEQASLAAVSQSLARTDDISVEALGEGLITSVOOSIGHLIDP IATAAKGRAQLGHKSTQLASYPEPILLAAVVASKLLUHOQOM TVLDQITKTLASSALOMLVAAKEGGONFACHTDATTEAAQLMK EAVDDIMVTINFAASSVOLVGGNVDA IAEAMSKLDEGTPPEPKG TVUNGTVUVKSKALAVTAGRAMTSVITSUGLASQMTSG VGHLAFQCGMAAATABPETGFGIRTRVOOLGHGCITLVOKAG ALQVCPTDSYTKKELIECARAVTEKVSULVSAGAKGTOACI TAATAVSGIIADLDTTINFATGATINAANSETFANHEENILKTA KALMEDTKALVSGASAT POKLAQAAQSSAATLABAVEKULOABVACAGA SIGSDPETQVULINAI KOVAKALSDLISATKGAAKKPODPSK VOLKGAAKWAVTINTSLLKTVKAVSDBATHSKATALARTIECIKG ELTVFGSKOVPERTSSFEESIKRTGITTMATAVAGNSCKORG DVIATAMLSKRAVSMUTJACKQASSHPDVSDEVRTRALBFGTEC TISSTLLEHVINIJCKPTELEKQQLAAPSKAJAGANSCKORG EMMOTTEWOPEDPTVIABTELLGAAASIEAAAKKLEOLKPRAK PKQADETLUPFEGILEAAKSIEKQQLAAPSKAJACHIACKGA EMMOTTEWOPEDPTVIABTELLGAAASIEAAAKKLEOLKPRAK PKQADETLUPFEGILEAAKSIEKQQLAAPSKAJACHIACKGATELOKAA RASADHAVAAOKAAFGGADDDOVVKTKRVGGIAOITAAQEEM LKKERELEBAKKLAQITRQQVKPLPPELEBEGN SEERLISSAKQVASATAGLUKAKADOSSAATELQAANAV RASADHAVRAAOKAAFGGADDDOVVKTKRVGGIAOITAAQEEM LKKERELEBAKKLAQITRQQVKPLPPELEBOR GREPPM\D\AHACHIAGASIATSALVKSAATRAQIAMTSALVATHITISTATACTMATTISTATAGATAGANAVATTARATAGATAGANATAGAMELAAACHAGAAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAA	6010	1	3533	IMPCGSSRLLRGCWTHPNEPVSDLSYFDC1ESVMENSKVLCFSM				
PRISOAGIGGLUPPIGPARAMOATOMACONLUPGESSESQUIJAA TIVAKHISALCMACRIASSKARMPVAKHENPEVAMITANI VATIKALIGADPSEDNINKCRIATAPI, IEAVENILTAFASNPEVAS IPAGISSEGGAQEPILVSAKUPHESSSYLTISALAIPKOPE PIWSVLAGHSHTVSDS IKSLITSIRDKAPGGRECDYSIDCINRC IRDIGASEGGAQEPILVSAKUPHESSSYLTISALAIPKOPE PIWSVLAGHSHTVSDS IKSLITSIRDKAPGGRECDYSIDCINRC IRDIGASEGGAQAEPILVSAKUPHESSSYLTISALAIPKOPE IATAARGBAAGLGHKGTOLASYPEPLILAAVOVASKILDHOQOM TVLDQTKTLAESALGMIVAAKEGGGIN PRACHTHOAITEAACIMK ERVDDINVITMARASEVCULOKOVOD IAEAMSKLDEGTPEPKG TVUNYQTTVVKYSKALAVTAQEMMYKSYTTPEELGGLASQMTSD VGHLAPGGGMAAATAEPEEIGFGIRTRVOLGGLASQMTSD VGHLAPGGGMAAATAEPEEIGFGIRTRVOLGHAREMILKTA KALVEDTKILVSGAASTEDKIAQAAQSSAATITOLAEVVKLGAA ALGVCPTDSYTKRELIECARAVTEKVSLVLSALQAGKKGTQACI TAATAVSGIIADLDTTINFATATATIANASHAFHEENILKTA KALVEDTKILVSGAASTEDKIAQAAQSSAATITOLAEVVKLGAA SIGSDPETGVVLINAI KDVAKALBDLISATKAARAHEENILKTA KALVEDTKILLVSGAASTEDKIAQAAQSSAATITOLAEVVKLGAA SIGSDPETGVVLINAI KDVAKALBDLISATKAARAHEENILKTA KALVEDTKILLVSGAASTEDKIAQAAQSSAATITOLAEVVKLGAA SIGSDPETGVVLINAI KOVAKALBDLISATKAARAHEENILTETIKO CHILTPGSKOUPEKTSSPEESI KRTKGITMARAARAHVAACHSCOED DVIATANILSRKAVSDMITACKQASPH PDVSDEVRTRALRRGTEC TIGYLDLEHVULJCKPTDELKQQLAAPEKAAAGNICQOE DVIATANILSRKAVSDMITACKQASPH PDVSDEVRTRALRRGTEC TIGYLDLEHVULJCKPTDELKQQLAAPEKAAGNICACK VGSIPANAADDCQMSQGLISAARMVAAATSICAANTSICAANOX KRASDDILVRAAQAKAFGKAADDUVVKTKRVCGIAQIIAAGKA VGSIPANAADDCQMSQGLISAARMVAAATSICAGANAVA KRASDDILVRAAQAKAFGKAADDUVVKTKRVCGIAQIIAAQGKA VGSIPANAADDCQMSGGLISAARMVAAATSICAGANAVA KRASDDILVRAAQAKAFGKAADDUVVVKTKRVCGIAQIIAAQGKA VGSIPANAADDCQMSGGLISAARMVAAATSICAGANAVA KRASDDILVRAAQAKAFGKAADDUVVVKTKRVCGIAQIIAAQGKA VGSIPANAADDCQMSGGLISAARMVAAATSICAGANAVA KRASDDILVRAAQAAFGKAADDUVVKTKRVCGIAQIIAAQGKA VGSIPANAVATAMOMPIACCKVKAADQOSEARREKQASLAQGK VGSIPAMAVATAMOMPIACCKVKAADQOSEARREKQANAY KRASDDILVRAAQAAFGKADDAVAATTICATARATICATARATICACDGAACMA KRASDDINAAVAATAMOMPIACCACKAADQOSEARREKQAATAGAACMAA KRASDDINAAVAATAMOMPIACCACKAADQOSEARREKAAATATSILAACDGGAACMA CIUPERTAGAACAAAAAGAAGAAGAAAAAAATTAAAAAAAAAAAA				AGISONAKTGDLPAFGECVGTASKALCGLTFAAAOAAVLVGTED				
TIVAKHTSALCHACRIAS KTANPVAKRHPVQSAKEVANSTANIL VKTIKALOGDFSEDNIKKCINITAPILEMITAPASNPEPUS IPAQISSEGSQAQBPILVSAKEMLESSYTLIRTARSLAINPKOP PPHWSVLAGHSHYVSDEIKSLITSIRDKAPGECOYSIGITIOR IRDIEQASILAAVSQSLATEDDISVEALQEQLTSVVOEIGHLIDP IATAARGEAAQLGHKGTQLASYFBPLILAAVGVASKILHOQQM TVLDQYKTLAESALQHLYAAKEGGGNPKAQHHDAITEAAQLMK EAVDDIMVTIAFAASSUGLVGGWVDALAEAMSKLIDHOQQM TVLDQYKTLAESALQHLYAAKEGGGNPKAQHHDAITEAAQLMK EAVDDIMVTIAFAASSUGLVGGWVDALAEAMSKLIDGTPEPKG TVNYQTTVVKYSKATAVTAQEMMYKSVINBELGGLASQMTSD YGHLAPGGQMAAATAEPESIGGGIRTRVQDLGHGCIFLVGKAGY ALQVCPTDSYTKRELEGARAVTEKVSLAQAGNKSTOACI TAATAVSGIIADLDTIMPATAGTIANAENSETPADHREBILKTA KALVEDTKILVSGAASTEPKALQAAGVSKATQASI SIGSDDFETOVVLINAIKDVAKALSDLISATKGASKPVDDPSM YQLKGAKAWATVNTSLIKATVAAVEDBAYTALAEATICLAEVVKLGAA SIGSDDFETOVVLINAIKDVAKALSDLISATKGASKPVDDPSM YQLKGAKAWATVNTSLIKATVAAVEDBAYTALAEATICLAEV BLTYGSKOUPEKYSSPESIRTMKGITMATAKAVAAGNSCRQE DVIATANLSRKAVSDMLTACKQASPHPDVSDEVETRARFETEC TIGYLDLEHUVILCKYPTPELKQQLAAFSKRVAGAVTELLQAA EAMKGTEWVDEDDTVIAATELLGAAASISEARAVAGAVTSLQAGK VGSIPANAADDGOWSGGIISAARWAAATSSLCBANNAYQGHA SEEKLISSAKQVAASTAGLAVACKVKADGSARMRIQAAGNAV KRASDALVBAAQKAAFGKADDDDVVKTKFVGGIAQITAQGEM KKERELEBERKKLAQIRQQYKFLPTEREBBG 6011 4466 1835 LLDBARKSPGISDCLWARVILLAGTTJTGRSYGOFSLQDELKDNT TVPPRILDBYLDGYDNRIRPGLGERVYTEVKTDIFVTSGVSHA DMEYTIDVPFRQSKODELKYKOPMTULENDINASKINTDTF FRIGKKSVAHNMTMPNKLLRITSDGILVTRRITVSLACCMAF GROFPM\O'AHACPLKFGSXAYTRACVYTENTIVALACCMAF GROFPM\O'AHACPLKFGSXAYTRACVYTENTIVALACCMAF GROFPM\O'AHACPLKFGSXAYTRACVYTENTIVALACCMAF GROFPM\O'AHACPLKFGSXAYTRACVYTENTIVALTIVSIS ARISLBKVAVAYATAMOMFIAVCYAFVSSALIEFATVPNLAGCODGIA TILKSATIEPKEVKPTKPPDPKKTTNSVSKIDRLSRIAPPLLF GUVQSSPCEABELRYSLHVOPWSTCSMPHSRQVGQRRKKUDDLITTSGV QVQSSPCEABELRYSLHVOPWSTCSMPHSRQVGQRRKMTRGDCG CUSEFSAWSECSKYCGSGIGHTRHVVAPGGGGGGCPLTTFC QVCQSSPCEABELRYSLHVOPWSTCSMPHSRQVGQRRKKNDIGIGYOR EWCINNTGKAADLSFCQCKLPTTRINTGPGGSGCPLTTFC QCCQSSPCEABELRYSLHVOPWSTCSMPHSRQVORGRRKNENE PCKKTCHMVSPAGTRVRTTTRIOPPOLAGGSCFWEPLSCORG GUVPCATYGRRTTENTECRODELLSQODKRRCNACPILCOGG IOTREVYCVOANSALLSQLIFTRAVYBORGGGGCPLOGC CULSTWSTWSMSCHIPCTVYHQTOSM				PNSOAGHOGL/DPTOFAPANOATOMACONL/DBGGGDGOVI CAN				
VKTIKALDGDFSEDNRIKCRIATAPLIEAVENITAPSKIPEVS IPAGISSEGSOAGDPILVSAKMMESSSYNIRTARSKETIPKD PRØSVLAGHSHYVSDSIKSLITSIRDKAPGQECOYSIBGINKC IRDTEQASILAAVSGULATAPDISVEALQEQLISVOSTIGHING IRTARARGEAAQLGHKSTQLASYFSPILLBAVVVASKILDHOQQM TVLDQTKTLASSALQMLYAAKEGGGNEKAQHTHDAITEAAQLMK ERVDDIMVTIMFAASSEUGLVGGWUDALBAGKLBGTPEPEKG TFUDYQTTVUKYSKALAVTAQEMMTKSVINPBELGGLSGVTSSO VGHLAPGGGMAATAPBEBEIGGJRTRVQDLGHGCTFLVOKAG\ ALGVUPTDSYTKRELIECARAVTEKVSUVLSALQAGKKTOAGI. TAATAVSGILJADLDTTIMBATTAGTILAARSTADHEMILKTA KALVEDTKLLIVSGAASTPDKLAQAQSSAATITOLAEVVKLGAA SLGSDDPETQVVLINAIKDVARALSDLISATKGAASKTOAGI. TAATAVSGILJADLDTTIMBATTAGTILAARSTPADHEMILKTA KALVEDTKLLIVSGAASTPDKLAQAQSSAATITOLAEVVKLGAA SLGSDDPETQVVLINAIKDVARALSDLISATKGAASKTOAGI. TAATAVSGILJADLTTIMSTATGTILAARSTPADHEMILKTA KALVEDTKLLIVSGAASTPDKLAQAAQSSAATITOLAEVVKLGAA SLGSDDPETQVVLINAIKDVARARSDLISATKGAASKTOAGI. TOLGGAAKMVTAVTSLLKTVKAVEDBEATGARGTALEATIECIKG BLTVFGSKOVPEKTSSPESSIRMTKGITTATAKAVAAGNSCROE DVIATAMLSRRANSDMLTACKQASFHENDEVTRALRFGTEC TLGYLDLLEHVLVILCKPTPELKGQLAAPSKRVAGAVTELIQAA EMMKGTEWDPEDDTVIARATSLLICAAASICEARANSVOGK VGSIPANAADDOOMSGGILSAARNVAAATSALVKSASAAGREUVAQGK VGSIPANAADDOOMSGGILSAARNVAAATSALVKSASAAGREUVAQGK VGSIPANAADDOOMSGGILSAARNVAAATSALVKSASAAGREUVAQGK VGSIPANAADDOOMSGGILSAARNVAAATSALVKSASAAGREUVAQGK VGSIPANAADDOOMSGGILSAARNVAAATSALVKSASAAGREUVAQGK VGSIPANAADDOOMSGGILSAARNVAAATSALVKSACEAANASVOGK VGSIPANAADDOOMSGGILSAARNVAAATSALVKSACEAANASVOGK VGSIPANARGKSAGARGKADDOOMVVKTKFOGGIAGTAAGEEK LKKERELBEARKALQGIRQQYKKLFUTEREBBG  6011  446  1835  LLDPARKSFGLSBCLMWATILLISTLTGRSVGOPSLOEMKNT TVFTRILDRALLDGVINLERPGLGEKTTEVKTOTTVLTWTTISTS PROKKSVANHAMMYNKLLALTSDGTLLIVTUTVA LOEPMAP GROPPN\DAATILOGVONSTASTATATSTTOKARGUNTATTITISTS ARSISPKVAVATAMODFILAVCXAFVSSALIEFATUNYTKRGYA WEGKSVVERKKVEDPLIKGTSTOTTVTTVATTISTTYNAACDOGGLA TIAKSATIEPEWKETKPPEPKKTTNSVSKIDRISRTAPPLLF QUCQSSPCEABELRYJARREPGUKKKNTNOKINGSRNYMTTRGYA WEGKSVVERKKVEDPLIKKKNTNKOKRGRENKYMDIGIGYOTR EVKCINKTGKAADLFFCQGKKFTTENTGYTPOLLGQCDLTPOQD CIVSEFSAMSECSKITGSGGLTRTHVVAPPOPGGGSGCPMLTTF QLCHIPCTYTGRATTISTREGTYDLLGQGOKKGFRURKRITT NEPTGG	1			TIVAKHTSALCNACRIASSKTANDUAKDUDUGGAKTURAGORAT				
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EAMKGTEWUDEBDPTVTAETELLGAAASIEAAAKKLEQLKPRAK PKQADETLDFEEQILEAAKSIAAATSALVKSASAAQRELVAGGK VGSTPANAADDCQWSQGLISAARNVAAATSSLCEAANASVQHA SEEKLISSAKQVAASTAQLLVACKVKADQDSEAMRRLQAAGNAV KRASDNLVRAAQKAAFGKADDDDVVXTKFVGGIAQITAAQEEM LKKERELEBARKLKAQIRQQQYKFLPTELREDBG LKKERELEBARKLKAQIRQQQYKFLPTELREDBG LLQPAMRKSPGLSDCLWAWILLLSTLTGRSYGGPSLQDELKDNT TVFTRILDRLLDGYDNRLRPGLGERVTEVKTDIFVTSRGPVSDH DMEYTIDVFFRQSWKDERLKFKGPMTVLRINNLMASKIWTPDTF FHNGKKSVAHMMTMPNKLLRITSDGTLLYTMRLTVR\ACCPMAF GRDFPM\D\AHACPLKFGSYAYTRAEVVYEWTREPARSVVVAED GSRLNQYDLLGGTVDSGTVQNSTTHFHLKKRIGYFVI QTYLDPCIMTVILSQVSFMLNRESVPARTVFGVTTVLTWTTLSIS ARNSLPKVAYATAMDWFIAVCYAFVFSALIEFATVNYFTKRGYA WDGKSVVPEKPKKVKDPLIKKNNTYAPTATSYTPNLARGDGLA TIAKSATIEPKEVKPETKPPEPKKTFNSVSKIDRLSRIAFPLLF GIPNLVYWATYLNREPQLKAPTPHQ GIPNLYWATYLNREPQLKAPTPHQ  6012 351 5013 PAELFQSFAIMHKELYDWRLGPWNQCOPVISKSLEKPLECIKGE EGIQVREIACIQKDKDIPAEDIICEYFERKPLLEQACLIPQOD CIVSEFSAWASGSKSTGSLGURTRHIVAPAPOFGSGCPNLTEP QVCQSSPCEAEELRYSLHVGPWSTCSMPHSRQVRQARRRGKNKE REKDRSKGVKDPEARELIKKKRNRRNRQNRGENKYWDIQIGYQTR EVWCINKTGKAADLSFCQQEKLPMTPQSCVITKECQVSEWSEWS PCSKTCHDMYSPAGTRVTRTTIRQFPIGSEKECPEFEKEPCLS QGGVVPCATYGWRTTEWTECRVDPLLSQQDKRRGNTALCGGG IQTREVYCVQANENLLSQLSTHKNREASKPMULKLCTGPIPNTT QLCHIPCPTRECVSPWSAWGPCTYSNCNDQQGKKGFKLRKRRIT NEPTGGSGVTGNCPHLLZAIPCEPPACYDWKAVRLGDCEPDNGK BCGPGTQVGEVVCINSDGBEUDRGLCRDAIFFIPVACDAPCPKD CVLSTWSTWSSCSHTCSGKTTEGKQIRARSILAYAGEBGGIRCP NSSALQEVRSCNEHPCTVYTHQATOPWGQCIEDTSVSSFNTTTTIW				DVIATANLSRKAVSDMLTACKQASFHPDVSDEVRTRALRFGTEC				
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VGSTPANAADDGGWSQGLISAARMWAAATSSLCEAANASVQGHA SEEKLISSAKQVAASTAGLLVACKVKADQDSEAMRRLQAAGNAV KRASDNLVRAQKAAFGKADDDUVVKTKEVGGIAQIIAAQEEM LKKERELEEARKKLAQIRQQQYKFLPTELREDBG  6011 446 1835 LLQPAMRXSPGLSDCLWAWILLSTLTGRSYGOPSLQDELKDNT TVFTRILDRLLDGYDNRLPGLGERVTEVKTDIFVTSPGPVSDH DMEYTIDVFFRQSWKDERLKPKGGMTVLRINNLMASKIWTPDTF FHNGKKSVAHNNTMPNKLLRITEDGTLLYTMRLTVR\AECPMAF GRDFPM\D\AHACPLKFGSYATRAEVVYEWTREPRASVVVAED GSRLNQYDLLGGTVDSGIVQSSTGEYVVMTHEHLKRKIGYFVI QTYLPCIMTVILSQVSFWLNRESVPARTVFGVTTVLTMTISIS ARNSLPKVAYATAMDWFIAVCYAFVFSALIEFATVNYFTKRGYA WDGKSVVPBKPKKVKVDPLIKKNNTYAPTATSYTPNLARGDPGLA TIAKSATIEPKSVKPETKPPEPKKTFNSVSKIDRLSRIAFPLLF GIPNLVWAATYLNREPQLKAPTPHQ 6012 351 5013 PAELFQSFALWKELYDDWRLGPWROCQPVISKSLEKFLECIKGE EGGIQVREIACIQKDKDIPAEDIICEYFEPKPLLEQACLIPCQQD CIVSEFSAWSECSKTCGSGLQHRTRHVVAPPQFGGSGCPNLTEF QVCQSSPCEAEELRYSLHVGPWSTCSMPHSRQVRQARRGKNKE REKDRSKGVKDPEARELIKKKRNRNRQNRQENKYWDIQIGYQTR EVMCINKTGKAADLSFCQQEKLPMTPQSCVITKECQVSEWSEWS PCSKTCHDMVSPAGTRVRTTIRQFPIGSEKECPBFEEKEPCLS QGGVVPCATTGWRTTEWTECRVDPLLSQQDKRGNQTALCGGG IQTREVYCVQANENLLSQLSTHKNKEBSKPMDLKLCTGPIPNTT QCHIPCPTECEVSPWSAWGPCTYENCNDQQGKKGFKLRRRIT NEPTGGSGVTGNCPHLLZAIPCEEPACYDWKAVRLGDCEPDNGK BCGPGTQVGEVVCINSDGEEURQLCRDAIFFIPVACDAPCPKD CVLSTWSTWSSCSHTCSGKTTEGKQIRARSILAYAGEEGGIRCP NSSALQEVRSCNEHPCTVYHMQTGPWGQCIEDTSVSSFNTTTTM				EAMKGTEWVDPBDPTVIAETELLGAAASIEAAAKKLEQLKPRAK				
VGSTPANAADDGGWSQGLISAARMWAAATSSLCEAANASVQGHA SEEKLISSAKQVAASTAGLLVACKVKADQDSEAMRRLQAAGNAV KRASDNLVRAQKAAFGKADDDUVVKTKEVGGIAQIIAAQEEM LKKERELEEARKKLAQIRQQQYKFLPTELREDBG  6011 446 1835 LLQPAMRXSPGLSDCLWAWILLSTLTGRSYGOPSLQDELKDNT TVFTRILDRLLDGYDNRLPGLGERVTEVKTDIFVTSPGPVSDH DMEYTIDVFFRQSWKDERLKPKGGMTVLRINNLMASKIWTPDTF FHNGKKSVAHNNTMPNKLLRITEDGTLLYTMRLTVR\AECPMAF GRDFPM\D\AHACPLKFGSYATRAEVVYEWTREPRASVVVAED GSRLNQYDLLGGTVDSGIVQSSTGEYVVMTHEHLKRKIGYFVI QTYLPCIMTVILSQVSFWLNRESVPARTVFGVTTVLTMTISIS ARNSLPKVAYATAMDWFIAVCYAFVFSALIEFATVNYFTKRGYA WDGKSVVPBKPKKVKVDPLIKKNNTYAPTATSYTPNLARGDPGLA TIAKSATIEPKSVKPETKPPEPKKTFNSVSKIDRLSRIAFPLLF GIPNLVWAATYLNREPQLKAPTPHQ 6012 351 5013 PAELFQSFALWKELYDDWRLGPWROCQPVISKSLEKFLECIKGE EGGIQVREIACIQKDKDIPAEDIICEYFEPKPLLEQACLIPCQQD CIVSEFSAWSECSKTCGSGLQHRTRHVVAPPQFGGSGCPNLTEF QVCQSSPCEAEELRYSLHVGPWSTCSMPHSRQVRQARRGKNKE REKDRSKGVKDPEARELIKKKRNRNRQNRQENKYWDIQIGYQTR EVMCINKTGKAADLSFCQQEKLPMTPQSCVITKECQVSEWSEWS PCSKTCHDMVSPAGTRVRTTIRQFPIGSEKECPBFEEKEPCLS QGGVVPCATTGWRTTEWTECRVDPLLSQQDKRGNQTALCGGG IQTREVYCVQANENLLSQLSTHKNKEBSKPMDLKLCTGPIPNTT QCHIPCPTECEVSPWSAWGPCTYENCNDQQGKKGFKLRRRIT NEPTGGSGVTGNCPHLLZAIPCEEPACYDWKAVRLGDCEPDNGK BCGPGTQVGEVVCINSDGEEURQLCRDAIFFIPVACDAPCPKD CVLSTWSTWSSCSHTCSGKTTEGKQIRARSILAYAGEEGGIRCP NSSALQEVRSCNEHPCTVYHMQTGPWGQCIEDTSVSSFNTTTTM	1			PKQADETLDFEEQILEAAKSIAAATSALVKSASAAQRELVAQGK				
SEEKLISSAKQVASTAGLLVACKVKADQDSEAMRRLQAAGMAV KRASDNLVRAAQKAAFGKADDDDVVVKTKFVGGIAQIIAAQEEM LKKERELEEARKKLAQIRQQQYKFLPTELREBEG  LLQPAMRKSPGLSDCLWAWILLLSTLTGRSYGQPSLQDELKDNT TVFTRILDRLLDGYDNRLRPGLGERVTEVKTDIFVTSFGPVSDH DMEYTIDVFFRQSWKDERLKFKGPMTVLRLNNLMASKIWTPDTF FHNGKKSVAHNMYMPNKLLRITEDGTLLYTMRLTVR\AECPMAF GRDFPM\D\AHACPLKFGSYAYTRAEVVYEWTREPARSVVVAED GSRLMQYDLLGGTVDSGIVQSSTGEYYVMTTHFHLKRKIGYFVI QTYLPCIMTVILSQVSFWLNRESVPARTVFGYTTVLTMTTLSIS ARNSLPKVAYATAMDWFIAVCYAFVFSALIEFATVNYFTKRGYA WDGKSVVPEKPKKVKDPLIKKNNTYAPTATSTYPNLARGDPGLA TIAKSATIEPKEVKPETKPPEPKKTFNSVSKIDRLSRIAFPLLF GIFNLVYWATYLNREPQLKAPTPHQ GIFNLVYWATYLNREPPQLKAPTPHQ CIVSEFSAWSECSKTGSGLQHRTRHVVAPPQFGGSGCPNLTEF QVCQSSPCEAEELRYSLHVOFWSTCSMPHSRQVRQARRGKNKE REKDRSKGVKDPEARELIKKRRNRRQNRQENKYWDIQIGYQTR EVMCINKTGKAADLSFCQQEKLPMTPGSCVITKEQCYSENSEMS PCSKTCHDMVSPAGTRVRTTIRQFPIGSEKECPEFEEKEPCLS QGGVVPCATYGWRTTEWTECRVDPLLSQDJKRRGNGTALCGGG IQTREVVCVQANENLLSQLSTHKNKEASKPMDLKLCTGPIPNTT QLCHIPCPTECEVSFWSAMGPCTYENCNDQGKKGFKLRKRRIT NEPTGGSGVTCNCPHLLEAIPCEEPACYDWKAVRLGDCEPDNGK BCGPGTQVGVVCINSDGBEVDRQLCRDAIFPIPVACDAPCPKD CVLSTWSTWSSCSHTCSGKTTEGKQIRARSILAYAGEEGGIRCP NSSALQEVRSCHEHPCTVYHWQTOPWGQCIEDTSVSSFNTTTTW	1			VGSIPANAADDGQWSQGLISAARMVAAATSSLCEAANASVOGHA				
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REKDRSKGVKDPEARELIKKKRNRNQNRQENKYWDIQIGYQTR EVMCINKTGKAADLSFCQQEKLPMTFQSCVITKECQVSEWSEMS PCSKTCHDMVSPAGTRVRTRTIRQFPIGSEKECPEFBEKEPPCLS QGGGVVPCATYGWRTTEWTECRVDPLLSQQDKRRGNQTALCGGG IQTREVYCVQANENLLSQLSTHKNKEASKPMDLKLCTGPIPNTT QLCHIPCPTECEVSPWSAWGPCTYENCNDQQGKKGFKLRKRRIT NEPTGGSGVTGNCPHLLEAIPCEEPACYDWKAVRLGDCEPDNGK ECGPGTQVQEVVCINSDGEEVDRQLCRDAIFPIPVACDAPCPKD CVLSTWSTWSSCSHTCSGKTTBGKQIRARSILAYAGEEGGIRCP NSSALQEVRSCNEHPCTVYHWQTGPWGQCIEDTSVSSFNTTTTW	Į. J	. [	i	OVCOSSPCEAERLRYSLINGDWGTCGMDUGDOUTGARDAGGGG				
EVMCINKTGKAADLSFCQQEKLPMTFQSCVITKECQVSEWSEWS PCSKTCHDMVSPAGTRVRTRTIRQFPIGSEKECPEFBEKEPCLS QGDGVVPCATYGWRTTEWTECRVDPLLSQQDKRRGNQTALCGGG IQTREVYCVQANENLLSQLSTHKNKEASKPMDLKLCTGPIPNTT QLCHIPCPTECEVSPWSAWGPCTYENCONQQGKKGFKLRKRRIT NEPTGGSGVTGNCPHLLEAIPCEEPACYDWKAVRLGDCEPDNGK ECGPGTQVQEVVCINSDGBEVDRQLCRDAIFPIPVACDAPCPKD CVLSTWSTWSSCSHTCSGKTTEGKQIRARSILAYAGEEGGIRCP NSSALQEVRSCNEHPCTVYHWQTGPWGQCIEDTSVSSFNTTTTW	} !		}	BEKDESKOVKDDEADELTVVVDNDADOVDODAVAVADECTOR				
PCSKTCHDMVSPAGTRVRTRTIRQFPIGSEKECPEFEEKEPCLS QGDGVVPCATYGWRTTEWTECRVDPLLSQQDKRRGNQTALCGGG IQTREVYCVQANENLLSQLSTHKNKEASKPMDLKLCTGPIPNTT QLCHIPCPTECEVSPWSAWGPCTYENCNDQQGKKGFKLRKRRIT NEPTGGSGVTGNCPHLLEAIPCEEPACYDWKAVRLGDCEPDNGK EGGPGTQVQEVVCINSDGEEVDRQLCRDAIFPIPVACDAPCPKD CVLSTWSTWSSCSHTCSGKTTEGKQIRARSILAYAGEEGGIRCP NSSALQEVRSCNEHPCTVYHWQTGPWGQCIEDTSVSSFNTTTTW	į l		1	EAMCINKLERY DITCE TOWNS TOWNS TO THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE O				
QGDGVVPCATYGWRTTEWTECRVDPLLSQQDKRRGNQTALCGGG IQTREVYCVQANENLLSQLSTHKNKEASKPMDLKLCTGPIPNTT QLCHIPCPTECEVSPWSAWGPCTYENCNDQQGKKGFKLRKRRIT NEPTGGSGVTGNCPHLLEAIPCEEPACYDWKAVRLGDCEPDNGK ECGPGTQVEVVCINSDGEEVDRQLCRDAIFPIPVACDAPCPKD CVLSTWSTWSSCSHTCSGKTTEGKQIRARSILAYAGEEGGIRCP NSSALQEVRSCNEHPCTVYHWQTGPWGQCIEDTSVSSFNTTTTW	1			PCSKTCHDMVSDACTDVDTDTTDCTDTTCCTPTCTTRECQVSEWSEWS				
IQTREVYCVQANENLLSQLSTHKNKEASKPMDLKLCTGPIPNTT QLCHIPCPTECEVSPWSAWGPCTYENCNDQQKKGFKLRKRRIT NEPTGGSGVTGNCPHLLEAIPCEEPACYDWKAVRLGDCEPDNGK ECGPGTQVQEVVCINSDGEEVDRQLCRDAIFPIPVACDAPCPKD CVLSTWSTWSSCSHTCSGKTTEGKQIRARSILAYAGEEGGIRCP NSSALQEVRSCNEHPCTVYHWQTGPWGQCIEDTSVSSFNTTTTW	1 1	1		OCDCIA/DCATYCHDTTEHMBOOLDD - COOLUND CATYCHDTEHMBOOLDD - COOLUND CATYCHDTEHMBOOLDD - COOLUND CATYCHDTEHMBOOLDD - COOLUND CATYCHDTEHMBOOLDD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD - COOLUND CATYCHD				
QLCHIPCPTECEVSPWSAWGPCTYENCNDQQGKKGFKLRKRRIT NEPTGGSGVTGNCPHLLEAIPCEEPACYDWKAVRLGDCEPDNGK BCGPGTQVQEVVCINSDGEEVDRQLCRDAIFPIPVACDAPCPKD CVLSTWSTWSSCSHTCSGKTTBGKQIRARSILAYAGEEGGIRCP NSSALQEVRSCNEHPCTVYHWQTGPWGQCIEDTSVSSFNTTTTW	I	i		TOTTE ELECTION NEW TECKY DPLLSQQDKRRGNQTALCGGG				
NEPTGGSGVTGNCPHLLEAIPCEEPACYDWKAVRLGDCEPDNGK  ECGPGTQVQEVVCINSDGEEVDRQLCRDAIFPIPVACDAPCPKD  CVLSTWSTWSSCSHTCSGKTTEGKQIRARSILAYAGEEGGIRCP  NSSALQEVRSCNEHPCTVYHWQTGPWGQCIEDTSVSSFNTTTTW	į l	1		OLGULDGOTTEGENGRANDA WORKERSKPMDLKLCTGPIPNTT				
ECGPGTQVQEVVCINSDGEEVDRQLCRDAIFPIPVACDAPCPKD CVLSTWSTWSSCSHTCSGKTTEGKQIRARSILAYAGEEGGIRCP NSSALQEVRSCNEHPCTVYHWQTGPWGQCIEDTSVSSFNTTTTW	}			WEDTCCCCOTTCNONT I TO TROTTE TO THE TOTAL TO THE TOTAL TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO THE TROTTE TO				
CVLSTWSTWSSCSHTCSGKTTEGKQIRARSILAYAGEEGGIRCP NSSALQEVRSCNEHPCTVYHWQTGPWGQCIEDTSVSSFNTTTTW	1	j		NEFTGGSGVTGNCPHLLEAIPCEEPACYDWKAVRLGDCEPDNGK				
NSSALQEVRSCNEHPCTVYHWQTGPWGQCIEDTSVSSFNTTTTW		1		BCGFGTQVQEVVCINSUGEEVDRQLCRDAIFPIPVACDAPCPKD				
NSSALQEVRSCNEHPCTVYHWQTGPWGQCIEDTSVSSFNTTTTW NGEASCSVGMQTRKVICVRVNVGQVGPKKCPESLRPETVRPCLL	1		1	CVLSTWSTWSSCSHTCSGKTTEGKQIRARSILAYAGEEGGIRCP				
NGEASCSVGMQTRKVICVRVNVGQVGPKKCPESLRPETVRPCLL	·		1	NSSALQEVRSCNEHPCTVYHWQTGPWGQCIEDTSVSSFNTTTTW				
				NGEASCSVGMQTRKVICVRVNVGQVGPKKCPESLRPETVRPCLL				

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F-Phenylalanine, G-Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ļ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ı	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
į.	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i i	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence .	· •	\=possible nucleotide insertion}
			PCKKDCIVTPYSDWTSCPS\SCKEGDSSIRKQSRHRVIIQLPAN
			GGRDCTDPLYEEKACEAPQACQSYRW\KTHKW\HRCQ\LVP\WS
- 1	İ	1	VQQDSP\GAQEGCGPGRQARAITCRKQDGGQAGIHECLQYAGPV
			PALTQACQIPCQDDCQLTSWSKFSSCNGDCGAVRTRKRTLVGKS
1			KKKEKCKNSHLYPLIETQYCPCDKYNAQPVGNWSDCILPEGKVE
1			VLLGMKVQGDIKECGQGYRYQAMACYDQNGRLVETSRCNSHGYI
i			BEACIIPCPSDCKLSEWSNWSRCSKSCGSGVKVRSKWLREKPYN
1			GGRPCPKLDHVNQAQVYEVVPCHSDCNQYLWVTEPWSICKVTFV
1			NMRENCGEGVQTRKVRCMQNTADGPSEHVEDYLCDPEEMPLGSR
	1		VCKLPCPEDCVISEWGPWTQCVLPCNQSSFRQRSADPIRQPADE
1		·	GRSCPNAVEKEPCNLNKNCYHYDYNVTDWSTCQLSEKAVCGNGI
' ·			KTRMLDCVRSDGKSVDLKYCEALGLEKNWQMNTSCMVECPVNCQ
	]		LSDWSPWSECSQTCGLTGKMIRRRTVTQPFQGDGRPCPSLMDQS
1	1		KPCPVKPCYRWQYGQWSPCQVQEAQCGEGTRTRNISCVVSDGSA
1			DDFSKVVDBEFCADIELIIDGNKNMVLEESCSQPCPGDCYLKDW
İ			SSWSLCQLTCVNGEDLGFGGIQVRSRPVIIQELENQHLCPEQML
ļ			ETKSCYDGQCYEYKWMASAWKGSSRTVWCQRSDGINVTGGCLVM
İ	!		SQPDADRSCNPPCSQPHSYCSETKTCHCEEGYTEVMSSNSTLEQ
			CTLIPVVVLPTMEDKRGDVKTSRAVHPTQPSSNPAGRGRTWFLQ
	ļ .		PFGPDGRLKTWVYGVAAGAFVLLIFIVSMIYLACKKPKKPQRRQ
			NNRLKPLTLAYDGDADM
6013	1161	710	GAFIAGVPVQPVLIRYPNSLDTTSWAWRGPGVLKVLWLTASQPC
			SIVDVEFLPVYHPSPEESRDPTLYANNVQRVMAQALGIPATECE
1			FVGSLPVIVVGRLKVALEPQL/WGTGKSASEGWAVRWLCGRWGR
			ARPESNDQPGRVCQAATAL
6014	2857	613	EAVAGGMEKSRMNLPKGPDTLCFDKDEFMKEDFDVDHFVSDCRK
			RVQLEELRDDLELYYKLLKTAMVELINKDYADF\VNLSTNLVGM
	İ		DKALNQLSVPLGQLREEVLSLRSSVSEGIRAVDERMSKQEDIRK
			KKMCVLRLIQVIRSVEKIEKILNSQSSKETSALEASSPLLTGQI
1 1			LERIATEFNQLQFHACQSK\GMPLLDKVRPRIAGITAMLQQSLE
1 1		1	GLLLEGLQTSDVDIIRHCLRTYATIDKTRDAEALVGQVLVKPYI
1 1			DEVIIEQFVESHPNGLQVMYNKLLEFVPHHCRLLREVTGGAISS
1			EKGNTVPGYDFLVNSVWPQIVQGLEEKLPSLFNPGNPDAFHEKY
)			TISMDFVRRLERQCGSQASVKRLRAHPAYHSFNKKWNLPVYFQI
	j	· i	RFRETAGSLEAALTDVLEDAPAESPYCLLASHRTWSSLRRCWSD
1			EMFLPLLVHRLWRLHSGRFWARYSVFV\N\BLSLRPISNESPKE
ĺĺ	į.	1	IKKPLVTGSKEPSITQGNTEDQGSGPSETKPVVSISRTOLVYVV
; · I			ADLDKLQEQLPELLEIIKPKLEMIGFKNFSSISAALEDSOSSFS
1		İ	ACVPSLSSKI IQDLSDSCFGFLKSALEVPRLYRRTNKEVPTTAS
		4	SYVDSALKPLFQLQSGHKDKLKQAIIQQWLEGTLSESTHKYYET
Į l			VSDVLNSVKKMEESLKRLKQARKTTPANPVGPSGGMSDDDKIRL
1 1		i	QLALDVEYLGEQIQKLGLQASDIKSFSALABLVAAAKDQATAEQ
			P
6015	13	2237	AEGCAERRGTEPVVELSMSWESGAGPGLGSQGMDLVWSAWYGKC
1			VKGKGSLPLSAHGIVVAWLSRAEWDOVTVYLPCDDHKLORYALN
1 1	ļ		RITVWRSRSGNELPLAVASTADLIRCKLLDVTGGLGTDELRLLY
] ]	İ	1	GMALVRFVNLISERKTKFAKVPLKCLAQEVNIPDWIVDLRHELT
[ [	ĺ	ï	HKKMPHINDCRRGCYFVLDWLQKTYWCROLENSLRETWELEEFR
] ]	1	1	EGIEEEDQEEDKNIVVDDITEQKPRPODDGKSTESDVKADGDSK
j			GSEEVDSHCKKALSHKELYERARELLVSYEEEOFTVLEKFRYLD
	1	i	KAIKAWNNPSPRVECVLAELKGVTCENREAVLDAFLDDGFLVPT
	1		FEQLAALQ1EYEENVDLNDVLVPKPFSQFWQPLLRGLHSQNFTQ
			ALLERMLSELPALGISGIRPTYILRWTVELIVANTKTGRNARRF
			SAGQWEARRGWRLFNCSASLDWPRMVESCLGSPCWASPOLLRIT
			F\KAMGQGLQDE\EQEKLLRICSIYTOSGENSLVOEGSEASPIG
			KSPYTLDSLYWSVKPASSSFGSEAKAOOOEEOGSVNDVKEEEKE
		<b>1</b>	EKEVLPDQVEEEEENDDQEEEEEDEDDEDDEEEDRMEVGPFSTG
1		l ·	QESPTAENARLLAQKRGALQGSAWOVSSEDVRWDTFP\LGRMPR
,	1	1 -	SRPRTPAELMLENYDTHVIFWTKPVL\EORLEPSTCK\TDTLGI.
6016.	13		\SCGVGS\GNCSNSSSSNFRGAFLLRARGSLH\GL\KTGLOLF
		2237	AEGCAERRGTEPVVELSMSWESGAGPGLGSQGMDLVWSAWYGKC

SEQ	Predicted	Predicted end	Amino acid cogmons control
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
- 1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine.
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine
	amino acid	residue of	S=Serine, T=Threonine, V=Valine.
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
<u> </u>	sequence		\=possible nucleotide insertion)
			VKGKGSLPLSAHGIVVAWLSRAEWDQVTVYLFCDDHKLQRYALN
1		1	RITVWRSRSGNELPLAVASTADLIRCKLLDVTGGLGTDELRLLY
Į.			GMALVRFVNLISERKTKFAKVPLKCLAQEVNIPDWIVDLRHELT
1			HKKMPHINDCRRGCYFVLDWLQKTYWCRQLENSLRETWELEEFR
1			EGIEEEDQEEDKNIVVDDITEQKPEPQDDGKSTESDVKADGDSK
			GSEEVDSHCKKALSHKELYBRARELLVSYEEEQFTVLEKFRYLP KAIKAWNNPSPRVECVLAELKGVTCENREAVLDAFLDDGFLVPT
l l	ļ	İ	FEQLAALQIEYEENVDLNDVLVPKPFSQFWQPLLRGLHSQNFTQ
ł			ALLERMISELPALGISGIRPTYILRWIVELIVANTKIGRNARRF
1	1		SAGQWEARRGWRLFNCSASLDWPRMVESCLGSPCWASPQLLRII
1			F\KAMGQGLQDE\EQEKLLRICSIYTQSGENSLVOEGSEASPIG
1			KSPYTLDSLYWSVKPASSSFGSEAKAQQQEEQGSVNDVKEEEKE
1			RKEVLPDQVEEEEKNDDQEEBEEDEDDEDDEEEDRMEVGPFSTG
			QESPTAENARLLAQKRGALOGSAWOVSSEDVRWDTFD\1GPMPR
I	1		SRPRTPAELMLENYDTHVIFWTKPVL\EORLEPSTCK\TDTLGL
	222		\SCGVGS\GNCSNSSSSNFRGAFLLEARGSLH\GL\KTGLOLF
6017	203	3469	SHQEIEQNSAMAPRKRGGRGISFIFCCFRNNDHPEITYRLRNDS
			NFALQTMEPALPMPPVEELDVMFSELVDELDLTDKHREAMFALP
1			AEKKWQIYCSKKKDQEENKGATSWPEFYIDQLNSMAARKSLLAL
			EKBEEEERSKTIESLKTALRTKPMRFVTRFIDLDGLSCILNFLK
1	,		TMDYETSESRIHTSLIGCIKALMNNSQGRAHVLAHSESINVIAQ
ļ:			SLSTENIKTKVAVLEILGAVCLVPGGHKKVLOAMLHYOKYASER TRFQTLINDLDXSTGRYRDEVSLKTAIMSFINAVLSQGAGVESL
1			DFRLHLRYE\FLMLGIHPVMDKLRKHENSTLDRHLDFFEMLRNE
	,		DELEFAKRFELVHIDTKSATQMPELTRKRLTHSEAYPHFMSILH
i	]		HCLQMPYKRSGNTVQYWLLLDRIIQQIVIQNDKGQDPDSTPLEN
1	1		FNIKNVVRMLVNENEVKQWKEQABKMRKEHNELQQKLBKKEREC
			DAKTQEKEEMMQTLNKMKEKLEKETTEHKQVKQQVADLTAQLHE
			LSRRAVCASIPGGPSPGAPGGPFPSSVPGSLLPPPPPPPPPLPGGM
	1		LPPPPPPLPPGGPPPPPGPPPLGAIMPPPGAPMGLALKKKSIPO
1 .			PTNALKSFNWSKLPENKLEGTVWTEIDDTKVFKILDLEDLERTF
1	1		SAYQRQQDFFVNSNSKQKEADAIDDTLSSKLKVKELSVIDGRRA
1			QNCNILLSRLKLSNDEIKRAILTMDEQEDLPKDMLEQLLKFVPE
1	1		KSDIDLLEEHKHELDRMAKADRFLFEMSRINHYQQRLQSLYFKK
			KFABRVAEVKPKVEAIRSGSEEVFRSGALKQLLEVVLAFGNYMN
			KGQRGNAYGFKISSLNKIADTKSSIDKNITLLHYLITIVENKYP
ł			SVLNLNEELRDIPQAAKVNMTELDKEISTLRSGLKAVETELEYQ KSQPPQPGDKFVSVVSQFITVASFSFSDVEDLLAEAKDLFTKAV
<b> </b>			KHFGEEAGKIQPDEFFGIFDQFLQAVSEAKQENENMRKKKEEEE
	]		RRARMEAQLKEQRERERKMRKAKENSEESGEFDDLVSALRSGEV
		1	FDKDLSKLKRNRKRITNOMTDSSRERPITKLNF
6018	13	2510	TISQSGGIRRRREAVWFEVVNMDFSRLHMYSPPQCVPENTGYTY
		ļ	ALSSSYSSDALDFETEHKLDPVFDSPRMSRRSLRLATTACTLGD
1 1			GEAVGADSGTSSAVSLKNRAARTTKORRSTNKSAFSINHUSROV
ļ l			TSSGVSYGGTVSLQDAVTRRPPVLDESWIREOTTVDHFWGLDDD
i i		1	GDLKGGNKAAIQGNGDVGAGAATGHNGFFCSNCNMLSERKDVLT
1		1	AHPAAPGPVSRVYSRDRNQKCDDCKGKRHLDAHPGRAGTLWHIN
			ACAGYFLLQILRRIGAVGQAVSRTAWSALWLAVVAPGKAASGVF
<u> </u>	1		WWLGIGWYQFVTLISWLNVFLLTRCLRNICKFLVLLIPLFLLLG
i !	1	Ì	LSLRGQG\NFFSFLPVLNWASMHRTQRVDDPQDVFKPTTSRLKQ
	1		PLQGDSEAFPWHWMSGVEQQVASLSGQCHHHGENLRELTTLLQK
		1	LQARVDQMEGGAAGPSASVRDAVGQPPRETDFMAFHQEHEVRMS
] [	j	İ	HLEDILGKLREKSEAIQKELEQTKQKTISAVGEQLLPTVEHLQL
	ŀ	1	ELDQLKSELSSWRHVKTGCETVDAVQERVDVQVREMVKLLFSED
		1	QQGGSLEQLLQRPSSQFVSKGDLQTMLRDLQLQILRNVTHHVSV TKOLPTSEAVVSAVSFAGASGITFAGABAILANAN VACCOUNTS
	ļ		TKQLPTSEAVVSAVSEAGASGITEAQARAIVNSALKLYSQDKTG MVDFALESGGGSILSTRCSETYETKTALMSLFGIPLWYFSQSPR
	1		VVIQPDIYPGNCWAFKGSQGYLVVRLSMMIHPAAFTLEHIPKTL
			SPTGNISSAPKDFAVYGLENEYQEEGQLLGQFTYDQDGESLQMF
			QALKRPDDTAFQIVELRIFSNWGHPEYTCLYRFRVHGEPVK
6019	2	1066	TPNDREPPPORPPSSRRASHLAQEITSAASLGDQTQILGSLTTA
			The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s

	SEQ	Predicted	Predicted end	l hmino poid assessment
	ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	NO:	nucleotide	location	Glutamic Acid, F-Phenylalanine, G-Glycine,
		location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
		corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
		to first	amino acid	P-Proline, Q-Glutamine, R-Arginine,
		amino acid	residue of	S=Serine, T=Threonine, V=Valine,
		residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
		amino acid	sequence	Codon, /=possible nucleotide deletion,
i		sequence	1	\=possible nucleotide insertion)
				PVITSAIRSMPGISSQILTNAQGQVIGTLPWVVNSASVAAPAPA
			ľ	QSLQVQAVTPQLLLNAQGQVIATLASSPLPPPVAVRK\PSTPES
				LLKSEVQPIKPTPTVPQPAVVIASPAPAAKPSASAPIPITCSET
		1		PTVSQLVSKPHTPSLDEDGINLEEIREFAKNFKIRRLSLGLTQT
				QVGQALTATEGPAYSQSAICRFEKLDITPKSAQKLKPVLEKWLN
ı				EAELRNQEGQQNLMEFVGGEPSKKRKRRTSFTPQAIEALNAYFE
			l	KNPLPTGQEITEIAKELNYDREVVRVWFCNRRQTLKNTSKLNVF
			<u>.</u>	QIP
1	6020	4953	549	EAIQFEVSIGNYGNKFDTTCKPLASTTQYSRAVFDGNYYYYLPW
I				AHTKPVVTLTSYWEDISHRLDAVNTLLAMAERLOTNIEALKSGI
İ				QGKIPANQLAELWLKLIDEVIEDTRYTLPLTEGKANVTVLDTOT
			1	RKLRSRSLSQIHEAAVRMRSBATDVKSTLAEIEDWLDKLMOLTE
-			·	EPONSMPDIIIWMIRGEKRLAYARIPAHOVLYSTSGENASGKYC
-1				GKTQTIFLKYPQEKNNGPKVPVELRVNIWLGLSAVEKKENSEAE
				GTFTVFAEMYENQALMFGKWGTSGLVGRHKFSDVTGKIKLKDER
				FLPPKGWEWEGEWIVDPERSLLTEADAGHTEFTDEVYONESRVP
.			•	GGDWKPAEDTYTDANGDKAASPSELTCPPGWEWEDDAWSYDING
- 1		1		AVDEKGWEYGITIPPDHKPKSWVAAEKMYHTHRRRRLVRKRKKD
1		1		LTQTASSTAGAMEELQDQEGWEYASLIGWKFHWKQRSSDTFRRR
			*	RWRRKMAPSETHGAAAIFKLEGALGADTTEDGDEKSLEKQKHSA
				TTVFGANTPIVSCNFDRDYIYHLRCYVYQARNLLALDKDSFSDP
ı				YAHICFLHRSKTTEIIHSTLNPTWDQTIIFDEVEIYGEPQTVLQ
				NPPKVIMELFDNDQVGKDEFLGRSIFSPVVKLNSEMDITPKLLW
T		. 1		HPVMNGDKACGDVLVTAELILRGKDGSNLPILPPQRAPNLYMVP
1				QGIRPVVQLTAIEILAWGLRNMKNFQMASITSPSLVVBCGGERV ESVVIKNLKKTPNFPSSVLFMKVFLPKEELYMPPLVIKVIDHRQ
l		1	•	FGRKPVVGQCTIERLDRFRCDPYAGKEDIVPQLKASLLSAPPCR
ı				DIVIEMEDTKPLLASKCLSSMSTALSKMASPATVHLTEKEEEIV
J		· '	·	DWWSKFYASSGEHEKCGQYIQKGYSKLKIYNCELENVABFEGLT
1		Į.		DFSDTFKLYRGKSDENEDPSVVGEFKGSFRIYPLPDDPSVPAPP
1				ROFRELPDSVPQECTVRIYIVRGLELQPQDNNGLCDPYIKITLG
1			j	KKVIE\DRDHYIPNTLNPVFGRMYELSCYLPQEKDLKISVYDYD
		]		TFTRDEKVGETIIDLENPF\LSRFG\SHCG\IPEEYCVSGVNTW
		'		RDSLR\PTQ\LLQNVARFKGFPQPILSEDGSRIRYGGRDYSLDE
		1		FEANKILHQHLGAPEERLALHILRTOGLVPEHVETRTIHSTEAD
1				NIS\RYYLRVIIWNTKDVILDEKSITGEEMSDIYVKGWIDGNEE
		1		NKQKTDVHYRSLDGEGNFNWRFVFPFDYLPAEOLCTVAKKEHEW
				SIDQTEFRIPPR\LIIQIW\DNDKFS\LDDYLGFPRTLTCPHTT
1				HFLQKSPGGNC/RGLDMIPDLKAMNPLKAKTASLFEOKSMKGWW
Ĺ		i		PCYAEKDGARVMAGKVEMTLEILNEKEADERPAGKGRDERNMND
ľ				KLDLPNRPETSFLWFTNPCKTMKFIVWRRFKWVIIGLLFLLILL
H	6021	4953	549	LFVAVLLYSLPNYLSMKIVKPNV
Ĺ		.555	549	EAIQFEVSIGNYGNKFDTTCKPLASTTQYSRAVFDGNYYYYLPW
				AHTKPVVTLTSYWEDISHRLDAVNTLLAMAERLQTNIEALKSGI
ļ			.	QGKIPANQLAELWLKLIDEVIEDTRYTLPLTEGKANVTVLDTQI
ı				RKLRSRSLSQIHEAAVRMRSEATDVKSTLAEIEDWLDKLMQLTE
1	i i		1	EPQNSMPDIIIWMIRGEKRLAYARIPAHQVLYSTSGENASGKYC
		. ]		GKTQTIFLKYPQEKNNGPKVPVELRVNIWLGLSAVEKKFNSFAE
ŀ	Ì			GTFTVFAEMYENQALMFGKWGTSGLVGRHKFSDVTGKIKLKREF FLPPKGWEWEGEWIVDPERSLLTEADAGHTEFTDEVYQNESRYP
	ì	1	1	GGDWKPAEDTYTDANGDKAASPSELTCPPGWEWEDDAWSYDINR
	l	•	1.	AVDEKGWEYGITIPPDHKPKSWVAAEKMYHTHRRRRLVRKRKKD
				LTQTASSTAGAMEELQDQEGWEYASLIGWKFHWKQRSSDTFRRR
	l		1.	RWRRKMAPSETHGAAAIFKLEGALGADTTEDGDEKSLEKQKHSA
	- 1		] .	TTVFGANTPIVSCNFDRDYIYHLRCYVYQARNLLALDKDSFSDP
			1.	YAHICFLHRSKTTEIIHSTLNPTWDQTIIFDEVEIYGEPQTVLQ
	i	1	1.	NPPKVIMELFDNDQVGKDEFLGRSIFSPVVKLNSEMDITDKL.LW
	- 1		11	HPVMNGDKACGDVLVTAELILRGKDGSNLPILPPORAPNLVMVP
		İ		QGIRPVVQLTAIEILANGLRNMKNFOMASITSPSLVVECGGERV
	1	İ	1	BSVVIKNLKKTPNPPSSVLFMKVFLPKERLYMPPLVIKVIDUPO
_				FGRKPVVGQCTIERLDRFRCDPYAGKEDIVPQLKASLLSAPPCR
		* *		

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
į.	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			DIVIEMEDTKPLLASKCLSSMSTALSKMASPATVHLTEKEEEIV
		1	DWWSKFYASSGEHEKCGQYIQKGYSKLKIYNCELENVAEFEGLT
į			DFSDTFKLYRGKSDENEDPSVVGEFKGSFRIYPLPDDPSVPAPP
		į	ROFRELPDSVPQECTVRIYIVRGLELQPQDNNGLCDPYIKITLG
	Ì		KKVIE\DRDHYIPNTLNPVFGRMYELSCYLPQEKDLKISVYDYD
			TFTRDEKVGETIIDLENPF\LSRFG\SHCG\IPEEYCVSGVNTW
			RDSLR\PTQ\LLQNVARFKGFPQPILSEDGSRIRYGGRDYSLDE
			FEANKILHQHLGAPEERLALHILRTQGLVPEHVETRTLHSTFQP
			NIS/RYYLRVIIWNTKDVILDEKSITGEEMSDIYVKGWIPGNEE
i			NKQKTDVHYRSLDGEGNFNWRFVFPFDYLPAEQLCIVAKKEHPW
			SIDQTEFRIPPR\LIIQIW\DNDKFS\LDDYLGFPRTLTCRHTI
ı	ľ		HPLQKSPGGNC/RGLDMIPDLKAMNPLKAKTASLFEQKSMKGWW
1			PCYAEKDGARVMAGKVEMTLEILNEKEADERPAGKGRDEPNMNP
i			KLDLPNRPETSFLWFTNPCKTMKFIVWRRFKWVIIGLLFLLILL
	1		LFVAVLLYSLPNYLSMKIVKPNV
6022	4953	549	EAIQFEVSIGNYGNKFDTTCKPLASTTQYSRAVFDGNYYYYLPW
1	1		AHTKPVVTLTSYWEDISHRLDAVNTLLAMAERLQTNIEALKSGI
1			QGKIPANQLAELWLKLIDEVIEDTRYTLPLTEGKANVTVLDTQI
			RKLRSRSLSQIHEAAVRMRSEATDVKSTLAEIEDWLDKLMQLTE
	ļ		EPQNSMPDIIIWMIRGEKRLAYARIPAHQVLYSTSGENASGKYC
			GKTQTIFLKYPQEKNNGPKVPVELRVNIWLGLSAVEKKFNSFAE
			GTFTVFAEMYENQALMFGKWGTSGLVGRHKFSDVTGKIKLKPER
1			FLPPKGWEWEGEWIVDPERSLLTEADAGHTEFTDEVYONESRYP
i i	Į.		GGDWKPAEDTYTDANGDKAASPSELTCPPGWEWEDDAWSYDINR
			AVDEKGWEYGITIPPDHKPKSWVAAEKMYHTHRRRRLVRKRKKD
			LTQTASSTAGAMEELQDQEGWEYASLIGWKFHWKORSSDTFRRR
į į			RWRRKMAPSETHGAAAIFKLEGALGADTTEDGDEKSLEKOKHSA
1			TTVFGANTPIVSCNFDRDYIYHLRCYVYOARNLLALDKDSFSDP
			YAHICFLHRSKTTEIIHSTLNPTWDQTIIFDEVEIYGEPOTVLO
1 1	· · · · · · · · · · · · · · · · · · ·		NPPKVIMELFDNDQVGKDEFLGRSIFSPVVKLNSEMDITPKLLW
ŀ	1		HPVMNGDKACGDVLVTAELILRGKDGSNLPILPPORAPNLYMVP
1			QGIRPVVQLTAIEILAWGLRNMKNFQMASITSPSLVVECGGRRV
1 ]			ESVVIKNLKKTPNFPSSVLFMKVFLPKEELYMPPLVIKVIDHRO
1 4			FGRKPVVGQCTIERLDRFRCDPYAGKEDIVPOLKASILSAPPCP
1	•		DIVIEMEDTKPLLASKCLSSMSTALSKMASPATVHLTEKERETV
1 1			DWWSKFYASSGEHEKCGQYIQKGYSKLKIYNCELENVAEFEGLT
1			DFSDTFKLYRGKSDENEDPSVVGEFKGSFRIYPLPDDPSVPAPP
1	1		RQFRELPDSVPQECTVRIYIVRGLELQPQDNNGLCDPYIKITLG
1	1		KKVIE \DRDHYIPNTLNPVFGRMYELSCYLPOEKDLKISVYDYD
] ]			TFTRDEKVGETIIDLENPF\LSRFG\SHCG\IPEEYCVSGVNTW
	į		RDSLR\PTQ\LLQNVARFKGFPQPILSEDGSRIRYGGRDYSLDE
į į	1	ļ	FEANKILHOHLGAPEERLALHIT.PTYCT.VPFLVPTPTT HEMPON
[ ]		. 1	NIS\RYYLRVIIWNTKDVILDEKSITGEEMSDIYVKGWIPGNEE
[	.	İ	NKQKTDVHYRSLDGEGNFNWRFVFPFDYLPAEOLCIVAKKEHFW
		i	SIDQTEFRIPPR\LIIQIW\DNDKFS\LDDYLGFPRTLTCRHTI
] {		1	HFLQKSPGGNC/RGLDMIPDLKAMNPLKAKTASLFEQKSMKGWW
1		ĺ	PCYAEKDGARVMAGKVEMTLEILNEKEADERPAGKGRDEPNMNP
			KLDLPNRPETSFLWFTNPCKTMKFIVWRRPKWVIIGLLFLLILL
6023	102		LFVAVLLYSLPNYLSMKIVKPNV
	102	916	SQELGMFVELNNLLNTTPDRAEQGKLTLLCDAKTDGSFLVHHFL
			SFYLKANCKVCFVALIQSFSHYSIVGOKLGVSLTMARERGOT.VF
			LEGL/IVCSGR\VFQAQKEPHPLQFLREANAGNLKPLFEFVREA
		i	LKPVDSGEARWTYPVLLVDDLSVLLSLGMGAVAVLDFIHYCRAT
			VCWELKGNMVVLVHDSGDAEDEENDILLNGLSHOSHLTLRAEGI.
ſ	1		ATGFCRDVHGQLRILWRRPSQPAVHRDQSFTYQYKIQDKSVSFF
6024	3		AKGMSPAVL
	-	3260	FLSFLCYPRFRCLFCLQFAIPASRMEQLNELELLMEKSFWBEAB
	į –		LPAELFQKKVVASFPRTVLSTGMDNRYLVLAVNTVONKEGNCEK
į		<b>j</b> .	RLVITASQSLENKELCILRNDWCSVPVEPGDIIHLEGDCTSDTW
]			IIDKDFGYLILYPDMLISGTSIASSIRCMRRAVLSETFRSSDPA
			TRQMLIGTVLHEVFQKAINNSFAPEKLQELAFQTIQEIRHLKEM

SEQ	Predicted	Predicted end	Daving
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
l l	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ĺ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
j	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
J	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion
ļ	sequence		\=possible nucleotide insertion)
			YRLNLSQDEIKQEVEDYLPSFCKWAGDFMHKNTSTDFPOMOLSL.
Į	İ		PSDNSKDNSTCNIEVVKPMDIEESIWSPRFGLKGKIDVTVGVKI
i	•	1	HRGYKTKYKIMPLELKTGKESNSIEHRSQVVLYTLLSOERRADD
			EAGLLLYLKTGQMYPVPANHLDKRELLKLRNOMAFSI, PHDISKS
1	į		ATROKTOLASLPQIIEEEKTCKYCSQIGNCALYSRAVEOOMDCS
ſ	İ		SVPIVMLPKIBEETQHLKQTHLEYFSLWCLMLTLESOSKDNKKN
J		}	HQNIWLMPASEMEKSGSCIGNLIRMEHVKIVCDGOYLHNFOCKH
ļ			GAIPVTNLMAGDRVIVSGEERSLFALSRGYVKEINMTTVTCLLD
}		ļ	RNLSVLPESTLFRLDQEEKNCDIDTPLGNLSKLMENTFVSKKLR
•		ĺ	DLIIDFREPQFISYLSSVLPHDAKDTVACILKGLNKPQRQAMKK
			VLLSKDYTLIVGMPGTGKTTTICTLVRILYACGFSVLLTSYTHS
			AVDNILLKLAKFKIGFLRSR\QIQKVHPAIQQFTEHEICRSKSI
1	}		KS\LALLEBLYTSQLIDATTCMGINHPIFSRKIFDFCIVDEASQ
i	1		ISQPICLGPLFFSRRFVLVGDHQQLPPLVLNREARALGMSESLF
1			KRLEQNKSAVVQLTVQYRMNSKIMSLSNKLTYEGKLECGSDKVA
ł	1		NAVINLRHFKDVKLELEFYADYSDNPWLMGVFEPNNPVCFLNTD KVPAPEQVEKGGVSNVTEAKLIVFLTSIFVKAGCSPSDIGIIAP
i			YRQQLKIINDLLARSIGMVEVNTVDKYQD\RDKSIVLVSFVRSN
1	,		KDGTVGELLKDWRRI.NVAITRAKHKLILLGCVPSLNCYPPLEKL
	<u>                                     </u>		LNHLNSEKLIIDLPSREHESLCHILGDFQRE
6025	3977	89	GGFPAQSDHLPPVFPLRSDLLITMSTLYVSPHPDAFPSLRALIA
			ARYGEAGEGPGWGGAHPRICLOPPPTSRTSFPPPRI.PALEOGPG
1			GLWVWGATAVAQLLWPAGLGGPGGSRAAVLVOOWVSYADTELTP
1	]		AACGATLPALGLRSSAQDPQAVLGALGRALSPLEEWIRLHTYLA
1			GEAPTLADLAAVTALLLPFRYVLDPPARRIWNNVTRWFVTCVRO
İ			PEFRAVLGEVVLYSGARPLSHQPGPEAPALPKTAAOLKKEAKKR
			EKLEKFQQKQKIQQQQPPPGEKKPKPEKREKRDPGVITYDLPTP
}			PGEKKDVSGPMPDSYSPRYVEAAWYPWWEQQGFFKPEYGRPNVS
1			AANPRGVFMMCIPPPNVTGSLHLGHALTNAIQDSLTRWHRMRGE
İ			TTLWNPGCDHAGIATQVVVEKKLWREQGLSRHQLGREAFLQEVW
			KWKEEKGDRIYHQLKKLGSSLDWDRACFTMDPKLSAAVTEAFVR
	]		LHEEGIIYRSTRLVNWSCTLNSAISDIEVDKKBLTGRTLLSVPG
I	] ]		YKEKVEFGVLVSFAYKVQGSDSDEEVVVATTRIETMLGDVAVAV
}	]		HPKDTRYQHLKGKNVIHPFLSRSLPIVFDEFVDMDFGTGAVKIT PAHDQNDYEVGQRHGLEAISIMDSRGALINVPPPFLGLPRFEAR
ŀ			KAVLVALKERGLFRGIEDNPMVVPLCNRSKDVVEPLLRPQWYVR
ļ			CGEMAQAASAAVTRGDLRILPERHQRTWHAWMDNIRE\WCMFPG
			KLWWG\HR\IPAYFVTVSDPAVPPGEDPDGRYWVSGRNEAEARE
			KAAKEFGVSPDKISLQQDEDVLDTWFSSGLFPLSILGWPNQSED
İ			LSVFYPGTLLETGHDILFFWVARMVMLGLKLTGRLPFREVYLHA
i			IVRDAHGRKMSKSLGNVIDPLDVIYGISLOGLHNOLLNSNLDPS
			EVEKAKEGQKADPPAGIPECGTDALRPGLCAVMSOGPDTMT.DVM
1			RILGYRHFCNKLWNATKFALRGLGKGFVPSPTSOPGGHESLVDP
1 1			WIRSRLTEAVRLSNQGFQAYDFPAVTTAOYSFWLYELCDVVLEC
		1	LKPVLNGVDQVAAECARQTLYTCLDVGLRLLSPFMPFVTERLFO
			RLPRRMPQAPPSLCVTPYPEPSECSWKDPEAEAALELALSTTRA
			VRP\LRADYNLHPESGPTCFLEVAD\EATGALASAVSGYVQGPG
		j	QAQVVVAVAEPWGLPAP\QGCAVALASDRCSI\HLQLQG\LLDP
			ARELG\KLQ\AKRVEAQ\RQAQ\RLR\ERRA\ASGNPVKVPL\E
6026	2674	514	VQEADEAKLQQTEAELRKVDEAIALFQKML
ĺ	-		GPITFLKKKAKMKDMPLRIHVLLGLAITTLVQAVDKKVDCPRLC
1		1	TCEIRPWFTPRSIYMEASTVDCNDLGLLTFPARLPANTQILLLQ TNNIAKIEYSTDFPVNLTGLDLSQNNLSSVTNINGKKMPQLLSV
ŀ	1	1	YLEENKLTELPEKCLSELSNLQELYINHNLLSTISPGAFIGLHN
1		İ	LLRLHLNSNRLOMINSKWFDALPNLEILMIGENPIIRIKDMNPK
Į	1		PLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRLIKVPH
-	1		VALQKVVNLKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPEL
		í	ISIDSLAVDNLPDLRKIEATNNPRLSYIHPNAPFRLPKLESIMI.
	1		NSNALSALYHGTIESLPNLKEISIHSNPIRCDCVIRWMNMNKTN
1		1	IRFMEPDSLFCVDPPEFOGONVROVHFRDMMEICLPLTAPEGFP
			SNLNVEAGSYVSFHCRATA\EPQPEIYWITPSGQKLLPNT\LTD

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NO:	nucleotide	location	Glutamic Acid, P=Phenylalanine, G=Glycine,
ŀ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
l	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
l	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence		\=possible nucleotide insertion)
			KFYVHSEGTLDINGVTPKEGGLYTCIATNLVGADLKSVMIKVDG
Í			SFPQDNNGSLNIKIRDIQANSVLVSWKASSKILKSSVKWTAFVK
			TENSHAAQSARIPSDVKVYNLTHLNPSTEYKICIDIPTIYQKNR
ı		ļ	KKCVNVTTKGLHPDQKEYEKNNTTTLMACLGGLLGIIGVICLIS
-		1	CLSPEMNCDGGHSYVRNYLQKPTFALGELYPPLINLWEAGKEKS
L		<u> </u>	TSLKVKATVIGLPTNMS
6027	5254	4148	GGRRAPGRPGRSIKDEEEETVFREVVSFSPDPLPVRYYDKDTTK
J		}	PISFYLSSLEELLAWKPRLEDGFNVALEPLACROPPLSSQRPRT
1	1		LLCHDMMGGYLDDRFIQGSVVQTPYAFYHWQCIDVFVYFSHHTV
I			TIPPVGWTNTAHRHGVCVLGTFITEWNEGGRLCEAFLAGDERSY
1		İ	QAVADRLVQIT\RFFRFDGWLINIENSLSLAAVGNMPPFLRYLT
1			TQLHRQVPGGLVLWYDSVVQSGQLKWQDELNQHNRVFFDSCDGF
			FTNYNWREEHLERMLGOAGERRADVYVGVDVFARGNINGGP PDT
l			DKVGGGFRPRASGPVPPLGPHFLMDLPFPSAPQRNDSSCSSQSG
			DPVALRNRCPAPAKLCPH
6028	120	3432	NCLLLQAKGFHGEIEDLQQWLTDTERHLLASKPLGGLPETAKEQ
	Î.		LNVHMEVCAAFEAKEETYKSLMQKGQQMLARCPKSAETNIDQDI
			NNLKEKWESVETKLNER\KT\KLEEALNLA\MEFHNSI.\ODRIN
i			WLTQAEQTLNVASRPSLILDTVLFOIDEHKVFANEVNSHDEGIT
İ			ELDXTGTHLKYFSQKQDVVLIKNLLISVOSRWEKUVOPLVERGE
1			SLDDARKRAKOFHEAWSKLMEWLRESEKSIDSELETANDEDVIV
-			TQLAQHKEFQKSLGAKHSVYDTTNRTGRSLKEKTSLADDNLKLD
1	·		DMLSELRDKWDTICGKSVERONKLEEA\LIFSGOFTDALORLID
l			WLYRVEPQLAEDQPVHGDIDLVMNLIDNHKAFOKELGKPTSSUO
			ALKRSARBLIEGSRDDSSWVKVOMOELSTRWETVCALSISKOTP
1			DEAALRQAEEFHSVVHALLEWLAEAEOTLRFHGVI.PDDPDat.pm
			LIDQHKEFMKKLEEKRAELNKATTMGDTVLAICHPDSITTIKUW
1	ļ		IT_IRARFEEVLAWAKQHQQRLASALAGLIAKOELLRALLAWIO
}			WAETTLTDKDKEVIPQEIEEVKALIAEHOTEMEEMTRKORDVDV
i .			VTKTYKRRAADPSSLQSHIPVLDKGRAGRKRFPASSLYPSGSOT
1	ľ		QIETKNPRVNLLVSKWQQVWLLALERRKLNDALDRLEELREFA
	l i		NFDFDIWRKKYMRWMNHKKSRVMDFFRRIDKDQDGKITRQEFID
i			GILSSKFPTSRLEMSAVADIFDRDGDGYIDYYEFVAALHPNKDA
	į		YKPITDADKIEDEVTROVAKCKCAKRFQVEQIGDNKYRFFLGNQ
!!!	ł		FGDSQQLRLVRILRSTVMVRVGGGWMALDEFLVKNDPCRAKGRT
ĺ			NMBLREKFILADGASQGMAAFRPRGRRSRPSSRGASPNRSTSVS
i l			SQAAQAASPQVPATTTPKILHPLTRNYGKPWLTNSKMSTPCKAA
l i			ECSDFPVPSAEGTPIQGSKLRLPGYLSGKGPHSGEDSGLITTAA
1			ARVRTQFADSKKTPSRPGSRAGSKAGSRASSRRGSDASDFDISE
1	ļ		IQSVCSDVETVPQTHRPTPRAGSRPSTAKPSKIPTPQRKSPASK LDKSSKR
6029	1	3533	
	1		IMPCGSSRLLRGCWTHPNEPVSDLSYFDCIESVMENSKVLGESM AGISQNAKTGDLPAFGECVGIASKALCGLTEAAAQAAYLVGIFD
			PNSQAGHQGLVDPIQFARANQAIQMACQNLVDPGSSPSQVLSAA
			TIVAKHTSALCNACRIASSKTANPVAKRHFVQSAKEVANSTANL
	·		VKTIKALDGDFSEDNRNKCRIATAPLIEAVENLTAFASNPEFVS
			IPAQISSEGSQAQEPILVSAKPMLESSSYLIRTARSLAINPKDP
			PTWSVLAGHSHTVSDSIKSLITSIRDKAPGQRECDYSIDGINRC
1		1	IRDIEQASLAAVSQSLATRDDISVEALQEQLTSVVQEIGHLIDP
			IATAARGEAAQLGHKGTQLASYFEPLILAAVGVASKILDHQQQM
1		]	TVLDQTKTLAESALQMLYAAKEGGGNPKAQHTHDAITEAAQLMK
			EAVDDIMVTLNEAASEVGLVGGMVDAIAEAMSKLDEGTPPEPKG
İ		ŀ	TPVDYQTTVVKYSKAIAVTAQEMMTKSVTNPEELGGLASQMTSD
ĺ		ĺ	YGHLAFQGQMAAATAEPEEIGFQIRTRVQDLGHGCIFLVQKAG\
- 1		1	ALQVCPTDSYTKRELIECARAVTEKVSLVLSALQAGNKGTQACI
1	1	1	TAATAVSGIIADLDTTIMFATAGTLNARNSETFADHDENTLYTA
1	1		KALVEDTKLLVSGAASTPDKLAOAAOSSAATITOLAEVVKLGDA
ļ			SLGSDDPETQVVLINAIKDVAKALSDLISATKGAASKPVDDPSM
}		i i	YQLKGAAKVMVTNVTSLLKTVKAVEDEATRGTRALBATIECIKO
	Ì	ľ	ELTVFQSKDVPEKTSSPEESIRMTKGITMATAKAVAAGNSCPOR
			DVIATANLSRKAVSDMLTACKQASFHPDVSDEVRTRALRFGTEC
			THE TOPPER TRANSPORTER

SEQ	Predicted	Predicted end	Amino paid goment contests
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	
1	to first		L-Leucine, M-Methionine, N-Asparagine,
,	amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine,
		residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	l	\=possible nucleotide insertion)
			TLGYLDLLEHVLVILQKPTPELKQQLAAFSKRVAGAVTELIQAA
			EAMKGTEWVDPEDPTVIAETELLGAAASIEAAAKKLEOLKPRAK
1	ļ		PKQADETLDFEEQILEAAKSIAAATSALVKSASAAQRELVAQGK
	]		VGSIPANAADDGQWSQGLISAARMVAAATSSLCEAANASVQGHA
	Į.		SEEKLISSAKQVAASTAQLLVACKVKADQDSEAMRRLQAAGNAV
1	1		KRASDNLVRAAQKAAFGKADDDDVVVKTKFVGGIAQIIAAQEEM
1	i :		LKKERELEEARKKLAQIRQQQYKFLPTELREDEG
6030	3	1777	FPGRGSPALQLEVLICLGLMGLERALNVLAPIFYRNIVNLLTEN
1	_	<b>-</b> ///	
i			APWNSLAWTVTSYVFLKFLQGGGTGSTGFVSNLRTFLWIRVQQF
1	<b>j</b> .		TSRRVELLIFSHLHELSLRWHLGRRTGEVLRIADRGTSSVTGLL
i			SYLVFNVIPTLADIIIGIIYFSMFFNAWFGLIVPLCMSLYLTLT
1		•	IVVTEWRTKFRRAMNTQENATRARAVDSLLNFETVKYYNAESYE
1			VERYREAIIKYQGLEWKSSASLVLLNQTQNLVIGLGLLAGSLLC
			AYFVTEQKLQVGDYVLFGTYIIQLYMPLNWFGTYYRMIQTNFID
1			MENMFDLLKK\ETEVKDLPGAGPFRFQKGRIEFENVHFSYADGR
		•	BTLQDVSFTVMPGQTLALVGPSGAGKSTILRLLFRFYDISSGCI
	[		RIDGQDISQVTQALFRFSHWELCPKDTVLFNDTIADNIRYGRVT
]	[		AGNDEVEAAAQAAGIHDAIMAFPEGYRTQVGERGLKLSGGEKQR
1			VAIARTILKAPGIILLDEATSALDTSNERAIQASLAKVCANRTT
l			IVVAHRLSTVVNADQILVIKDGCIVERGRHEALLSRGGVYADMW
			QLQQGQEETSEDTKPQTMER
6031	160	1694	LRMSENLDKSNVNEAGKSKSNDSEEGLEDAVEGADEALQKAIKS
	·	•  -	DSSSPQRVQRPHSSPPRFVTVEELLETARGVTNMALAHEIVVNG
		•	DFQIKPVELPENSLKKRVKEIVHKAFWDCLSVQLSEDPPAYDHA
			IKLVGEIKETLLSFLLPGHTRLRNQITEVLDLDLIKQBAENGAL
1			DISKLAEFIIGMMGTLCAPARDEEVKKLKDIKEIVPLFREIFSV
			LDLMKVDMANFAISSIRPHLMQQSVEYERKKFQEILERQPNSLD
	. 1		FVTQWLEEASEDLMTQKYKHALPVGGMAAGSGDMPRLSPVAVQN
	·		
l I	i ' i		YAYLKLLKWDHLQRPFPETVLMDQSRFHBLQLQ\REQLTILGAV
			LLVTFSMAAPGISSQADFAEKLKMIVKILLTDMHLPSFHLKDVL
	ŀ	• •	TTIGEKVCLEVSSCLSLCGSSPFTTDKETVLKGQIQAVASPDDP
1	! · · · · · · · · · · · · · · · · · · ·		IRRIMESRILTFLETYLASGHQKPLPTVPGGLSPVQRELEEVAI
			KFARLVNYNKMVFCPYYDAILSKILVRS
6032	39	2415	AARLCRAQPTKSAWMIRDLSKMYPQTRHPAPHQPAQPFKFTISE
			SCDRIKEEFQFLQAQYHSLKLECEKLASEKTEMQRHYVMYYEMS
			YGLNIEMHKQAEIVKRLNAICAQVIPFLSQEHQQQVVQAVERAK
-[		•	QVTMAELNAIIGQQQLQAQHLSHGHGLPVPLTPHPSGLQPPAIP
	,		PIGSSAGLLALSSALGGQSHLPIKDEKKHHDNDHQRDRDSIKSS
	j		SVSPSASFRGAEKHRNSADYSSESKKQKTEEKEIAARYDSDGEK
1			SDDNLVVDVSNEDPSSPRGSPAHSPRENGLDKTRLLKKDAPISP
			ASIASSSTPSSKSKELSLNEKSTTPVSKSNTPTPRTDAPTPGS
			NSTPGLRPVPGKPPGVDPLASSLRTPMAVPCPYPTPFGIVPHAG
{ ·		ļ	MNGELTSPGAAYAGLHNISPOMSAAAAAAAAAAAYGRSPVVGFD
( l			PHHHMRVPAIPPNLTGIPGGKPAYSFHVSADGQMQPVPFPPDAL
.	ŀ	ſ	IGPGIPRHARQINTLNHGEVVCAVTISNPTRHVYTGGKGCVKVW
1 1		,	DISHPGNKSPVSQLDCLNRDNYIRSCRLLPDGRTLIVGGEASTL
] ]		]	SIWDLAAPTPRIKAELTSSAPACYALAISPDSKVCFSCCSDGNI
( )	1		AVWDLHNQTLVRQFQGHTDGASCIDISNDGTKLWTGGLDNTVRS
[	j,		
] ]			W\DLREGRQLQQHD/FFTSPVFSLGYCP\TEEWLAVGMENSN\V
1 1	į		EVLHVTKPDKYQLHLHESCVLSLKFAHCGKWF\VSTGKDNLLNA
	1		W\RTPYG\ASIF\QSKESSS\VLSCDI\SVDDKYIVTGS\GDK\
6033	<del></del> _		RATVYEVIY
6033	39	2415	AARLCRAQPTKSAWMIRDLSKMYPQTRHPAPHQPAQPFKFTISE
			SCDRIKEEFQFLQAQYHSLKLECEKLASEKTEMQRHYVMYYEMS
1 1		ł	YGLNIEMHKQAEIVKRLNAICAQVIPFLSQEHQQQVVQAVERAK
			QVTMAELNAIIGQQQLQAQHLSHGHGLPVPLTPHPSGLQPPAIP
ļ l	į	1	PIGSSAGLLALSSALGGQSHLPIKDEKKHHDNDHQRDRDSIKSS
			SVSPSASFRGAEKHRNSADYSSESKKOKTEEKEIAARYDSDGEK
		. 1	SDDNLVVDVSNEDPSSPRGSPAHSPRENGLDKTRLLKKDAPISP
[		}.	ASIASSSTPSSKSKELSLNEKSTTPVSKSNTPTPRTDAPTPGS
j J		į	NSTPGLRPVPGKPPGVDPLASSLRTPMAVPCPYPTPFGIVPHAG
	<del></del>		

SEO	Predicted	Predicted end	Denis
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidinc, I=Isoleucine, K=Lysine,
ļ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Ī	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	] "	\=possible nucleotide insertion)
			MNGELTSPGAAYAGLHNISPQMSAAAAAAAAAAYGRSPVVGFD
1		1	PHHIMRVPAIPPNLTGIPGGKPAYSFHVSADGQMQPVPFFPDAL
	•		IGPGIPRHARQINTLNHGEVVCAVTISNPTRHVYTGGKGCVKVW
1	ļ	ľ	DISHPGNKSPVSQLDCLNRDNYIRSCRLLPDGRTLIVGGEASTL
1	1	1	SIWDLAAPTPRIKAELTSSAPACYALAISPDSKVCFSCCSDGNI
1	İ	1	AVWDLHNQTLVRQFQGHTDGASCIDISNDGTKLWTGGLDNTVRS
ı			W\DLREGRQLQQHD/FFTSPVFSLGYCP\TBEWLAVGMENSN\V
1			EVLHVTKPDKYQLHLHESCVLSLKFAHCGKWF\VSTGKDNLLNA
ì			W\RTPYG\ASIF\QSKESSS\VLSCDI\SVDDKYIVTGS\GDK\
ł	1	l	RATVYEVIY
6034	2683	714	ESGRRRLXRRRSPCPGTAGGPGETNPGPGACPRGPREEAAAAM
1			EIAPQEAPPVPGADGDIEEAPAEAGSPSPASPPADGRLKAAAKR
1	1		VTFPSDEDIVSGAVEPKDPWRHAQNVTVDEVIGAYKQACQKLNC
[			BOLDKIT'S OU OEE AD LOCK DE MODERA DAMAGE OF MANAGEMENT
1			RQIPKLLRQLQEFTDLGHRLDCLDLKGEKLDYKTCEALEEVFKR LQFKVVDLEQTNLDEDGASALFDMIEYYESATHLNISFNKHIGT
j .			RGWQAAAHMRKTSCLQYL\DARNTPLLDHSAPFVARALRIRSS
1			LAVLHLENASLSGRPLMLLATALKMNMNLRELYL\ADNKLNGLQ
· ·		,	DSAQLGNLLKFNCSLQILDLRNNHVLDSGLAYICEGLKEQRKGL
1			VTL\VLWNNQLTHTGMAFLGMTLPHTQSLETLNLGHNPIGNEGV
1			RHLKNGLISNRSVLRLGLASTKLTCEGAVAVAEFIAESPRLLRL
1.			DLRENEIKTGGLMALSLALKVNHSLLRLDLDREPKKEAVKSFIE
ł		,	TOKALLAEIQNGCKRNLVLAREREEKEQPPQLSASMPETTATEP
1	1		QPDDEPAAGVQNGAPSPAPSPDSDSDSDSDSDGEEEEEEGERDET
ł			PSGAIDTRDTGSSEPQPPPEPPRSGPPLPNGLKPEFALALPPEP
1		,	PPGPEVKGGSCGLEHELSCSKNEKELEELLLEASQESGQETL
6035	19	404	SVTYLGIILHKNTGALPADPVQLISQTPTPSTKQQLLSFLGMVG
			YFYLWIPGFAILTKPLCKLTKENLADAIDPKSFSHSSFRSLKTA
L	· ·		LENASTLALPDSSQPF\SLHTAEVQGCVVEILTQGLGPLPV
6036	1745	356	LPDVEKLGRRRGRKMDSVEKGAATSVSNPRGRPSRGRPPKLQRN
1. 1	1		SRGGQGRGVEKPPHLAALILARGGSKGIPLKNIKHLAGVPLIGW
			VLRAALDSGAFQSVWVSTDHDEIENVAKQFGAQVHRRSSEVSKD
	1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 -		SSTSLDAIIEFLNYHNEVDIVGNIQATSPCLHPTDLQKVAEMIR
1.			EEGYDSVFSVVRRHQFRWSEIQKGVREVTEPLNLNPAKRPRRQD
ŀ			WDGELYENGSFYFAKRHLIEMGYLQGGKMAYYEMRAEHSVDIDV
1			DIDWPIAEQRVLRYGYFGKEKLKEIKLLVCNIDGCLTNGHIYVS
			GDQKEIISYDVKDAIGISLLKKSGIEVRLISERACSKQTLSSLK
			LDCXMEVSVSDKLAVVDEWRKEMGLCWKEVAYLGNEVSDEECLK
}			RVGLSGAPADACSTAQKAVGYICKCNGGRGA\IREFAEHIC\LL
			MEKGLINFMPKNRNLAVNIGEKK
6037	2936	1919	WISWWMSSVLTILLFSLQGNKMLNYSAPSAGGYLLPRKPVGTPA
1 1		į	GGGFPRRHSVTLPSSKFRQNQLLSSLKGEPAPALSSRDSRFRDR
] [	İ	ļ	SFSEGGERLLPTOKOPGGGOVNSSRYKT\ELCRPFFFNGACKYC
<b>,</b>	,		DKCQFAHGIHELRSLTRHPKYKTELCRTFHTIGFCPYGPRCHFI
1 1			HNAEERRALAGARDLSADRPRLOHSFSFAGFPSAAATAAATGLI.
] [	· .	,	DSPTSITPPPILSADDLLGSPTLPDGTNNPF\AFSSOELASLFA
<u> </u>			PSMGLPGGGSPTTFLFRPMSESPHMFDSPPSPQDSLSDQEGYLS
			SSSSSHSGSDSPTLDNSRRLPIFSRLSISDD
6038	1450	426	SSALQEFGTRNHTFGVPLPHRRKQIISCNICQLRFNSDSOAAAH
1 1		]	YKGTKHAKKLKALEAMKNKOKSVTAKDSAKTTFTSITTNTINTS
1. 1		Í	SDKTDGTAGTPAISTTTTVEIRKSSVMTTEITSKVEKSPTTATG
1 1		,	NSSCPSTETEERKAKRLL\YCSLCKVAVNSASQLEAHNSGTKHK
			TMLEARNGSGTI KAFPRAGVKGKGPVNKGNTGLQNKTFHCEICD
1	1	.	VHVNSETQLKQHISSRRHKDRAAGKPPKPKYSPYNKLOKTAHPI.
1 1	İ	ŀ	GVKLVFSKEPSKPLAPRILPNPLAAAAAAAAVAVSSPFSLRTAP
<del> </del>			AATLFOTSALPPALLRPAPGPIRTAHTPVLFAPY
6039	4073	1000	LDEYEARLTLANLDDFEEDNEDDDENRVNOEEKAAKITELINKI.
1	!	j	NFLDEAEKDLATVNSNPFDDPDAAELNPFGDPDSEEPITETASP
	1		RKTEDSFYNNSYNPFKEVQTPQYLNPPDEPEAFVTIKDSPPQST
[	İ	i i	KKKNIRPVDMSKYLYADSSKTEEBELDESNPFYEPKSTPPPNNL
L			VNPVQELETERRVKRKAPAPPVLSPKTGVLNENTVSAGKDLSTS
	· -		

	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
	ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
		location	corresponding	H-Histidine, I=Isoleucine, K=Lysine,
		corresponding	to first	L=Leucine, M=Methionine, N=Asparagine
		to first	amino acid	P=Proline, Q=Glutamine, R=Arginine
		amino acid	residue of	S=Serine, T=Threonine, V=Valine
		residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown +_c+-
		amino acid	sequence	Codon, /=possible nucleotide deletion
		sequence		\=possible nucleotide insertion)
ı				PKPSPIPSPVLGRKPNASQSLLVWCKEVTKNYRGVKITNETTEN
ı			1	RNGLSFCAILHHFRPDLIDYKSLNPODIKENNKKAYDGFASIGI
ı		f	1	SRLDEPSDMVLLAIPDKLTVMTYLYOIRAHFSGOELNVVOTERN
-1				SSKSTYKVGNYETDTNSSVDOEKFYAELSDIKREDELOODIGA
- 1			į	VDFLSQDDSVFVNDSGVGESESEHQTPDDHLSPSTASPYCRRTK
ı		İ		SDTEPQKSQQSSGRTSGSDDPGICSNTDSTQAQVLLGKKRLLKA
ı				ETLELSDLYVSDKKKDMSPPFICEETDEQKLQTLDIGSNLEKEK
-		}		LENSRSLECRSDPESPIKKTSLSPTSKLGYSYSRDLDLAKKKHA
-1				SLRQTESDPDADRTTLNHADHSSKIVQHRLLSRQEELKERARVL
1		}		LEQARRDAALKAGNKHNTNTAAPFCNRQLSDQQDEERRRQLHER ARQLIAEARSGGKMSELPSYGERAAEKLKERSKASGDENDNIEI
-				DTNEEIPEGFVVGGGDELTNLENDLDTPEQNSKLVDLKLKKLLE
1				VQPQVANSPSSAAQKAVTESSEQDMKSGTEDLRTERLQKTTERF
1				RNPVVFSKDSTVRKTQLQSFSQYIENRPEMKRQRSIQEDTKKGN
1	•	· · · · · · · · · · · · · · · · · · ·		EEKAAITETQRKPSEDEVLNKGFKDS\SQYVVGELAALENEQKQ
1				IDTRAALVEKRLRYLMDTGRNTBEBEAMMQEWFMLVNKKNALIR
1				RMNQLSLLEKEHDLERRYELLNRELRAMLAIEDWOKTRAOKDDE
ı				QLLLDELVALVNKRDALVRDI DAQEKQAEEEDEHLERTLEONKG
$\vdash$	6040	475		KMAKKEEKCVLQ
1	30.10	. 4/3	1052	PTALMTAPSCAFPVQFRQPSVSGLSQITKSLYISNGVAANNKLM
Ī	. }		•	LSSNQTTMVINVSVEVVNTLYEDIQYMQVPVADSPNSRLCDFFD
ı				PIADHIHSVEMKQGR\TLLHCAAGVSRSAALCLAYLMKYHAMSL
				LDAHTWTKSCRPIIRPNSGFWEQLIHYEFQLFGKNTVHMVSSPV GMIPDIYEKEVRLMIPL
Γ	6041	2	3886	TEKDEKTAHNLENVLIHPWERLSEICVAKISEPEADVESVLGVS
1				NLLCVLQKPKGSLKSSKKKNGKVRFADEILESNKENEKCVSSEG
ı		· }		EKIECWELTTEPSLTHNSSGLLSPLRKKPLEDLVCKLADISTNY
	- 1			VNERKSEQHLRFLSTLLDSFSSSRVFKMLLGDEKOSIVOAKDLE
	- 1			TAKLVQKNPAVQFLYQKLIGWLNEDORKDFGFLVDILYSALRCC
1	- 1	j		DNDMERKKVLDDLTKVDLKWNSLLKIIEKACPSSDKHALVTDWL.
		• 1	,	KGDILGEKLVNLADCLCNEDLESRVSSESHFSERWTLLSLVLSQ
			•	HVKNDYLIGDVYVERIIVRLHETLFKTKKLSEAKSSDSSVSFIC DVAYNYFSSAKGCLLMPSSEDLLLTLFQLCAQSKEKTHLPDFLI
1	J	1		CKLKNTWLSGVNLLVHQTDSSYKESTFLHLSALWLKNQVQASSL
L	- 1	į.		DINSLQVLLSAVDDLLNTLLESEDSYLMGVYIGSVMPNDSEWEK
	1			MRQSLPMQWLHRPLLEGRLSLNYECFKTDFKEODIKTLPSHLCT
	•	1	Ì	SALLSKMVLIALRKETVLENNELEKILAELLYSLOWCEELDNPP
l			i	IFLIGFCEILQKMNITYDNLRVLGNMSGLLOLLFNRSREHGTLW
	1			SLITAKLILSRSISSDEVKPHYKRKESFFPLTEGNLHTTOSLCP
	. !	<u> </u>		FLSKEEKKEFSAQCIPALLGWTKKDLCSTNGGFGHLAIFNSCLQ
	1			TKSIDDGELLHGILKIIISWKKEHEDIFLFSCNLSEASPEVLGV
ı			Ĭ	NIEIIRFLSLFLKYCSSPLAESEWDFIMCSMLAWLETTSENQAL YSIPLVQLFACVSCDLACDLSAFFDSTTLDTIGNLPVNLISEWK
	- 1		·	EFFSQGIHSLLLPILVTVTGENKDVSETSFQNAMLKPMCETLTY
	l l			ISKEQLLSHKLPARLVADQKTNLPEYLQTLLNTLAPLLLFRARP
				VQIAVYHMLYKLMPELPOYDODNLKSYGDEEEEPALSPDAALMS
	- 1	1	j	DESIQUED LENVLGCIPVGOIVTIKPLSEDFCYVLGYLLTWKLT
	1	1	•	LTFFKAASSQLRALYSMYLRKTKSLNKLLYHLFRLMPENDTVAR
	1	1	•	TAVEVPNKDPKTFFTEELQLSIRETTMLPYHIPHLACSVYHMTI
	- 1		1	KDLPAMVRLWWNSSEKRVFNIVDRFTSKYVSSVI.SFORTSGUOT
				STQLFNGMTVKARATTREVMATYTIEDIVIELIIQLPSNYPLGS
		1		IIVESGKRVGVAVQQWRNWMLQLSTYLTHQNGSIMEGLALWKNN
				VDKRFEGVEDCMICFSVIHGFNYSLPKKACRTCKKKFHSA\CLY KWFTSSNKSTCSLCRETFF
	6042	1306	253	MAELAPASPSDIKASVSNGDTTLLCSRRQSCGMNEVRQVSLTYP
	ļ	[	ł	GSPAPSHSLPLQPRSGGSLCPSRAW/PDPHQLFDDTSSAQSRGY
				GAQRAPGGLSYPAASPTPHAAFLADPVSNMAMAYGSSLAACGKE
			i i	LVDKNIDRFIPITKLKYYFAVDTMYVGRKLGLLFFPYLHODWEV
	1		L.	QYQQDTPVAPRFDVNAPDLYIPAMAFITYVLVAGLALGTODFFC
			i	PDLLGLQASSALAWLTLEVLAILLSLYLVTVNTDLTTIDLVagi.
				GYKYVGMIGGVLMGLLFGKIGYYLVLGWCCVAIFVFMIRTLRLK

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	, , ,	H=Histidine, I=Isoleucine, K=Lysine,
	to first	to first	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid		P=Proline, Q=Glutamine, R=Arginine,
	residue of	residue of	S=Serine, T=Threonine, V=Valine,
		amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			ILADAAAEGVPVRGARNQLRMYLTMAVAAAOPMLMYWLTFHLVR
6043	403	599	LCLFFFFPCATPVLPLPSLISAL/CLSHLSVSSWFCPCQPPLPC
			PLPPLONKTAKGSLSTEQSERG
6044	793	412	KLEMWNFTLISKVKISREVTMIASKFGIGQQVRHSLLGYLGVVV
1		!	DIDPVYSLSEPSPDELAVNDELRAAPWYHVVMEDDNGLPVHTYL
1 !	Í		AEAQLSSELQDEHP\EQPSMDELAQTIRKQLQAPRLRN
6045	155	2299	SPLPQVAAMNYLRRRLSDSNFMANLPNGYMTDLQRPQPPPPPPG
1 1			AHSPGATPGPGTATAERSSGVAPAASPAAPSPGSSGGGGFFSSL
			SWAVKOTTA A A ATTECHOUSE GROUP OF COMMENT
			SNAVKQTTAAAAATFSEQVGGGSGGAGRGGAASRVLLVIDEPHT
1 [			DWAKYFKGKKIHGEIDIKVEQAEFSDLNLVAHANGGFSVDMEVL
			RNGVKVVRSLKPDFVLIRQHAFSMARNGDYRSLVIGLQYAGIPS
1			VNSLHSVYNFCDKPWVFAQMVRLHKKLGTEEFPLIDQTFYPNHK
1 1			EMLSS\TTYPVVVKMGHGTLWGWGKVKVDNQHDFQDIASVVALT
].	•		KTYATAEPFIDAKYDVRVQKIGQNYKAYMRTSVSGNWKTNTGSA
			MLEQIAMSDRYKLWVDTCSEIFGGLDICAVEALHGKDGRDHIIE
1 1			VVGSSMPLIGDHQDEDKQLIVELVVNKMAOALPRORORDASDGR
	į		GSHGQTPSPGALPLGRQTSQQPAGPPAQQRPPPOGGPPOPGPGP
1 1			QRQGPPLQQRPPPQGQQHLSGLGPPAGSPLPORLPSPTSAPOOP
] [			ASQAAPPTQGQGRQSRPVAGGPGAPPAARPPASPSPOROAGPPO
i l		•	ATROTSVSGPAPPKASGAPPGGOOROGPPOKPPGPAGPTROASO
1 1			AGPVPRTGPPTTQQPRPSGPGPAGRPKPQLAOKPSODVPPPATA
]. [	i		AAGGPPHPQLNKSQSLTNAFNLPEPAPPRPSLSQDEVKAETIRS
			LRKSFASLFSD
6046	212	1075	EGLTGPCERVPFLLGRGPPHGATRAGHRRAVRWAGPESLPPLPR
1 1			SLIMDSPRAGTHQGPLDAETEVGADRCTSTAYQEQRPQVEQVGK
1			QAPLSPGLPAMGGPGPGPCEDPAGAGGAGAGGSEPLVTVTVQCA
] [			PTVALRARRGADLSSLRALLGQALPHQ\AQLGQLSYLAPGEDGH
1			WVPIPEEESLQRAWQDAAACPRGLQLQCRGAGGRPVLYQVVAQH
1			SYSAQGPEDLGFRQGDTVDVLCEVDQAWLEGHCDGRIGIFPKCF
1 1			VVPAGPRMSGAPGRLPRSQQGDQP
6047	49	1405	PVLVTSLRMREADTLRPPQLMEVSADIISTVEFNHTGELLATGD
1 1	:		KGGRVVIFQREPESKNAPHSQGEYDVYSTFQSHEPEFDYLKSLE
1 1	. 1	· · ·	TERKINKIYMI DOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOMAAHGI TOOM
1 1			IEBKINKIKWLPQQNAAHSLLSTNDKTIKLWKITERDKRPEGYN
! !			LKDBEGKLKDLSTVTSLQVPVLKPMDLMVEVSPRRIFANGHTYH
1			INSISVNSDCETYMSADDLRINLWHLAITDRSFTP\NIVDIKPA
1 1			NMEDLTEVITASEFHPHHCNLFVYSSSKGSLRLCDMRAAALCDK
			HSKLFEEPEDPSNRSFFSEIIS\SVSDVKFSHSDRYMLTR\DYL
·		•	TVKVWDL\NMEARPIETYQVHDYLRSKLCSLYENDCIFDKFECA
1 1	,	j	WNGSDSVIMTGA\YNNFFRMFDRNTKRDVTL\EASRESSKPRAV
1	1		LKPRRVCVGGKRRRDDISVDSLDFTKKILHTAWHPAENIIAIAA
6048		3194	TNNLYIFQDKVNSDMH
	•	J174	GIRTPKFCDSPTSDLEMRNGRGRGKRMRPNSNTPVNETATASDS
		i	KGTSNSSKTRAGANSKGRRGSQNSSEHRPPASSTSEDVKASPSS
1 1	1		ANKRKNKPLSDMELNSSSEDSKGSKRVRTNSMGSATGPLPGTKV
]	1	i	EPTVLDRNCPSPVLIDCPHPNCNKKYKHINGLKYHQAHAHTDDD
[	1	ł	SKPEADGDSEYGEEPILHADLGSCNG\ASVSOK\GSLSPARSAT
]	ļ	ł	PKVRLVEPHSPSPSSKFSTKGLCKKKLSGEGDTDLGALSNDGSD
[	j	İ	DGPSVMDETSNDAFDSLERKCMEKEKCKKPSSLKPEKIPSKSLK
	ĺ		SARPI/APLAIPPQQIYTFQTATFTAASPGSSSGLTATVAQAMP
	İ		NSPQLKPIQPKPTVMGEPFTVNPALTPAKDKKKKDKKKKESSKE
ļ İ		1	LESPLTPGKVCRAEEGKSPFRESSGNGMKMEGLLNGSSDPHOSP
		i	LASIKAEADKIYSFTDNAPSPSIGGSSRLENTTPTOPLTPLHTV
		i	TONGAEASSVKTNSPAYSDISDAGEDGEGKVDSVKSKDAEOLVK
	j		EGAKKTLFPPQPQSKDSPYYQGFESYYSPSYAQSSPGALNPSSQ
l		1	AGVESQALKTKRDEEPESIEGKVKNDICEEKKPELSSSSQQPSV
		- 1	IQQRPNMYMQSLYYNQYAYVPPYGYSDQSYHTHLLSTNTAYRQQ
'	1	1	YEEQQKRQSLEQQQRGVDKKAEMGLKEREAALKEEWKQKPSIPP
i			
	İ	] .	TLTKAPSLTDLVKSGPGKAKEDGADDAVGUTTOVI DDGGVT BOO
i			TLTKAPSLTDLVKSGPGKAKEPGADPAKSVIIPKLDDSSKLPGO
			TLTKAPSLTDLVKSGPGKAKEPGADPAKSVIIPKLDDSSKLPGQ APEGLKVKLSDASHLSKEASEAKTGAECGRQAEMDPILWYRQEA EPRMWTYVYPAKYSDIKSEDERWKEERDRKLKEERSRSKDSVPK

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
- l	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
- [	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
•	to first	amino acid	L-Leucine, M-Methionine, N-Asparagine,
ļ	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
Į	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	sequence	Codon, /=possible nucleotide deletion,
<del> </del>		<del> </del>	\=possible nucleotide insertion)
}			EDGKESTSSDCKLPTSEESRLGSKEPRPSVHVPVSSPLTQHQSY
1		Ì	IPYMHGYSYSQSYDPNHPSYRSMPAVMMQNYPGSYLPSSYSFSP
ŀ			YGSKVSGGEDADKARASPSVTCKSSSESKALDILQQHASHYKSK
•		j	SPTISDKTSQERDRGGCGVVGGGGSCSSVGGASGGERSVDRPRT
	1		SPSQRLMSTHHHHHHLGYSLLPAQYNLPYAAGLSSTAIVASQQG
6049	215	1089	STPSLYPPPRR
1 4415	1 22	1089	AMTGVFDRRVPSIRSGDFQAPFQTSAAMHHPSQESPTLPESSAT
1			DSDYYSPTGGAPHGYCSPTSASYG\KALNPYQYQYHGVNGSAGS
1			YPAKAYADYSYASSYHOYGGAYNRVPSATNOPEKEUTE DEVIDMU
			NGKPKKVRKPRTIYSSFOLAALORRFOKTOYLALPPRAELAASI.
1	1		GLTQTQVKIWFQNKRSKIKKIMKNGEMPPEHSPSSSDDMACNSD
			QSPAVWEPQGSSRSLSHHPHAHPPTSNOSPASSYLENGASWYTG
6050	- FCC		AASSINSHLPPPGSLOHPLALASGTLY
0030	566	1718	KGLERTCCAMEESDSEKTTEKENLGPRMDPPLGEPG\GSLGWVL
			PNTAMKKKVLLMGKSGSGKTSMRSIIFANYTARDTRRLCATTLD
]			RIHSLQINSSLSTYSLVDSVGNTKTFDVEHSHVRFLGNLVLNLW
i i			DCGGQDTFMENYFTSQRDNIFRNVEVLIYVFDVESRRLEKDMHV
			YQSCLEAILQNSPDAKIFCLVHKMDLVOFDORDI.TRKRRFEDIR
1			RLSRPLECSCFRTSIWDETLYKAWSSIVYOLIPNVOOT.FMNT.DN
			FAEITEADEVLLFERATFLVISHYOCKEORDAHREEKIGNITVO
1 1			FKLSCSKLAASFQSMEVRNSNFAAFIDIFTSNTVVMVVMSDD91
6051			PSAATLINIRNARKHFEKLERVDGPKOCLLMR
0021	566	1718	KGLERTCCAMEESDSEKTTEKENLG?RMDPPLGEPG\GSICWVI
1			PNTAMKKKVLLMGKSGSGKTSMRSIIFANYIARDTRRLGATTID
			RIHSLQINSSLSTYSLVDSVGNTKTFDVRHSHVRFTGNLVLNI.W
[			DCGGQDTFMENYFTSQRDNIFRNVEVLIYVFDVESRELEKDMHV
1 1	j		YQSCLEAILQNSPDAKIFCLVHKMDLVORDORDLIFKRPREDLD
1 1	1		RLSRPLECSCFRTSIWDETLYKAWSSIVYOLIPNVOOLEMNLEN
1			FABILEADEVLLFERATFLVISHYOCKEORDAHRFRKTSNITKO
1 1			FKLSCSKLAASFQSMEVRNSNFAAFIDIFTSNTYVMVVMSDDSI
6052	566		PSAATLINIRNARKHFEKLERVDGPKOCLLMR
1 0032	566	1718	KGLERTCCAMEESDSEKTTEKENLGPRMDPPLGEPG\GSLGWVL
1 1	1		PNTAMKKKVLLMGKSGSGKTSMRSIIPANYIARDTRRIGATILD
[ ]			RIHSLQINSSLSTYSLVDSVGNTKTFDVEHSHVRFLCNLVLNLW
]			DCGGQDTFMENYFTSQRDNIFRNVEVI,IYVPDVESPELEKDMUV
	ļ	•	YQSCLEAILQNSPDAKIFCLVHKMDLVOEDORDLIPKERFEDIR
·			RLSRPLECSCFRTSIWDETLYKAWSSIVYOLIPNVOOLEMNIDN
] ]	j		FABIIEADEVLLFERATFLVISHYOCKEORDAHRFFKTSNITVO
	[·		FKLSCSKLAASFQSMEVRNSNFAAFIDIFTSNTYVMVVMSDDST
6053	201		PSAATLINIRNARKHFEKLERVDGPKOCLLMR
"""	201	1704	KGTEMNKSRWQSRRRHGRRSHQONPWFRLRDSEDRSDSRAAOPA
			HDSGHGDDESPSTSSGTAGTSSVPELPGFYFDPEKKRVFPLLDG
			HNNCNPLTKESIRQKEMESKRLRLLQEEDRRKKIARMGFNASSM
1		I	LRKSQLGFLNVTNYCHLAHELRLSCMERKKVOTRSMDBSatash
·	'		RENLI LADTNSDRLFTVNDVTVGGSKYGT INTOSI KTDTT KVEM
i			HENLYFTNRKV\NSVCWASLNHLDSHILLCLMGLARTDGCDTLL
1		. [	PASLFVNSHPAGIDRPG\MLCSFRIPGANSCAWSINTOANNCRC
- 1	1	i	TGLSRRVLLTNVVTGHROSFGTNSDVLAOOFALMADI.LENGODE
1	İ	i	GZIFAIDLRCGNQGKGWKATRLFHDSAVTSVRTI.ODEOVIMAGD
ľ			MAGKIKLWDLRTTKCVRQYEGHVNEYAYLPLHVHEEEGTLVDVG
	1	}	QUCYTRIWSLHDARLLRTIPSPYPASKADIPSVAFSSRIGGSRG
6054			APGLLMAVGQDLYCYSYS
0034	1	1054	P?IARLQEFGTSRRHMAAPSGVHLLVRRGSHRIFSSDLNUTVIU
- 1		ı	KQSSSQQRRNFFFRRQRDISHSIVLPAAVSSAHPVPKHIKKDDV
1	1	ł	VTTGIVPDWGDSIEVKNEDOIOGLHOACOLARHVLLLAGKSI.KV
- 1	1		DMTTEEIDALVHREIISHNAYPSPLGYGGFPKSVCTSVNNVT.CH
1	,	ŀ	GIPDSRPLQDGDIINIDVTVYYNGYHGDTSETFLVGNVDECGKK
			LVEVARRCRDEAIAACRAGAPFSVIGNTISHITHONGFOVCPUE
- 1		ſ	VGHGIGSYFHGHPEIWHHANDSDLPMEEGMAFTIEDTTTEGGDR
			FKVLEDAWTVVSLD/TSKVSAQFEHTVLITSRGAQILTKLPHEA
			THE THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF TH

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Cocation corresponding to first contraponding to first contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding contraponding co	ID			Time dota segment containing signal papride
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Leucine, M-Methionine, N-Asparagine, saino acid residue of amino acid sequence silvertic properties of the control of amino acid sequence source of the control of the control of amino acid sequence source of the control of the control of the control of sequence source of the control of the control of the control of sequence source of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of	1	lccation		Halistidine Talcoleucine K turing
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Sequence  6055  6056  6057  6057  6058  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  6059  60		residue of	amino acid	Wallyptophan, Yallyrosine Yallyknown turner
Sequence   Spossible nucleotide insertion	ł	amino acid	sequence	Codon. /spossible nucleotide deletion
### PPYPLISFIAMWINGSDRIFTDISGSAGPPGTICGSAINING  GCANGSPRENGESTOPACCHTHUPPGNAINGNOPPELSRITALI  SERPPRKKKSGTTTGKERERTSFLOGGKRFEIGHGLGGIG  TLLITGBISVBARDWHUTHARNELBKRAGDYKLVALDASKNOW  MKGQIDDEGGRFFAS FYRLWANNEDEVEBGBDJONGGLDENDG  CLCLGRFQURNDDRARVINEIDSFRHIYKLKLDGLGCYLKQC  RKRRDMFSDBQLKVIFONIEDIYRPQMSYRDLEKQYNDDDPLI  SIGPFLERQDGFWITSSYLVANHLOMELSKUMDGRVGHFP  EACRLLQOMIDIA\IOFFLIPPQKICKYPLOLAELLKYTACOM  SDYRYVARALAMMINYQGINEKKRERINDKLRQADGSVLDFRED  GDZLDRSSELIYTGSNANIVQA\CKYPLOLAELLKYTACOM  SDYRYVARALAMMINYQGINEKKRERINDKLRQADGSVLDFRED  GDZLDRSSELIYTGSNANIVQA\CKYPLOLAELLKYTACOM  NETEBIHLFFAKKLEKIRHLBAFREERWOODEKIGFEISE  NOKROAMTURKVYROKGWORASSPESYPPPOPDETANGYLVP  LOGIAGSGVPEFTEPKRSQSPFKOPFSRLTPFKK  SOKGROVARSSOLGSPAROVSGOLGSGREFISLEPPFBRA  LAPTRAPDTALTIMEVALVESPINPSCKIMTFRSWEFFEFRIK  VLAAMSSKGAHRAGLAVIPKSKWAPCOVDINLLIPPETO  WTGGGLFTOYNIQKKAMTVKSPEOLANSGKYCTPRYLDYEDL  ERKYWKINTEVAPIYCAGDINGSIYDEVOVENHIALRINVLDVVE  ECCISISGNYPPLYFOMMKTFAMITEDMOLYSINVLHPGEB  KSWAITPPENGRIELBLAGGFFFSSGOCDAFLRHMITLSPNU  LIKKGIFPDKITQBAGEFMITFPYGYVAGGRNGCHARSTNIPAT  VENIDYGKVALKCTGKOMWKISNIGLYSKGARAVKLANESPOCASTSKEP  KSWAITPPENGRELBLAGGFFFSSGOCDAFLRHMITLSPNU  LIKKGIFPDKITQBAGEFMITFPYGYVAGGRNGCHARSTNIPAT  VENIDYGKVALKCTGKOMWKISNIGLYSKGARAVKLANERS  SSEESSSASRMOVSGNLSBHIKLGGNSCLSTSVYEDLKTEDDKA  ANDESEVSDEVGARAVENDSVIDDKVSKSGARAVKLANER  SSEESSSASRMOVSGNLSBHIKLGGNSCLSTSVYEDLKTEDDKA  SSEESSSASRMOVSGNLSBHIKLGGNSCLSTSVYEDLKTEDDKA  SSEESSSASRMOVSGNLSBHIKLGGNSCLSTSKYPELKTEDDKA  ANDESEVSBEVGARAMPHONITURGQAFSDEELBPVLSI  EESVEETESNAAPLHILMOTKOPMFAAGGENAVTVARMKPHCAL  CTLLMPHYKODSSSENDTFEDDISHPARSPRITTURGQAFSDEELBPVLSI  EESVEETESNAAPLHALMOTKOPMFAAGGENAVTVARMKPHCAL  TYSERNIESSPHAAPLEEDGTSLLISGAKCCVAVRAGCTGIFSH  WORDCSSCATHVYREGERGIDARGENGKORGHARAMPHCA  VANFSVFSTSGERGHOFFTANAFTHACCCCLLIRGGALMOTKINKAMAMPMCA  VANFSVFSTSGERGHOFFTANAFTHACCCCLLIRGGALMOTKINKAMAMPMCA  VANFSVFSTSGERGHOFFTANAFTHACCCCLLIRGGALMOTKINKAMAMPMCA  VANFSVFSTSGERGHTANAFTHACCCCLLIRGGALMOTKINKAMAMPMCA  VANFSVFSTSGARDHVOTVERGHKKTLTCCRHEVYRNOSG  THE HUPPANGLESSFRANGERGRAGGERGRERKONLTPRCCVVILOG		sequence	1	\=possible nucleotide insertion\
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SGGGDPURVESSQLSPSACEVSQLSISLIGERPLSSLPPPSPSR, LAPPTRAPPTRAPTIMENGAVESSPINDSCHIMFTRPSMEERTEFINK YLAAMESKGAHRAGLAKVI DYKEWKPRQCYDDIDMLLIPAP IOO MVTGGGGLFTQYNIQKKAMIVKEPRQLANSGKYCFRYLDVEDL ERKYWKNLTFVAPI YGAD INGSI YDEGDDENHTARLITYLDVED ERKYWKNLTFVAPI YGAD INGSI YDEGDDENHTARLITYLDVED ERKYWKNLTFVAPI YGAD INGSI YDEGDDENHTARLITYLDVED EECCI SI EGVNTPYLLYGMMKTFAMHTEDMDLYS INVLHFGED KSWYAI PSPHGKRIERIAGGFFFSSCOFFIRHAMIT LISPSV LKKYGI PFDKITQEAGEFMI TTPYGYHAGPNHGFNCASSTWFAT VRWIDYGKVAKLCTCRAWWKI SMD IPVRKPQDDRYQLHKQGKD IYTIDHTKFTPASTPEVKAMLQRRRKVRKASRSFQCARSTKKRP KADBEEEVSDEVDGAVVRPDSVTDDLKVSEKSEAAVKLRRTEK SSEESSASRMQV&GNUSDHI KLSGGNSCLSTSVTEDI KIEDDKA YAYNSVPSISSEADDSI PLSTGYKEPEKSDPSGLBWFKSPSCS SVAESMGVITGGESSDVSEGHINGEFI PAVDSGERNSFKVDS IARGENKTSKSWRIPLSRPPARSPMTLUKQQASDEELPRVLGS  SVAESMGVITGGESSDVSESHGKGLBPGEI PAVDSGERNSFKVDS IARGENKTSKSWRIPLSRPPARSPMTLUKQQASDEELPRVLGS CTLLMPYHKPDGSNEENDARWETKLDEVVTSGGKTKPLIFEMCP IYSEENI EYSPFPARFLEEDGTS LLISCGAKCCVAVHASCYGIPSH EICCGGLCARCKRNAMTARCCCCLNEGALGYTMAKARHYMCA VAVPEVRFTNVPERTQIDDGRI PLQRIKKLKCIFCHRVKRVSGA CLQCSYGGCPASFEVTCAHAGAVL NAPUNKPDCKAYD MFDOKS FSROTPPPDI VERDCLKLGPDARGEVKNPCGKNGAR CLQCSYGGCPASFEVTCAHAGAVL NAPUNKPDCKAYD MFDOKS FSROTPPPDI VERDCLKLGPDARGEVKNPCGCGGG AKYFGSNI AHMYQVEPEOGSQLAMKREDIYTTLDEELPKRVKARF VSAGRCHLGTCQVNSLSSPHVSOAQOETYLGFWINKKSQCRIF SSTY SAGNASTILGLLAPPGEAWG ILGQPPNRPNHSPPPSAKVKKIFG WGGDFYSNIKTVALNLLVTGKLYDHGNGTTSVHPQHNATGGGNIS SLVPPSKAVEFFIGEOGTIFRAKASTIRC\RMWEKEX HORG TSLFTHPDAKICSRPHAQSSATMSCSQPPKVVCVYIAPYSTDYR LVQKVCPDYNHSDTPYPPSG  1 986 HPLPSASIGFPSTRPFOVAIYLVBERMGTSVHPCHANTGGGNIS SILVPSPSKAVEFFIGEOGTIFRAKASTIRC\RMWEKEX HORG TSLFTHDPAKICSRPHAQSSATMSCSQPPKVVCVYIAPYSTDYR VLDACSSEATHVWMETSABEAVSWGERMAAAPPGCTPPALD ISMLTESLGAGQPVVECRIRLEVAGPSKGPLLFTCRAFSVIKAL PSPVTTILSGLGCLPHFGEHSSRVVQELLEHOVCEVERVRRSP/ RLFTQ1FGVVXTADRWYRGGLRTLDDLREGORLITTCLARSKGFR VLDACSSEATHVWMETSABEAVSWGERMMAAAPPGCTPPALD ISMLTESLGAGQPVVECRIRLEVAGPSKGPLLFTCRAFSVIKAL PSPVTTILGLGELBIL LLARAGFGESGRRILLTTCRAFSVIKAL PSPVTTILGLGELBIL LLARAGFGESGRRILLTTCRAFSVIKAL PSPVTTILGLGELBILGHAPROF		<u></u>		\DGIAQSQVFEFTEPKRSQSPFWQNFSPLTPFVV
LAPTRAPDTALTIMEVAEVESPINPSCKIMTEPSNEBERSFERN VIATMESSCAHRAGIARXI PPKSKHPCYDDIDNLI PAPIQO WYTOGSCLFTQYNICKKAMTVKEPROLANSGKYCTPRYLDYKDL ERKWKKULTYVAPIYGADINGSIYDEGVUDENTALINTALINTVLDVVB EECCISIEGVATPYLYPGMMKTTFAMHTEDMDLYSINYLHPGEB KSWYAIPPEHGRIERLAQGFFFSSSQCCDAFIRHMTLISPSU LKKYGIPFKLTQSAEGFMITFFYGYHAGPNHGFNCABSTHFAT VRWIDYGKVAKLCTCRKDWYKISMDIPYRKQDDRYQLMKQGKD IYTIDHTKFTPASTPBEVKANLQRRKKVRKARSFQCARSTSKRR KADBEBEVSDBVDGABVPRPDSVTDDLKVSEKSEAGAVKIRNTER SSEBESSASRNQVEQNLSDHIKLSGNSCLSTSVTEDIKTBEDKR YAYNSVPSISSEADDSIPJSTYSKEPEKSPDSELSWPKSPSGC SVAESNGVLTEGERSDVESHGNGLBPGEIPAVPSGGRNSFKVDS IARGENKTKSKWRHPLSERPPASSPMTLVGQAFSDELPBVLGI EEBVETESMAKDLIHLWQTKPPNFAABQSTVALTVANKKHCCAI CTILMPYHKPDSSNEENDARMSTKLDEVVISGKKRFLIEBMGR IYSERNIEYSPRAPLEEDGTSLLISCAKCCVRVASSCYGIPSH EICDGNLCARCKRNANTABCCLCNLRGGALKGTKNNKAAHYMCA VAYPSWFTNVPERTOLDGGR PIQDKLKGTPGKRVVUSGC CIQCSYGRCPASFRVTOAHAAGVI\MEPDDMPYVVNITCPRHKV NPNVKSKACEKVISVGGVTITKHNTTKYYSCXWAVTSGCFTYEKV MFDDSSTSRDTFPEDIVSRDCLKLGPPARGEWOVNKPDGKLYG AXYPGSNITAHMYQUFEDOSQLAKKREDIYTLDEELPKRVKARF VSAGKCHLGTCQVNSLSSPHVSOAQQETYLGFWINSKXSQCNIF LGGTY  FVARLKEQEGEGGLGPRKEKGRARGRERRKMQLTRCCFVFLVQ GSLHLVICGQDDGPPGSEDPSDHBGGPRRVPRKKARFI VSAGKCHLGTCQVNSLSSPHVSOAQQETYLGFWINSKXSQCNIF LGGTY  FVARLKEQEGGGLGPRKEKGRARGRERRKMQLTRCCFVFLVQ GSLHLVICGQDDGPPGSEDPSRDHBGGPRRVPRKKRHISPKS RPMANSTLLGLLAPPGEAWGILGQPPNRNHSPPPSAKVKKIFG WGDFYSNIKTVALNLLVTKALVBKUTGVTAPFTYDYR LYQKVCPDYNYHSDTPYYPSG  1 986 HPLPSASLGJPSVSLGVVSLALEAVVPNLEKRRRARVGSP SOADASSTFYSTFPGVATILVEPRINGSRRAFITGLARSKGFR VLDACSSEATHVVMETSAEAVSNQERRMAAAPPGCTPPALLD ISMLTESLGAQQPVPVCCNIFLEVAGPSKGPLEFTCRAASVLRAL PSPVTTLSCLAGQUPVPCCRRFLEVAGPGRATGCARS LIFTQIFGVYKTADRWYRGGLRTLDDLREPQCPKLTQQKAGGP SSEAGPMASINCTLDPSASTP  00DFSLADLTDHRAHRCFGDGDDDDDPGLSWVASSFSKDVASPT VLDACSSEATHVVMETSASCPPCCVKKFSSRAPMATACOG SCARASTFYGVKYTADRWYRGGLRTLDDLREPQCPKLTQQKAGGP SSEAGPMASINCTLDPSASTP 0NIGDCCLUGGEEGGTGLPYPCCPCKSFILLSVLKRHEQIH SDKLPFKCTYCSRIFKHKKRSRDRHKKLHTGDKKYHCHECEAAFS SSEALKHLKKHISSSKPHCTTVCTVKGSTSLOGHMOAHKWY	6056	43	3358	SGGRGPVRVRSEOLSPSAEOVSOISOISIGPPPLSSI PRPPSTA
VILAYMESKGAHRAGIAKVI PPKEMKRRCYDDIDILLI PAPIOO  WYTGGSGLETGVINICKKAMTVKEPKGLANSGKYCTPTAJDYKDL  ERKYWKNITFVAPI YGADINGSI YDEGGDEMNIARLNTVLDVVE  EEKOISI EGWNTPYLY PGWNKTTFAMTEDULYSINVLHEGEE  KSWYAI PEHGKELERLAGGFFSSSGCCDAFLRHKMILI SPSV  LKKYGI PFDKI TDEAGEFMITFYGYHAGFNHCHFCABSTHFAIT  VRHIDIGKVAKLCTCRAGWYKISMI PYRKYGDBYROLMKGKGK  IYTIDHTKFTPASTPEVKAMLQRRKVYKASHSFGCANSTSKRR  KABBEEDVSDBVCAGEVYPRDSVTDULKVSEKSEAAVKLRNTEA  SSEESSASRMOVEONLSDHI KLSGNSCLSTSVTEDIKTEDDKA  YAYRSVPSI SSEADDSI PLSTGYKEPEKSDPSELESHKYKEPSS  SVAESNGVLTEGEESDVESHNGKLEBEFJAPSSEPSTVPS  IARGENKTSKSWRHPLSTPPASSPMTLVKQAPSDEELPRULSI  EERVEETESMAKPLI HUMOTVPPWFAAGSVANTAARKYPCAI  CTILLMPYHKPDSSNEENDARWETKLDEVYTSGGKYKPLIPEMCE  IYSEENI ESSPANTHUNGTYPPWFAAGSVANTAARKYPCAI  CTILLMPYHKPDSSNEENDARWETKLDEVYTSGGKYKPLIPEMCE  IYSEENI ESSPANTHUNGTYPPWFAAGSVANTAARKYPCAI  CTILLMPYHKPDSSNEENDARWETKLDEVYTSGGKYKPLIPEMCE  IYSEENI ESSPANTHUNGTYPPWFAAGSVANTAARKYPCAI  CTILLMPYHKPDSSNEENDARWETKLDEVYTSGGKYKPLIPEMCE  IYSEENI ESSPANTHUNGTYPPWFAAGSVANTAARKYPCAI  CTILLMPYHKPDSSNEENDARWETKLDEVYTSGGKYKPLIPEMCE  IYSEENI ESSPANTHUNGTYPPRAGGSVANTAARKYPCAI  CTILLMPYHKPDSSNEENDARWETKLDEVYTSGGKYKPLIPEMCE  IYSEENI ESSPANTHUNGTYPPRAGGSVANTAARKYPCAI  CTILLMPYHKPDSSNEENDARWETKLDEVYTSGGKYKPLIPEMCE  IYSEENI ESSPANTHUNGTYPPRAGGSVANTAARKYNGAA  VAVPEVRETTUVKGAPSOPELIPEMCHECUTVERNEYSEVIPEMCH  INSTANTAALSTANTAARCY  NEWKSKACERVI SVOGTVITKHNTKYYSCEVMAVTSOTFYHEV  MFDOKS FSROTFPEDI VSEDCLKLIG PILORHKLKCTFCHRVKWSGAA  CYGSYSGKCAPSFIVTVCAHAGAULTVERNEYVORVERVEKAGHISPKS  RPMANSTLLGILAPPGEAAGILGOPPNEPNHSPPSAKVKKIFG  WGDSYSNI KYVALILLVYKIVUNINGTYFURCKFVFIVV  GSSLYLVI CGODDGPOSEDPSDCHDHEGOPPRVENKRGHISPKS  RPMANSTLLGILAPPGEAAGILGOPPNEPNHSPPSAKVKKIFG  WGDSYSNIKTVALILLVYKIVALVERVARMEVEVYKKERFRAKVGSF  SUDANSSTYLVYNHSDTPYYPGG  1 986 HPLPSASLGUPSVGCORSHAAAPPGCTYARSE/  KLPTOIFGVYKTADRWYKTARMYNTULVEPRAGRSRALLFTCRAASVIKAL  PSPVTTILSULGGGOPPVECRIRLEVAGPSKOPLSPAMPAYACOR  PTPLITHINTGLEALET LALARAGFESSGRILTTCRAASVIKAL  PSPVTTILSULGGGOPPVECRIRLEVAGPSKOPLSPAMPAYACOR  RIFTOIFGVGVKTADRWYKRGLKTLDDLEEPOTKLOGGENAMPAYACOR  SEAGPPA	1			LAPTRAPDTALTIMEVAEVESPINDSCKIMTEDDSMERPEREDE
### WTGGSLFTQ**NIGKKMTVKERQLANSGYCTPRYLIPUDL ERKYWKNITPAPHT (SADINGS I DEGUDEMI NALHTVLDOVUE EECGISIEGUNTPYLYPGMWKTTFAWHTEDMDLYSINYLHPGEP KSWYAIPPEHGKRLERLAQGFFPSSSQCDAFLRIKWTLIEPGU KSWYAIPPEHGKRLERLAQGFFPSSSQCDAFLRIKWTLIEPGU KSWYAIPPEHGKRLERLAQGFFPSSSQCDAFLRIKWTLIEPGU KSWYAIPPEHGKRLERLAQGFFPSSSQCDAFLRIKWTLIEPGU LKKYGIPFPKITQEAGERMITFPYGYHAGFNIGFRKAGESITFAT VRWIDVGKVAKLCTCRKDMVXISMD I PVRKFQDERYDLWKGGKO I YITIDHIKPTPASTEVVAMUQARVKASSESPCASTSKER KADBEEEVSDEVDGARVENDSVIDDIKVSEKSEAAVKLRNTEA SSEEESSASRMOVEONLSDHI KLSGMSCLSITVTEDIKTEDDIGA YAYRSVPSISSEADDSI PLSTGYKEKEKSDFSELSWKSESPESC SVAESNGVLTEGESDVESHGNGLERGEI PAVLGII LABGEMKTKSKSWHRPLERPPARSFMILVRQOAPSDEELPBVLGII EERVEETSSWARPLIHLWQTVEPDMFAAGGYMATVARMKPHCAI CTLLMPYHKPDSSGNEENDARWETKLDEVVTSEGKTKELIPEMGF IYSEENIEYSPPNAPLEEDGTSLLISCAKCCVRVHASCYGIPSH EICOGWLCARCKRNAWTAECCLCNLRGGGLKGTKNNXWAHVMCA VAPFEWRTFNVPEERTOIDVORI PLGKIKKGIFGFREVKWSGAC CIQCSYGRCPASFHVTCAHAAGVI,MEPDDMPYVVNITCFRHKV NPAVKSKACEKVIS VAGGTVITKHRNITRYSCRVMAVTSGTFFEV MFDDGSFSRDTFPPDIVSRDCLKLGFPAEGEVVQVKMPDCKLYG AXYFGSNIAHWQVEFEDGSGLMRREDIYTLDEFLPKRVKARF VSAGRCHAGTGVOWSLSSPHVSOAQQETVLGFWINSKSGCNIF WFDRAKSTLLGLLAPPGEAGGLIGOPPNPHNSPPBSAKVKKIFG GSLYLVICGQDDGPPGSEPPERDDHEGGPRRVPRKRGHISPKS RPMANSTLLGLLAPPGEAGGLIGOPPNPHNSPPBSAKVKKIFG WGGPFSNIKTVAINLUTTGKIVDHGNTSSVHOCHMSTGCGNIS ISLVPPSRAVEFRIGEQQIFIRAKASKIFNC\REWEKVB\RGR TSLFTHPAALICSRDFVAITVTGKVHTATGSVHTCHMSTGCGNIS ISLVPPSRAVEFRIGEQQIFIRAKASKIFNC\REWEKVB\RGR TSLFTHPAALICSRDFVAITVTGKVHTATGSVHTCHMSTGCGNIS ISLVPPSRAVEFRIGEQOIFIRAKASKIFNC\REWEKVB\RGR TSLFTHPAALICSRDFVAITVTGKVHTATGSVHTCHMSTGCGNIS ISLVPPSRAVEFRIGEGGLIFFCRASVLKAL PSPYTTLSQLQGLPHIGEHSSRVVQELLERGVCEEVERVRSSP VLDAGSSEATHVVMEETSAERSVWQERRMAAAPPGCTPPALLD ISMTESLGAGQDVPVPCHRILEVAGPSKOPLSPAMMPAYACQR PTPLTHHNTCLSEALEILBAAGFGSGGLLTFCCRASVLKAL PSPYTTLSQLQGLPHIGEHSSRVVQELLERGVCEEVERVRSSE/ RLFTQ1FGVVKTADRWYREGLRTLORGOPQKLTQQCKAGGP SREAGPHASINCTLDPSASTP ONIGGEOLIGLEEEGGGGLDPPCQFCDKSFTRLSYLKRHEGIH SDLXPFKCTYCSRLFKHRSBRORHIKHTGERGPGSTSLOSHMOMAHKWW RSDLKLHKKHTISSSKFPKCTVCKRGFSSTSLOSHMOMAHKWW	1			YLAYMESKGAHRAGLAKVI PPKEWKPROCYDDIDMLI IRRBIOO
ERKYWKNILTYAPIYGADINGSIYDEGUDEMNIARLINTULDUVE EECGISIEGWIPPYLYPGMWKTTEMTEDMILYSINTLHFGEBY KSWYAIPPERGRELERLAQGFPSSSQCDAPLRHKMTLISPSY LKKYGIPPDKITQEAGEMITFPYGYHAGFNIGFNCABSTITFAT VRHIDYGKVAKLCTCRKDMYKISMIYENGPDRYDLWKGKGK IYTIDHTKPTPASTEEVKAMLQRRRKVKKASRSFQCAASTISKR KABBEESUSDEVDGAEVVPNDSVTURKKGKDSKAKKRINTEA SSEEESSASRMQVEQNLSDHIKLSGNSCLSTSVTEDLKTEDDKA YAYRSVPSISSEADDSIPLSTGYEKEEKSDPSBLSWPKSPESGS SVAESSMUTEGEESDVBESGMOLEGEPTPAYPSGERRSFKVDS IABGEMKTSKSWRHPLSRPPARSPMTLVKQQAPSDEELPBYLGI EERVETETSWARPLIHLWQYTXPPHAGGYNATVARMKPHCAI CTLLMPYHKPDSSNEENDARWETKLDEVVTSEGKTKFLIFEMGF IYSERNIEYSPRAFLEEDDTSLLISCAKCCTWHASCYGIPSH EICDGMCARCKRMAWTABCCLCHLDRGGALKQTKNNKAWYMCA VAVPEWFTNVPERTOLDVGRIPLGRGALKQTKTVANKAWYMCA VAVPEWFTNVPERTOLDVGRIPLGRGALKGCTKVANKAWYMCA VAVPEWFTNVPERTOLDVGRIPLGRGALKGCTVANKAWYMCA VAVPEWFTNVPERTOLDVGRIPLGRGALKGCTVFLVVG RODGSSRATAHMYQVEPEDGSGIAMREDIYTLDEELBFKWKARF VSAGRCHLGTCOVNSLSSPHVSOAQQETYLGFWINSKKSCCRIF LSGTY VSAGRCHLGTCOVNSLSSPHVSOAQQETYLGFWINSKKSCCRIF LSGTY VSAGRCHLGTCOVNSLSSPHVSOAQQETYLGFWINSKKSCCRIF LSGTY VSAGRCHLGTCOVNSLSSPHVSOAQQETYLGFWINSKKSCCRIF LSGTY VSAGRCHLGTCOVNSLSSPHVSOAQQETYLGFWINSKKSCCRIF LSGTY VGGDGDGPGSEDPERDDHEGGPRRPVPRKRGHISPKS RPMANSTLLGLLAPPGEAMGILGGPPRRPVPRKRGHISPKS RPMANSTLLGLLAPPGEAMGILGGPPRRPVPRKRGHISPKS RPMANSTLLGLLAPPGEAMGILGGPPRRPVPRKRGHISPKS RPMANSTLLGLAPPGEAMGILGGPPRRPVPRKRGHISPKS RPMANSTLLGLAPPGEAMGILGGPPRRPVPRKRGHISPKS RPMANSTLLGLAPPGEAMGILGGPPRRPVPRKRGHISPKS RPMANSTLLGLAPPGEAMGILGGPPRRPVPRKRGHISPKS RPMANSTLLGLAPPGEAMGILGGPPRRPVPRKRGHISPKS SGDAASSTPSTRFPGVAITYLUFRMGSRGARGERRARLTCLLARSKGFR VLDACSSEATHVVMEETSAEERAVSNQERRMAAAPPGCTPPALLD ISWLTESLGAGQPVPVCCHRLEVAGROPALLD ISWLTESLGAGQPVPVCCHRLEVAGROPALLD ISWLTESLGAGGPUPVCCHRLEVAGROPALLD ISWLTESLGAGGPUPVCCHRLEVAGROPALLD ISWLTESLGAGGPUPVCCHRLEVARROPQKLTQQCKAGEP SREAGPHASINCTLDPSASTP QNIGDGCLGLEFEGGTGLPYPCQCCDKSFTRLSYLKRHEGIH SDLLFTCIFGGLIGHTRARCFGGGDDDDPQLSWVASSFSSKDVASPT QNIGDGCLGLEFEGGTGLPYPCQCCDKSFTRLSYLKRHEGIH SDLLFTCIFGCHGRAFKFKTCVCKGRGFSSTSLOSHMOAHKVAY RSDLLAFKCTYCSRLFKHRSSROPRIKLHTCREAPPS				MVTGQSGLFTQYNIOKKAMTVKEFROLANSGKYCTPPVLDVPDI
EECGISIEGWTPYLYFOMWKTTFAMHTEDMDLYSINTLHFGER KSWYAIPPENGKRIERLAGGFFFSSGCCARLIRKWILISPSV LKKWGIPFDKITQEAGERMITFPYGYHAGFNHGFNCAESTWFAT VRWIDYGKVAKLCTCKKDMYKISMDIFVRKPGDRYQLMKQGKD IYTIDHTKPTPASTTEVKAMLQRRKVRKASRSFQCARSTKRKR KADDEGEVSDRVDGAEVENPDSVTDDLKVSEKSEAWVLRNTEA SSEESSASRMQVEGNLSDHIKLGSCLSTVYTEDLIKTEDDKA YAYRSVPSISSEADDSIPLSTGYEKPEKSDPSELSWPKSPESCS SVAESNGVUTEGEESDVESHGNLEBGEIPAVLSIT LAGGENKTSKEWRHPLSRPARSPMILVKQQAFSDEELPAVLSI EERVESTESWARPLIHLMQTKPPNFAABGSYNATVARNKPHCAI CTLLMPYHKPDSSNEEBNDAWETKLEVTSGETKTELIPEMCP IYSERNIEYSPNAPLEEDGTSLLISCAKCCVRVHASCYGIPSH EICDGRLCARCKRNAWTAECCLCNLRGGALKGTKNNKWARVMCA VAVPEVRFTNVPERTQIDVGRIPLGRKLKGITCRHRVKVSGA CIQCSYGRCPASFHVTCAHAAGVL/MEPDDWPVVNITCPRHKV NRVKKSKACEKVISVGGTVITKHRNTYYSCRVMAVYSGOFFYEN MFDDGSFSRDTPPBDLVSRDCLKLGPPAEGEVQVVKWPDGKLYG AKYFGSNIAHMYQVEPEDGSQLAMRGBDIYTLDEELPKRVKASGA CIQCSYGRCPASFHVTCAHAAGVL/MEPDDWPVVNITCPRHKV NRVKKSKACEKVISVGGTVITKHRNTYYSCRVMAVYSGOFFYEN MFDDGSFSRDTPPBDLVSRDCLKLGPPAEGEVQVVKWPDGKLYG AKYFGSNIAHMYQVEPEDGSQLAMRGBDIYTLDEELPKRVKASF VARJRCHLGTCQVNSLSSPHVSQAQCETYLGFMINGKKSGCNIF LSSTY  553  FVARLKEGGEGGLGPKEKGRARGRERRRKMQLTRCCFVFLVQ GSLYLVIGGDDGPPGSEDPERDDHEGOPRPRVRRKGHISPKS RPMANSTLLGLLAPPGEARGILGOPPNEPNHSPPSAKVKKIFG WGDFYSNIKTVALNLLVTGKIDHENGTSVHYCHMATGQGNIS ISLVPPSKAVEFFIGEQQIFIRAKASKIFNC\RWEWEKVE\AGRR TSLFFTHPAKICSRDHAASSATWSCSQPFKVVCVYIAPYSTDYR LVQKVCPDYNYHSDTPYYPSG  6058  1  986  1  986  HPPSASLGLPSVSLOVSLCVRSALLEAVVPMCHKRRARVGSP SGDAASSTPPSTTFPGVAITYLVEFMGRSRRAFLTGLARSKGFR VLDACSSEATHVVMEETSAERAVSWQERRMAAAPPGCTPPALLD ISMLTELGAGQVEVPUCHRLEVAGPSKOPLSPAMMPAYACOR PTPLTHHNTGLSEALEILARAGFGSGGRLTFCCAASVLKAL PSPVTTLSQLQGLPHFGEHSSRVVQELLERGVCEVERVRSSP VLDACSSEATHVVMEETSAERSRVVQCLLERGVCEVERVRSSP SGEAGPMASINCTLDPSASTP ONIGDSCLGLEFEGGGGLPYCOPCDKSFTRLSYLKRHEGIH SDKLFTGIGVVKTADRWYREGLRTLORGVKTGDCPQKLTQQCKAGBP SREAGPMASINCTLDPSASTP ONIGDSCLGLEFEGGGGLPYCOPCDKSFTRLSYLKRHEGIH SDKLFTGIGVVKTADRWYREGLRTLORGPSSTSLONMOAHKVNY SDKLFKCTYCSRLFKKRSRDRHIKLHTDGKKYGFGSTSSLONMOAHKNY				ERKYWKNLTFVAPIYGADINGSIYDEGVDEWNIADINTULDURE
LKKWG1FPKITDEAGEMHITPYGYHAGFHNGPKCAESTNFAT  URWIDYGKUAKLCTCRKDWYKISMDIFVRKPQPDRYQLMKQGKD  IYTIDHTKPTPASTPEVKAMLQRRKVKRASRSPQCARSTSKRP  KADDEEEVSDEVDGAAVENPDSVTDLKVSKKSEAAVKLRNTEA  SSEESSASRMQVEQNLSDHIKLSGNSCLSTSVTEDLKTEDDKA  YAYKSVPSISSEADDSIPLSTGYEKPEKSDPSELSWPKSPESCS  SVAESNGVLTEGEESDVESHANGLEPGEIPAVPSGERNSFKVPS  IABGENKTSKSWRHPLSRPPARSPMTLVKQQAFDGELBPVLSI  GERVEETESWAKPLLHLWGYTUPFAAGGFWATVARMKPHCAI  CTLLMPYHKPDSSNEENDARWETKLDEVVTSEGKTKPLIPEMCP  IYSEENIEYSPPNAPLEEDGTSLLISCAKCCVRVHASCGIPSH  EICDGWLCARCKRNAWTAECCLCHLRGGALKQTKNKWAHVMCA  VAVPEVRFTNVERTQIDVGRIPLQRIKKGIFCRIRVKRVSGA  CIQCSTGRCPASFHVTCAHAGAVLAMEDDDWPYVAVITCTRIRVKNSGA  VAYPEVRFTNVERTQIDVGRIPLQRIKKGIFCRIRVKRVSGA  AXYFGSNIAHMYQVEFEDSGJAHKRBDITTLDEELPKRVKAFF  VSAGRCHLGTCQVNSLSSPHVSQAQQETYLGFWINSKXSQCNIF  LSGTY  6057  1 853  FVARLKEQEGEGGLGPRKEKGRARGRERRRKMQLTRCCFVFLVQ  GSLYLVIGGDDGPFGSEDERDDHEGOPRRVPNKRGHISFKS  RPMANSTLIGLLAPGEGAMGIGPPRRYPNKRGHISFKS  RPMANSTLIGLLAPGEGAMGIGPPRRYPNKRGHISFKS  RPMANSTLIGLLAPGEAWGILGGPPRRYPNKRGHISFKS  RPMANSTLIGLLAPGEAWGILGGPPRRYPNKRGHISFKS  RPMANSTLIGLLAPGEAWGILGGPPRRYPNKRGHISFKS  RPMANSTLIGLLAPGEAWGILGGPPRRYPNKRGHISFKS  RPMANSTLIGLLAPGEAWGILGGPPRRYPNKRGHISFKS  RPMANSTLIGLLAPGEAWGILGGPPRRYPNKRGHISFKS  RPMANSTLIGLAPGEAWGILGGPPRRYPNKRGHISFKS  RPMANSTLIGLLAPGEAWGILGGPPRRYPNKRGHISFKS  RPMANSTLIGLLAPGEAWGILGGPPRRYPNKRGHISFKS  RPMANSTLIGLLAPGEAWGILGGPPRRYPNKRGHISFKS  RPMANSTLIGLLAPGEAWGILGGPPRRYPNKRGHISFKS  RPMANSTLIGLLAPGEAWGILGGPPRRYPNKRGHISFKS  RPMANSTLIGLLAPGEAWGILGFRANGESGPPKVVCVVIAFYSTDYR  LUQKVCDDYNYHSDTPYYPGG  6058  1 986  HELPSALGLGPVYDVCRHILELYGPSKOPLSPAMMPAYACQR  PPPLTHINTGLSEALEILAEAAGFEGSEGRLLTFCRASVLKAL  PSPVTTLSQLQGLPHGEHISRVVQELEHGVCEVERVRRSF/  VLDACSSEATHVVMEETSAGEAPSWQERMMAAPPGCTPPALLD  ISWLTESLIGAGQVPVPCCHRILELYGPSKGPLSPAMMPAYACQR  PPPLTHINTGLSEALEILAEAAGFEGEGGRLTFCRASVLKAL  PSPVTTLSQLQGLPHGGEHSRRVQELEHGVCEVERVRRSF/  SERAGPMASLNCTLDPSAGTP  OMFESSLADITOHRARECPGDGDDDPQLSWVASSPSSKDVASPT  OMIGDGCDLGLEGEGGTGLPVPQCFCKSFIRLSYLKREGIH  SDKLPFKCTYCSSLFKHKRSRDPRHIKLHTGKYCHGUECRAPS				EECGISIEGVNTPYLYFGMWKTTFAWHTEDMDLYSTNYLHPGER
LKKYGI-PFKITQEAGEBHITPYGYHAGFHGFNCAESTMFAT VRWIDVGKVAKLCTCRKDWYKISMI PVRKPQPDPYQLWKQKU IYTIDHTKPTPASTPEVKAWLQRRRKVRKASRSFQCARSTSKRP KADEBEEVSDBVDGAEVENPDSVTDDLKVSEKSEAAVKLRNTER SSEEESSASRMOVEONLSBHI KLIGONSCLSTSVTEDLKTEDDKA YAYRSVPSISSEADDSIPLSTGYERPEXSDSELSWPKSPESCS SVAESNGVLITEGEESDVESHGNGLEPGEIPAVPSGERNEFKVPS IAEGEMKTSKSWRHPLSRPPARSPMTLUKQQAPSDEELPBVLGI EEEVETESWAKPLIHLWOTKPPRFAABGYNATVARMKPHCAI CTLLMPYHKPDSSNEENDARWETKLDEVYTSEGKTKFLIPEMCF IYSEENIEYSPPNAPLEEDGTSLLISCAKCCVEVHASCYGITSH EICDGWLCARCKRNAWTAECCLCNLRGGALKQTKNNKWAHVMCA VAVPBVFTNVPSETQIDVGRIPLOFALKLKCIFCRHVKRVSGA CIQCSYGRCPASFHVTCAHAAGVL\MEPDDWPYVVNITCFRHKV NPNVKSKACEKVISVGGTVITKHNNTHYSCRWAAVTSGTFFEV WFDDGSFSRDTFPBDIUSRDCLKAPPAGECWYWRPDGKLYG AKYFGSNIAHMYQVEFBIGSGLAMKRBDIYTLDEELPKRVKARF VSAGRCHLGTCQVNSLSSPHVSQAQCETTLGFWINKSCAGCTIF LSGTY  6057  1 853 FVARLKEGEGGLGPRKEKGRAARGRERRKWDLTRCCFVPLVQ GSLYLVICGODDGPPGSEDPBROUHGOOPPRRVPRKRGHISPKS RPMANSTLLGLLAPPGEAWGILGOPPNRNHSPPSAKVKKIFG WGDFYSNIKTVALNLLUTGKIVDHGNGTTSVHFQHNATGGONIS ISLVPPSKAVEFHGQOIFTERAKIFMC\MEMEKVE\RGRR TSLFTHPPAKICSRDHAJSSATWSCSQPPKVVCVYIAPYSTDYR LVQKVCPDYNYHSDTPYYPSG  6058  1 986 HELPSASLGLPSVSLGVSLCVRSALLEAVVPMLPKRRRARVGSP SGDAASSTPPSTRPGVAITLVEPRGRSGRAFLTGLARSKGFR VLDACSSATHVVMEETSAEZAVSWGERRMAAAPPGCTPPALLD ISWLTESLGAGQVPVPCCRRILEVAGPSKGPLSPAMMPAYACOR PTPLTHHNTGLSEALEILABAGFGESGGRLLTFCRAASVLKAL PSPVTTLSQLQGLPHFGGHSRRVQAERRMAAPPGCTPPALLD ISWLTESLGAGQVPVPCRRRLEVAGPSKGPLSPAMMPAYACOR PTPLTHINTGLSEALEILABAAGFGESGGRLLTFCRAASVLKAL PSPVTTLSQLQGLPHFGGHSRRVQAERREAAPSPGCTPPALLD ISWLTESLGAGQVPVPCRRRLEVAGPSKGPLSPAWMPAYACOR PTPLTHINTGLSEALEILABAAGFGESGGRLLTFCRAASVLKAL PSPVTTLSQLQGLPHFGGHSRRVQAERREAAPSPGCTPPALLD ISWLTESLGAGQVPVPCRRRLEVAGPSKGPLSPAMMPAYACOR PTPLTHINTGLSEALEILABAAGFGESGGRLLTFCRAASVLKAL PSPVTTLSQLQGLPHFGGEBSRVQUELVEVRSB/ SERAGPWASLNCTLDPSASTP COURTESAADLTDLBSASTP COURTESAADLTDLBSASTP SKDLKKTYCKSRLFKKKRSRDRHIKLHTGDKYHCGECELRAPS RSDALKHLKTHSSSSRPFKCTVCKRGFSSTSSLOSHMOAHKKWY	1			KSWYAIPPEHGKRLERLAOGFFPSSSOGCDARLDWWATLTCDCV
VRMIDYGKVAKLCTCRKDWYKISMDIFVRKPOPDRYQLWKQGKO IYTIDHTKPTPASTPEVKAMLORRRKVRKASRSFQCARSTSKRP KADBEEEVSDEVDGAEVPNPDSVTDDLKVSKKSEAAVKLRNTEA SSEEESSASRMOVEONLSDHIKLGGNSCLSTSVTEDIKTEDDKA YAYKSVPSISSEADDSIPLSTGYERPEKSDDSELSJWKSPESCS SVAESNGVLTEGEESDVESHGNGLEPGEIPAVPSGERNSFKVPS IABGEKKTSKSWRHPLSRPARSPMTLVKQOAPSDEELBFULSI EERVEETESWAKPLHLWGTVPPNFAARGEVNATVAAMKPHCAI CTLLMPYHKPDSSNEENDARWETKLDEVVTSEGKTKPLIPEMCP IYSEENIEYSPPNAFLEEDGTSLLISCAKCVRVHASCYGIPSH EICDGMLCARCKRNAWTAECCLCHLRGGALKQTKNKWAHVMCA VAVPEWFFTNVPERTOIDVGRIPLGALKKCIFCRHRVKRVSGA CIQCSYGRCPASFHVTCAHAAGVT\MSPDDPVVVNITCFRHKV MPDMSFSRDTFPBDIVSRDCLKLGPPAEGEVQVVKWPDGKLYG AKYFGSNIAHMYQVEFEDGSQIAWKEDIYTLDEELPKKVKAFF VSAGRCHLGTCQVNSLSSPHVSOAQQETYLGFWINSKKSQCNIF LSGTY GSLYLVICGQDDGPPGSEDEERDHEGOPRPRVPKRCHISFKS RPMANSTLIGLIAPPGEAWGILGGPPNRPNHSPPPSAKVKXIFG GSLYLVICGQDDGPPGSEDEERDHEGOPRPRVPKRCHISFKS RPMANSTLIGLIAPPGEAWGILGGPPNRPNHSPPPSAKVKXIFG GSLYLVICGQDDGPPGSEDEERDHEGOPRFRVPKRCHISFKS RPMANSTLIGLIAPPGEAWGILGGPPRRVPKRCHISFKS RPMANSTLIGLIAPPGEAWGILGGPPRRVPKRCHISFKS RPMANSTLIGLIAPPGEAWGILGGPPRRVPHSPPSAKVKXIFG GSLYVVCOPDYNHSDTYPYPSG GDAASSTPPSTRPFGVAITLVEPRMGSRSRAFITGGLARSKGFR TSLFTHDPAKICSRDHAQSSATWSCSQPPKVVCVYIAPFSTDVR LVGKVCPDYNHSDTYPYPSG SGDAASSTPPSTRPFGVAITLVEPRMGSRRFFLTGGLARSKGFR SGDAASSTPPSTRPFGVAITLVEPRMGSRRFFLTGGLARSKGFR PPTPLTHHNTGLSEALEILAEAGFGSSGGLLTFCRAASKURAL PSPVTTISQLOGGLPHGEHSRYCWGEVERSPLICHCRAASKURAC PSPTTILSQLOGGLPHGEHSRAVGELBHGVCEEVERVRSB/ RLFTQIFGVGVKTADRWYREGLRTLDDLREGPGCEPVERVRSB/ RLFTQIFGVGVKTADRWYREGLRTLDDLREGPGCEPVERVRSB/ RLFTQIFGVGVKTADRWYREGLRTLDDLREGPGKLTGQOKAGBP SREAGPMASLNCTLDPSASTP OMIGGCCOLGGEEGGTGLPYPCQFCDKSFIRLSYLKREQIH SDKLPFKCTYCSRLFKHKRSRDRHIKLHTGKKYHGEGARAFS	1 1			LKKYGI?FDKITOEAGEFMITFPYGYHAGENUGENCAEGTNEAT
IYTIDHTKPTPASTPEVKANLQRRRKYRKASRSFQCARSTSKRP KADBEEEVSDEVDSAEVVPNDDVTDDLKVSEKSEAAVKLRNTEA SSEEESSASRMQVEQNLSDHIKLSGNSCUSTSVTEDIKTEDDKA YAYKSYPSISSEADDSIPLSTGYEKEEXSPSELSBPKSPESGS SVAESNOVITEGEESDVESBUNGLEPGEIPAVPSGERNSFEKVPS LAEGENKTSKSMRHPLSRPPARSFMTLVKQQAPSDEELPEVLSI EEEVETESWAKPLIHLWQTKPPNFARAGGSYNATVARMKPHCAI CTLLMPYHKPDSSNEENDARWEYKLDEVVTSGKKTPFLIPEMCP IYSEENIEYSPPNAFLEEDGTSLLISGAKCCVRVHASCYGIPSH EICDGMLCARCKRNAWTAECCLCNLRGGALKQTKNKWAHVWCA VAVPEVRFTNVEERTQIDVGRIPLOKLKCIFCRHRVKRYGGA CIQCSYGRCPASFHYTCAHAAGULYNEPDWPYVVNITCPRHKV NPAVKSKACEKVISVQGTVITHRHRNTRYYSCRVMAVTSQTFYEV MFDDGSFSRDTFPEDIVSRDCLKLGPPAEGEVQVXWPDGKLYG AKYFGSNIAHMYQVEFEDGSQIAMKREDIYTLDEELPKRVKARF VSAGRCHLGTCQVNSLSSPHVSQAQQETYLGFWINSKKSQCNIF LSGTY  FVARKKEQEEGGLGPRKEKGRARGERRRKMQUTRCCFVFLVQ GSLYLVICGQDDGPPGSEEDPERDDHEGOPRRVPRKRGHISPKS RPMANSTLIGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKIFG WGDFYSNIKTVALNLLVTGKIVDHGNGTFSVHFQHNATGQCNIS ISLVPPSKAVEFHGEQQIFIBRKASKIFNCYRMEWEKVB.FGRR TSLFFHDPAKICSRDHAGSSATWSCSQPPKVVCVYIAPYSTDYR LUQKVCPDYNYHSDTPYYPSG  6058  1  986 HPLPSASIGLPSVSLGVBLCVRSALLEAVVPMLPKRRRARVGSP SGDAASSTPPSTRFFGVAIYLVEPRMGRSRRAFLTGLARSKGFR VLDAKSEATHLVWBETSAEEAVSWQERRMAAAPPGCTPPALLD ISWLTESLGAGQPVPVECRHRLEVAGPSKGPLSPAMMPAYACQR PTPLTHHNTGLSEALEILAEAAGFEGSGRILTTCRAASVLKAL PSPVYTLSQLGGLPHFGEHSSRVVQGLLEHGVCEEVERVRRSE/ RLFTQIFGVGVKTADRWYRGSLRTLDDLREGPQKLTQCRAGGP SREAGPMASINCTLDPSASTP GNIGDGCDLGLGEEGGTGLPYPCQCCKSFIRLSVLKREQIH SDKLPFKCTYCSRLPKKKRSRDRHIKLHTDKKYHCHECEDARS RSDKLKHLKHTRSSKPFKCVCKRGFSSTSLOSMOMANKNYK	] i			VRWIDYGKVAKLCTCRKDMVKISMDIFURKFOPDRVOLWKOGKD
SEBESASARMOVEQNLISHLIKGSINSCLSTSVTEDIKTEDDKA SSEBESASARMOVEQNLISHLIKGSINSCLSTSVTEDIKTEDDKA YAYRSVPSISSEADDSIPLSTGYEKEEKSDPSELSWPKSPESGS SVAESMOVLTEGEESDVESHGNGLEPGEIPAVPSGERNSPKVPS IAEGENKTSKSWRHPLSRPPARSPMTLVKQOAPSDEELPEVLSI EEEVEETESWAKPLIHLWQTKPPNFAAEGEYNATVARMKPHCAI CTLLMPYHKPDSSNEENDARWETKLDEVVTSEGKTKPLIPEMGF IYSEEMIE YSPPNAFLEEDGTSLLISCAKCCVRYHASCYGIPSH EICOGMLCARCKRNAWTAECCLCNLRGGALKQTKNNKKMAHVMCA VAVPBVRFTNVERTQIDVGRIPLORLKKCTFCRHRVKRVSGA CIQCSYGRCPASFHYTCAHAGUL/NEPDDWPVVMITCPRIKV NPNVKSKACEKVISVGQTVITKHRNTRYYSCRVMAVTSQTFYEV MFDDGSFSRDTFPBDIVSRDCLKLGPPAGEGVVQVKMPDGKLYG AKYFGSNIAHMYQVBFEDGSQLMKRBDIYTLDEELPRKVKRFF VSAGRCHLGTCQVNSLSSPHVSQAQQETYLGFWINSKXSQCNIF LSGTY FVARLKEQEGEGGLGPRKEKGRARGRERRRKMQLTRCCFVFLVQ GSLYLVICQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISFKS RPMANSTLLGLLAPPGBANGILGQPPNAPNHSPPPSAKVKNIFG WGDFYSNIKTVALNILLVTGKIVDHGNGTFSVHFQHNATGQONIS ISLVPPSKAVEFHQEQQIFIBAKASKIFNC\RMEWEKVE\RGRR TSLFTHDPAKICSRDHAQSSATWSCSQPFKVVCVYIAPYSTDYR LVQKVCPPYNHSDTPYYPSG SGDAASSTPPSTRPFGVAIYLVEPRMGSRRAFITGLARSKGFR VLDACSSEATHVVMEETSAESAVSWGERRMAAPPGCTPPALLD ISWLTESLGAGQPVPVECRHRLEVAGPSKGPSERLUTTCRAASVIKAL PSPVTTLSQLGGLPHFGEHSSRVVQELLEHGVCEVERVRRSB/ RLFTQIFSVGVKTADRWYRBGLRTLDDLREQPQKLTQQCKAGBP FSPVTTLSQLGGLPHFGEHSRVVQELLEHGVCEVERVRRSB/ RLFTQIFSVGVKTADRWYRBGLRTLDDLREQPQKLTQQCKAGBP SREAGPWASLNCTLDPSASTP GNIGGGCLGLGEEGGTGLPYPCQFCKSFIRLSYLKRHEQIH SDKLPFKCTYCSRLFKKKRSRDRHIKLHTGKKYHCHECEAARS RSDALKHLKTHESSEPFKCTVCKRGFSSTSLOSMOANKKNYK				IYTIDHTKPTPASTPEVKAWLORRRKVRKASRSEOCARSTSKER
SSEEESSARMQVBQNLSDHIKLEGNSCLSTSVTEDIKTEDDKA YAYKSVPSISSEADDSS PLSTGYEKPEKSDPSELSWPKSPESCS SVAESNGVLTEGEESDVESHGNGLEPGET PAVPSGERNSFKVPS IAEGENKTSKSWRHPLSRPPARSPMTLVKQOAPSDEELPBVLSI EEBVETTESWAKPLIHLWQTKPPNFAAEQEYNATVARMKPHCAI CTLLMPYHKPDSSNEENDARWETKLDEVVTEGKTKPLIPEMCF IYSEBHIEYSPPNAFLEEDGTSLLISCAKCCVGVARASCYGIPSH EICCGMLCARCKRNAWTAECCLCNLRGGALKQTKNNKWAHYMCA VAVPEVRFTNVPERTQIDVGRIPLQRLKLKCIFCRHRVKRVSGA CIQCSYGRCPASFHVTCAHAAGVL\MEPDDMPYVVNITCFRHKV NPNVKSKACEKVISVGQTVITKRNTRYYSCRVMAVTSQTFYEV MFDDGSFSRDTFPEDIVSRDCLKLGPPAEGEVQOVKWPDGKLYG AKYFGSNIAHMYQVEFEDGSQIAMKREDIYTLDEELPKRVKARF VSAGRCHLGTCQVNSLSSPHVSQAQETYLGFWINSKKSQCNIF LSGTY  FVARLKEQEGEGGLGPRKEKGRARGRERRKMQLTRCCFVFLVQ GSLYLVICGQDDGPPGSEDPERDDHEGOPAPRVPRKRGHISPKS RPMANSTLIGLLAPPGEAMGILGOPPNR PHNSPPSAKVKKIFG WGDFYSNIKTVALINLLVTGKIVDHGNGTFSVHPQHNATGQGNIS ISLVPPSKAVEFHQEQQIFIERAKASIFINC\RMEWEKVE\RGRR TSLFFHDPAKICSRDHAQSSATWSCSQPFKVVCVYIAFYSTDYR LVQKVCPDYNYHSDTPYYPSQ  6058  1  986 HPLPSASIGLESVSIGVSLCVRSALLEAVVPMLPKKRRARVGSP SGDAASSTPSTRFPCAVITYLVEPRMGRSRAFLTGLARSKGFR VLDACSSEATHVVMEETSAEZAVSMCERRMAAAPPGCTPPALLD ISWLTESLGAGGPVPVECHRLEVAGPSKGPLSPAMMPAYACQR PTPLTHHNTGLSEALEILAEAAGFEGSEGRLTFCRAASVLKAL PSPVTTLSQLGGLEHFGEHSSRVVQELLEHGVCEEVERVERSE RLFTQIFGVGVKTADRWYREGLRTLDDLREQPQKLTQQKAGBP SREAGPWASINTLDPSASTP OQPFSIADLTDHRAHRCPGGCDDDDPOLSWVASSPSKDVASFT QNIGGGCLGLIGEEEGGTGLPYPCQFCDKSFIRLSYLKRHEQIH SDKLPFKCTYCSRLFKHKRSRDRHLKHTGDKKYNCHECENAFS RSDHLKHLKTHSSSKPFKCTYCKRGFSSTSSLOGHMOANKNW	l i			KADBEEEVSDEVDGAEVPNPDSVTDDLKVSEKSEAAVKI. PNTEA
SVARSNOVLYGGESDUSHPEKSPESGESGENBPKSPESGS SVARSNOVLYGGESSDUSHPEKSDESHGNGLEPGEIPAVPSGERNSFKVPS IAEGENKTSKSWRHPLSRPPARSPMTLVKQQAPSDEELPEVLSI EERVEETESWAKDLIHWQTKPPNFAARGEYNATVARMKPHCAI CTLLMPYHKPDSSNEEDDARMETKLDEVVTSEGKTKPLIPEMCP IYSEENIEYSPPNAFLEEDGTSLLISCAKCCVRVHASCYGIPSH EICDGMLCARCKRNAWTAECCLCHRGGALKQTKNNKWAHVMCA VAVPEVRFTNVERTQLDVGRIPLORLKLKCIFCRHRVKRVSGA CIQCSYGRCPASFHVTCAHAAGVL\MEDDDWPYVVNITCFRHKV NPRVKSKACEKVISVGGTVITKHRNTRYSCRVMAVTSGTFYEV MPDDGSFSRDTPPBDIVSCDLKLGPPAEGEVVQVKWPDGKLYG MPDDGSFSRDTPPBDIVSCDLKLGPPAEGEVVQVKWPDGKLYG AKYFGSNIAHMYQVEFEDGSQLMKRBDIYTLDEELPKRVKARF VSAGRCHLGTCQVNSLSSPHVSQAQQETYLGFWINSKXSQCNIF LSGTY  6057  1 853 FVARLKEQEGEGLGPRKEKGRARGRERRRKMQLTRCCFVFLVQ GSLYLVICQODDGPPGSEPPERDHEGOPRPRVPRKGHISPKS RPMANSTLLGLLAPPGGAWGILGQPPNRPNHSPPPSAKVKKIFG WGDFYSNIKTVALNLLVTGKIVDHGNGTFSVHFQHNATGQCNIS ISLVPPSKAVEFHQEQQIFIEAKASKIFNC\RMEWEKVE\RGRR TSLFTHDPAKICSRDHAQSSATWSCSQPFKVVCVYIAFYSTDYR LVQKVCPPYNYHSDTPYYPSG  6058 1 986 HPLPSASLGLPSVSLGVSLGVSLGVSLGVKSALLEAVVPMLPKRRRARVGSP SGDAASSTPPSTRPPGVAIYLVEPRMGRSRRAFLTGLARSKGFR VLDACSSEATHVVMEETSAEEAVSWQERRMAAAPPGGTPPALLD ISWLTESLGAGQPVPVECHRILEVAGPSKGPLSPAMMPAYACQR PTPLTHHNTGLSEALEILAEAAGFEGSGCRLLTFCRAASVLKAL PSPPTTLSQLGGLPHIFGEHSRVVQELLERGVCEEVERVRSB/ RLFTQIFGVGVKTADRWYREGLRTLDDLREQPQKLTQQKAGEP SREAGPWASLNCTLDPSASTP QNIGGCCLGLGEEGGTGLPYPCQFCDKSFIRLSYLKRHEGIH SDKLPFKCTYCSRLFKHKRSRDRHLKLHTGDKKYNCHECENAFS RSDHLKHLKTHSSKPFKKTKSTSSLOSHMOANKNW	[ [	1		SSEEESSASRMOVEONLSDHIKLSGNSCLSTSVTFDTKTFDDVA
SVARSNOVLTEGESDVESHGNLEPGEIPAVPSGERNSFKVPS IAEGENNISKSWHPLSRPPARSPMTLVKQQAPSDEELPEVLSI EEEVETESWAKPLIHLWQTKPPNFAAEGSYNATVARMKPHCAI CTLLMPYHKPDSSNEENDARWETKLDEVVISEGKTKPLIPEMCP IYSEENIEYSPPNAFLEEDGTSLLISCAKCCVRVHASCYGIPSH EICDGWLCARCKRNAWTAECCLCNLREGALKQTKNRKNAHVMCA VAVPBVRFTRVPERTQIDVGRIPLORLKLKCIFCRHRVKRVSGA CIQCSYGRCPASFHVTCAHAAGVL\MEPDDWPYVVNITCPRHKV NPNVKSKACEKVISVGQTVITHRNTRYYSCRWAMVISQTPYEV MFDDGSFSRDTFPBDIVSRDCLKLGPPAEGEVVQVKWPDGKLYG MFDDGSFSRDTFPBDIVSRDCLKLGPPAEGEVVQVKWPDGKLYG MFDDGSFSRDTFPBDIVSRDCLKLGPPAEGEVVQVKWPDGKLYG AKYFGSNIAHWQVEFEDGSQIAMKREDIYTLDEELPKRVKRAF VSSAGCHLGTCQVNSLSSPHVSQAQQETYLGFWINSKKSQCNIF LSGTY  6057  1 853 FVARLKEQEGEGGLGPRKEKGRARGRERRKMQLTRCCFVPLVQ GSLYLVICGQDDGPPGSEDPERDDHEGQPPRRVPKKRGHLSPKS RPMANSTLLGLLAPPGEAWGILGQPPNRNHSPPPSAKVKKIFG WGDFYSNIKTVALNLLVTGKIVDHGNGTFSVHFQHNATGQGNIS ISLVPPSKAVEFHQEQQIFIEAKASKIFNC\RMEWEKVER,RGRR TSLFTHDPAKICSRDHAQSSATWSCSQPFKVVCVYIAFYSTDYR LVQKVCPPVNYHSDTPYYPSG  6058 1 986 HPLPSASLGLPSVLGVSLCVRSALLEAVVPMLPKRRRARVGSP SGDAASSTPSTRFPGVAIVLVEPRMGRSRRAFLTLLARSKGFR VLDACSSEATHVVMEETSAEZAVSWQERRMAAAPPGCTPPALLD ISWLTESLGAGQPVPVECRRLEVAGPSKGPLSPAWMPAYACQR PTPLTHHNTGLSEALEITAGAGFGSGEGRLLTFCRAASVLKAL PSPVTTLSQLQGLPHFGEHSSRVVQELLEHGVCEEVERVRRSS/ RLFTQIFGVGVKTADRWYRGGLRTLDDLREQPQKLTQQQKAGEP SREAGPMASLNCTLDPSASTS GREAGPWASLNCTLDPSASTS OQPFSLADLTDHRAHRCPGDGDDDPQLSWVASSFSSKDVASFT QNIGDGCDLGLGEEEGGTGLPYPCQFCDKSFIRLSYLKRHEQIH SDKLJPFKCTYCSRLFFKHKRRSDRAHKLHTGDKKYHCHSCEAAFS RSDBLKHLKTHSSSKPFKTYCKRGFSSTSSLOSHOAAPKNYK	]			YAYRSVPSISSEADDSIPLSTGYEKPEKSDPSELSWPKSDEGG
IABGENKTSKSWRHPLSRPMRASPMTLVKQQAPSDEELPBULGI EEEVEFTESWAKPLIHLWOTKPPNFAABQEYNATVARMKPHCAI CTLLMPYHKPDSSMEENDARWETKLDEVYTSEGKTKPLIPEMCF IYSEENIEYSPPNAFLEEDGTSLLISCAKCCVRVHASCYGIPSH EICDGWLCARCKRNAWTAECCL.CHLRGGALKQTKINKKAHVMCA VAVPBVRFTRVPERTOIDVGRIPLORGRAIKQTKINKKAHVMCA CIQCSYGRCPASFHVTCAHAAGVL\MEPDDWPYVNTTCFRHKV NPRVKSKACEKVISVGQTVITHRNTRYYSCRMAVYTSQTFYEV MFPDGSFSRDTFPBDIVSRDCLKLGPPAEGEVVQVKWPDGKLYG AKYFGSNIAHMYQVEFEDGSQIAMKREDIYTTLDEELPKRVKRAF VSAGRCHLGTCQVNSLSSPHVSQAQQETYLGFWINSKKSQCNIF LSGTY  6057  1 853 FVARLKEQEGEGGLGPRKEKGRARGRERRKMQLTRCCFVFLVQ GSLYLVICGQDDGPPGSEDPERDDHEGGPRPRVPRKRGHISPKS RMANSTLLGLLAPPGEAWGILGPPNRPNHSPPPSAKVKKIFG WGDFYSNIKTVALNLLVTGKIVDHGNGTFSVHFQHNATGGGNIS ISLVPPSKAVEFHQEQQIFIRAKASKIFNC\RMEXEVE\RGRR TSLFTHDPAKICSRDHAQSSATWSCSQPPKVVCVYIAFYSTDYR LVQKVCPDYNYHSDTPYYPSG  6058 1 986 HPLPSASLGLPSVSLGVSLCVRSALLEAVVPMLPKRRRARVGSP SGDAASSTPPSTRFPGVAIYLVBPRMGRSRRAFLTGLAKSKGFR VLDACSSEATHVVMEBTSABEAVSWQERRMAAPPGCTPPALLD ISWLTESLGAGQPVPVECRRIELEVAGPSKGPLSPAWMPAYACQR PTPLTHHNTGLSEALBILAEAGFEGSGRLLTFCRAASVLKAL PSPVTTLSQLQGLPHFGEHSSRVVQELLEHGVCEEVERVRSE/ RLFTQIFGVGVKTADRWYRGBLRTLDDLREQPQKLTQQQKAGBP SREAGPWASJNCTLDPSASTP 6059 2 3650 QQDFESLADLTDHRAHRCPGDGDDDPQLSWVASSFSKDVASFT QNIGDGCDLGLGEEEGGTGLPYPCQFCDKSFIRLSYLKRHEQIH SDKLJPFKCTYCSRLFKHKRSRDRHIKLHTGDKKYHCHECEAAFS RSDBLKHLKTHSSSKPFKCTVCKRGFSSTSSLOSHMOAHKWVK				SVAESNGVLTEGEESDVESHGNGLEPGEIPAVPSGERNSRKUPS
CTLLMPYHKPDSSNEEMDARWETKLDEVVTSEGKTKPLIPEMCF IYSEBNIEYSPPNAFLEEDGTSLLISCAKCCVRVHASCYGIPSH EICDGWLCARCKRNANTAECCLCNLRGGALKQTKNKWAHVMCA VAVPEVRFTNVPERTQIDVGRIPLORLKLKCIFCRHRVKRVGGA CLQCSYGRCPASFHVTCAHAAGVL/MEPDDWPYVNITCPRHKV NPNVKSKACEKVISVGQTVITKHRNTRYYSCRVMAVTSQTFYEV MFDDGSFSRDTFPBDIVSRDCLKLGPPABGBVVQVKWPDGKLYG AKYFGSNIAHMYQVEFEDGSQLAMKREDIYTLDEELPKRVKRVGA AKYFGSNIAHMYQVEFEDGSQLAMKREDIYTLDEELPKRVKRVGR AKYFGSNIAHMYQVEFEDGSQLAMKREDIYTLDEELPKRVKRYGF VSAGRCHLGTCQVNSLSSFHVSQAQQETYLGFWINSKXSQCNIF LGGTY  FVARLKEQEGEGGLGPRKEKGRARGRERRRKMQLTRCCFVFLVQ GSLYLVICGQDDGPPGSEDPERDDHEGQPPRRVPKRGHISPKS RPMANSTLLGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKIFG WGDFYSNIKTVALNLLLVTGKUTDHGNGTFSVHFQHNATGGGNIS ISLVPPSKAVEFHGEQOIFIBAKASKIFNC\RMEWKVE\RGRR TSLFTHDPAKICSRDHAQSSATWSCSQPFKVCVYIAFYSTDVR LVQKVCPDYNYHSDTPYYPSG  6058  1 986 HPLPSASLGLPSVSLGVSALLEAVVPMLPKRRRARVGSP SGDAASSTPPSTRFPGVAIYLVEPRMGRSRRAFTTGLARSKGFR VLDACSSEATHVVMEETSAEEAVSWQERRMAAAPPGCTPPALLD ISWLTESLGAGQPVPVECHELEVAGPSKGPLSFAWMPAYACQR PTPLTHHNTGLSEALEILAEAAGFEGSEGRLLTFCRAASVLKAL PSPVTTLSQLQGLPHFGEHSRVVQELLEHGVCEEVERVRSE/ RLFTQIFGVGVKTADRWYREGLRTLDDLREQPQKLTQQCKAGBP SREAGPWASJNCTLDPSASTP  6059  2 3650 QQFESLADLTDHRARRCPGCBDDDPQLSWVASSPSSKDVASPT QNIGDGCLIGLGEEGGTGLBYPCQFCDKSPIRLSYLKRHEQIH SDKLJFKCTYCSRLFHKKRSRRHIKLKHTOKKYHCHECEAAFS RSDHLKHLKTHSSSRPFKCTVCKRGFSSTSSLOSHMOAHKWNK		į.		IAEGENKTSKSWRHPLSRPPARSPMTLVKOOAPSDEELPRVLST
CTLLMPYHKPDSSNEENDARWETKLDEVVTSEGKTKPLIPEMCF IYSEENIEYSPPNAPLEEDGTSLLISCAKCCVRVHASCYGIPSH EICDGMLCARCKRNAWTAECCLCNLRGGALKGYKNNKWAHVMCA VAVPEVRFTNVPERTQIDVGRIPLORLKLKCIFCRHRVKRVSGA CIQCSYGRCPASFHVTCAHAAGVL\MEPDDWPYVVNITCPRHKV NPNVKSKACEKVISVGQTVITKHRNTRYYSCRVMAVTSQTFYEV MFDDGSFSRDTFPEDIVSRDCLKKGPPAEGEVVQVKWPDGKLYG AXYFGSNIAHMYQVEFEDGSQIAMKREDIYTLDEELPKRVKARF VSAGRCHLGTCQVNSLSSPHVSQAQQETYLGFWINSKKSQCNIF LSGTY  6057  1 853 FVARLKEQEGEGGLGPRKEKGRARGRERRKMQLTRCCFVFLVQ GSLYLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKS RPMANSTLLGLLAPPGEAWGILGQPPNRPNHSPPSAKVKKIFG WGDFYSNIKTVALNLLVTGKIVDHGNGTFSVHFQNNATGGGNIS ISLVPPSKAVEFHQEQQIFIEAKASKIFNC\RMEWEKVE\RGRR TSLFTHDPAKICSRDHAQSSATWSCSQPFKVVCVYIAFYSTDYR LVQKVCPDYNYHSDTPYYPSG  6058 1 986 HPLPSASLGLPSVSLGVSLCVRSALLEAVVPMLPKRRRARVGSP SGDAASSTPPSTRFPGVAIYLVEPRMGRSRRAFLTGLARSKGFR VLDACSSEATHVVMEETSAEEAVSWQERRMAAAPPGCTPPALLD ISWLTESLGAGQPVPVCRHRLEVAGPSKGPLSPAMMPAYACQR PTPLTHHNTGLSEALEILAEAAGFEGSEGRLLTTCRAASVLKAL PSPVTTLSQLQGLPHFGEHSSRVVQELLEHGVCEEVERVRSE/ RLFTQIFGVGVKTADRWYRESLRTLDDLREQPQKLTQQQKAGEP SREAGPWASLNCTLIDPSASTP  6059 2 3650 QQDFSSLADLTDHRAHRCPGDGDDDPQLSWVASSFSSKDVASPT QNIGDGCDLGLGEEGGTGLPYPCQPCDKSFIRLSYLKRHEQIH SDKLPFKCTYCSRLFKHKRSRDRHIKLHTGKKYHCHECEAAFS RSDHLKHLKTHSSSRPFKCTVCKRGFSSTSSLOSHMOAHKWNK	1 1	ŀ		EEEVEETESWAKPLIHLWQTKPPNFAAEOEYNATVARMKPHCAT
I TYSEENLEYSPNAFLEEDGTSLLISCAKCCVRVHASCYGIPSH EICDGWLCARCKRNAWTABCCLCNLRGGALKQTKNNKWAHVMCA VAVPBVRFTNVPERTQIDVGRIPLQRLKLEGTCRHRVKRVSGA CIQCSYGRCPASFHVTCAHAAGVL\MEPDDWPYVVNITCFRHKV NPNVKSKACEKVISVGGTVITKHRNTRYYSCRVMAVTSQTFYEV MFDDGSFSRDTFPBDIVSRDCLKLGPPAEGEVVQVKWPDCKLYG AXYFGSNIAHMYQVEFEDGSQIAMKREDIYTLDEELPKRVKARF VSAGRCHLGTCQVNSLSSPHVSQAQQETYLDFWINSKKSQCNIF LSGTY  6057  1 853 FVARLKEQEGEGGLGPRKEKGRARGRERRKMQLTRCCFVFLVQ GSLYLVICGQDDGPPGSEDPERDDHEGQPPRVPNKKGHISPKS RPMANSTLLGLLAPPGEAMGILGQPPNRPNHSPPPSAKVKKIFG WGDFYSNIKTVALNLLVTGKIVDHGNGTFSVHPQHNATGQGNIS ISLVPPSKAVEFHQEQQIFIEAKASKIFMC\RMEWEKVE\RGRR TSLFTHDPAKICSRDHAQSSATWSCSQPPKVVCVYIAFYSTDYR LVQKVCPDYNYHSDTPYYPSG  6058 1 986 HPLPSASLGLPSVSLGVSLCVRSALLEAVVPMLPKRRRARVGSP SGDAASSTPPSTRPPGVAITJVEPRMGSSRAFLTGLARSKGFR VLDACSSEATHVVMEETSABEAVSWQERRMAAAPPGCTPPALLD ISWLTESLGAGQPVPVECHRLEVAGPSKGPLSPAWMPAYACQR PTPLTHHNTGLSEALEILAEAAGFEGSEGRLLTFCRAASVLKAL PSPVTTLSQLQGLPHFGEHSSRVVQELLEHGVCEEVERVRSB/ RLFTQIFGVGVKTADRWYREGLRTLDDLREQPQKLTQQQKAGEP SREAGPWASLNCTLDPSASTP OMIGDGCDLGLGEEGGTGLPYPCQFCDKSFIRLSYLKRHEQIH SDKLPFKCTYCSRLFKKNRSRDRHIKLHTGDKKYHCHECEANFS RSDKLKHLKKHESSKPPKCTYCKRGFSSTSSLOSHMOAHKKNK	1 1	ļ		CTLLMPYHKPDSSNEENDARWETKLDEVVTSEGKTKPLIPEMCR
EICDGWLCARCKRNAWTAECCL:CNLRGGALKQTKNNKWAHVMCA VAVPEVRFTNVPERTQIDVGRI PLQRLKKCI FCHRVKRVSGA CIQCSYGRCPASFHVTCAHAAGVI\MEPDDWPYVNI ITCPHKVV NPNVKSKACEKVISVGQTVITKHRNTRYYSCRVMAVTSQTFYEV MPDDGSFSRDTFPEDIVSRDCLKLGPPAEGEVQQVKWPDGKLYG AKYFGSNIAHMYQVEFEDGSQIAMKREDIYTLDEELPKRVKARF VSAGRCHLGTCQVNSLSSPHVSQAQQETYLGFWINSKKSQCNIF LSGTY  6057  1 853 FVARLKEQEGEGLGPRKEKGRARGRERRKMQLTRCCFVFLVQ GSLYLVICGQDDGPPGSEDPERDDHEGOPPRPVRFKGHISPKS RPMANSTLLGLLAPPGEAMGILGOPPNRPNHSPPPSAKVKKIFG WGDFYSNIKTVALNLLVTGKIVDHCNGTFSVHFQHNATGQGNIS ISLVPPSKAVEFHQEQQIFIEAKAGKIFMC\RMEWEKVE\RGRR TSLFTHDPAKICSRDHAQSSATWSCSQPPKVVCVYIAPYSTDYR LVQKVCPDYNYHSDTPYYPSG  6058  1 986 HPLPSASLGLPSVSLGVSLCVRSALLEAVVPMLPKRRRARVGSP SGDAASSTPPSTRPFGVAIYLVEPRMGRSRRAFLTGLARSKGFR VLDACSSEATHVVMEETSAEEAVSWQERRMAAAPPGCTPPALLD ISWLTESLGAGQPVPVECRHRLEVAGPSKGPLSPAMMPAYACQR PTPLTHHNTGLSEALEILAEAAGFEGSEGRLLTFCRAASVLKAL PSPVTTLSQLQGLPHFGEHSSRVVQELLEHGVCEEVERVRSB/ RLFTQIFGVGVKTADRWYREGLRTLDDLREQPQKLTQQQKAGEP SREAGPWASLNCTLDPSASTP QMIGDGCDLGLGEEGGTGLPYPCQFCDKSFIRLSYLKRHEQIH SDKLPFKCTYCSRLFKKNRSRDRHIKKLHTGDKKYHCHECEANFS RSDKLKHLKENSSKPPKCTYCKRGFSSTSSLOSHMOAHKKDK	1 1	ľ		IYSEENIEYSPPNAFLEEDGTSLLISCAKCCVRVHASCYGIPSH
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CIQCSYGRCPASFIVTCAHAAGVL\MEPDDWPYVVNITCFRHKV NPNVKSKACEKVISVGQTVITKHRNTRYYSCRVMAVTSQTFYEV MPDDGSFSRDTFPBDIVSRDCLKLGPPAEGEVVQVKWPDGKLYG AKYFGSNIAHMYQVEFEDGSQIAMKREDIYTLDEELPKRVKARF VSAGRCHLGTCQVNSLSSPHVSQAQQETYLGFWINSKKSQCNIF LSGTY  FVARLKEQEGEGGLGPRKEKGRARGRERRRKMQLTRCCFVFLVQ GSLYLVICGQDDGPPGSEDPERDDHEGOPRRVPRKRGHISPKS RPMANSTLLGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKIFG WGDFYSNIKTVALNLLVTGKIVDHGNGTFSVHFQHNATGQGNIS ISLVPPSKAVEFHQEQQIFIEAKASKIFNC\RMEWEKVE\RGRR TSLFTHDPAKICSRDHAQSSATWSCSQPFKVVCVYIAPYSTDYR LVQKVCPDYNYHSDTPYYPSG  6058  1  986  HPLPSASIGLPSVSLGYSLCVRSALLEAVVPMLPKRRRARVGSP SGDAASSTPPSTRPGVAIYLVEPRMGRSRAFLTGLARSKGFR VLDACSSEATHVVMEETSAEEAVSWQERRMAAAPPGCTPPALLD ISWLTESLGAGQPVPVECRHRLEVAGPSKGPLSFAWMPAYACQR PTPLTHHNTGLSEALETLAEAAGFEGSEGRLLTFCRAASVLKAL PSPVTTLSQLQGLPHFGEHSSRVVQELLEHGVCEEVERVRRSE/ RLFTQIFGVGVKTADRWYREGLRTLDDLREQPQKLTQQQKAGEP SREAGPWASLNCTLDPSASTP  OQDFESLADLTDHRAHRCPGDGDDDPQLSWVASSFSKDVASPT QMIGDGCDLGLGEEEGGTGLPYPCQFCCKSFIRLSYLKRHEQIH SDKLPFKCTYCSRLFKHKRSRDRHIKLHTGDKKYHCHECEANAFS RSDHLKIHLKTHSSSKPFKCTYCKRGFSSTSSLOSHMOAHKKNK				VAVPBVRFTNVPERTQIDVGRIPLORLKLKCIFCRHRVKRVSGA
NPNVKSKACEKVISVGQTVITKHRNTRYYSCRVMAVTSQTFYEV MFDDGSFSRDTFPEDIVSRDCLKLGPPAEGEVVQVKWPDGKLYG ARYFGSNIAHMYQVEFEDGSQIAMKREDIYTLDEELPKRVKARF VSAGRCHLGTCQVNSLSSPHVSQAQQETYLGFWINSKKSQCNIF LSGTY  1 853 FVARLKEQEGEGGLGPRKEKGRARGRERRKKMQLTRCCFVFLVQ GSLYLVICGQDDGPPGSEDPERDDHEGQPRRPKPKRKGHISPKS RPMANSTLLGLLAPPGEAWGILGQPPNRPNHSPPSAKVKKIFG WGDFYSNIKTVALNLLVTCKIVDHCHGTFSVHFQHNATGQGNIS ISLVPPSKAVEFHQEQQIFIEAKASKIFNC\RMEWEKVE\RGRR TSLFTHDPAKICSRDHAQSSATWSCSQPFKVVCVYIAPYSTDYR LVQKVCPDYNYHSDTPYYPSG  5GDAASSTPPSTRFPGVAIYLVEPRMGRSRRAFLTGLARSKGFR VLDACSSEATHVVMEETSAEEAVSWQERRMAAAPPGCTPPALLD ISWLTESLGAGQPVPVECRHRLEVAGPSKGPLSPAWMPAYACQR PTPLTHHNTGLSEALEILAEAAGFEGSSGRLLTFCRAASVLKAL PSPVTTLSQLQGLPHFGBHSRVVQELLEHGVCEEVERVRRSE/ RLFTQIFGVGVKTADRWYREGLRTLDDLREQPQKLTQQQKAGEP SREAGPWASLNCTLDPSASTP QMIEDGCDLGLGEETGGTGLPYPCQFCDKSFIRLSYLKREQIH SDKLPFKCTYCSRLFKHKRSRDRHIKLHTGDKKYHCHECENAFS RSDHLKIHLKTHSSSKPFKCTYCKRGFSSTSSLOSHMOAHKKNK	1 1			CIQCSYGRCPASFHVTCAHAAGVI,\MEPDDWPYVVNITCFPUVV
MFDDGSFSRDTFPEDIVSRDCLKLGPPAEGEVVQVKWPDGKLYG AKYFGSNIAHMYQVEFEDGSQLAMKREDIYTLDEELPKRVKARF VSAGRCHLGTCQVNSLSSPHVSQAQQETYLGFWINSKKSQCNIF LSGTY  853 FVARLKEQEGEGGLGPRKEKGRARGRERRKMQLTRCCFVFLVQ GSLYLVICGQDDGPPGSEDPERDDHEGQPRRVPRKRGHISPKS RPMANSTLLGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKIFG WGDFYSNIKTVALILLUTGKIVDHGNGTFSVHFQHNATGQGNIS ISLVPPSKAVEFHQEQQIFIEAKASKIFNC\RMEWEKVE\\RGRR TSLFTHDPAKICSRDHAQSSATWSCSQPFKVVCVYIAFYSTDYR LVQKVCPDYNYHSDTPYYPSG  HPLPSASLGLPSVSLGVSLCVRSALLEAVVPMLPKRRRARVGSP SGDAASSTPPSTRFPGVAIYLVEPRMGRSRRAFLTGLARSKGFR VLDACSSEATHVVMEETSAEEAVSWQERRMAAAPPGCTPPALLD ISWLTESLGAGQPVPVECRHRLEVAGPSKGPLSPAWMPAVACQR PTPLTHHNTGLSEALEILAEAAGFEGSEGRLLTFCRAASVLKAL PSPVTTLSQLQGLPHFGEHSSRVVQELLEHGVCEEVERVRSE/ RLFTQIFGVGVKTADRWYREGLRTLDDLREQPQKLTQQQKAGEP SREAGPWASLNCTLDPSASTP QMIGDGCDLGLGEEGGTGLPYPCQFCDKSFIRLSYLKRHEQIH SDKLJFFKCTVCSRLFKHKRSRDRHIKLHTGDKKYHCHECEAAFS RSDHLKIHLKTHSSSKPFKCTVCKRGFSSTSSLOSHMOAHKKNK	i j			NPNVKSKACEKVISVGQTVITKHRNTRYYSCRVMAVTSOTEVEV
ARYFGSNIAHMYQVEFEDGSQIAMKREDIYTLDEELPKRVKARF VSAGRCHLGTCQVNSLSSPHVSQAQQETYLGFWINSKKSQCNIF LSGTY  6057  1 853 FVARLKEQEGEGGLGPRKEKGRARGRERRKKMQLTRCCFVFLVQ GSLYLVICGQDDGPPGSEDPERDDHEGOPRRVPRKRGHISPKS RPMANSTLLGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKIFG WGDFYSNIKTVALNLLVTGKIVDHGNGTFSVHFQHNATGQGNIS ISLVPPSKAVEFHQEQQIFIEAKASKIFNC\RMEWEKVE\RGRR TSLFTHDPAKICSRDHAQSSATWSCSQPFKVVCVYIAFYSTDYR LVQKVCPDYNYHSDTPYYPSG  6058  1 986 HPLPSASLGLPSVSLGVSLCVRSALLEAVVPMLPKRRARVGSP SGDAASSTPPSTRFPGVAIYLVEPRMGRSRRAFLTGLARSKGFR VLDACSSEATHVVMEETSAEEAVSWQERRMAAAPPGCTPPALLD ISWLTESLGAGQPVPVECRHRLEVAGPSKGPLSPAWMPAVACQR PTPLTHHNTGLSEALEILAEAAGFEGSEGRLLTFCRAASVLKAL PSSPVTTLSQLQCLPHFGEHSSRVVQELLEHGVCEEVERVRRSE/ RLFTQIFGVGVKTADRWYREGLRTLDDLREQPQKLTQQQKAGEP SREAGPWASLNCTLDPSASTP  QMIGDGCDLGLEGEEGGTGLPYPCQFCDKSFIRLSYLKRHEQIH SDKLWFKCTVCSRLFKHKRSRDRHIKLHTGDKKYHCHECEAAFS RSDHLKIHLKTHSSSKPFKCTVCKRGFSSTSSLOSHMOAHKKNK		J		MFDDGSFSRDTFPEDIVSRDCLKLGPPAEGEVVOVKWPDGKLVG
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FVARLKEQEGEGGLGPRKEKGRARGRERRRKMQLTRCCFVFLVQ GSLYLVICGQDDGPPGSEDPERDDHEGQPPRPVPRKGHISPKS RPMANSTLLGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKIFG WGDFYSNIKTVALNLLVTGKIVDHGNGTFSVHFQHNATGQCNIS ISLVPPSKAVEFHQEQQIFIEAKASKIFNC\RMEWEKVE\RGRR TSLFTHDPAKICSRDHAQSSATWSCSQPFKVVCVYIAFYSTDYR LVQKVCPPVYNYHSDTPYYPSG  HPLPSASLGLPSVSLGVSLCVRSALLEAVVPMLPKRRRARVGSP SGDAASSTPPSTRFPGVAIYLVEPRMGRSRRAFLTGLARSKGFR VLDACSSEATHVVMEETSAEEAVSWQERRMAAAPPGCTPPALLD ISWLTESLGAGQPVPVECHRLEVAGFSKGPLSPAWMPAYACQR PTPLTHHNTGLSEALEILAEAAGFEGSEGRLTFFCRAASVIKAL PSPVTTLSQLQGLPHFGEHSSRVVQELLEHGVCEEVERVRSE/ RLFTQIFGVGVKTADRWYREGLRTLDDLREQPQKLTQQQKAGEP SREAGPWASLNCTLDPSASTP  QMIGDGCDLGLGEEGGTGLPYPCQFCDKSFIRLSYLKRHEQIH SDKLPFKCTYCSRLFKHKRSRDRHIKLHTGDKKYHCHECEAAFS RSDHLKIHLKTHSSSKPFKCTVCKRGFSSTSSLOSHMOAHKKNK	ľ			VSAGRCHLGTCQVNSLSSPHVSQAQQETYLGFWINSKKSQCNIF
FVARLEQUEGEGGLEPREKEGRARGRERREMQLTRCCFVFLVQ GSLYLVICGQDDGPPGSEDPERDDHEGDPRPRVPRKRGHISPKS RPMANSTLLGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKIFG WGDFYSNIKTVALNLLVTGKIVDHGNGTFSVHPQHNATGQGNIS ISLVPPSKAVEFHQEQQIFTBAKASKIFNC\RMEWEKVE\RGRR TSLFTHDPAKICSRDHAQSSATWSCSQPPKVVCVYIAFYSTDYR LVQKVCPDYNYHSDTPYYPSG HPLPSASIGLFSVSLGVSLCVRSALLEAVVPMLPKRRARVGSP SGDAASSTPPSTRPFGVAIYLVEPRMGRSRRAFLTGLARSKGFR VLDACSSEATHVVMEETSAEEAVSWQERRMAAAPPGCTPPALLD ISWLTESLGAGQPVPVECRHRLEVAGPSKGPLSPAMMPAYACQR PTPLTHHNTGLSEALEILAEAAGFEGSEGRLLTFCRAASVLKAL PSPVTTLSQLQGLPHFGEHSSRVVQELLEHGVCEEVERVRRSE/ RLFTQIFGVGVKTADRWYREGLRTLDDLREQPQKLTQQQKAGEP SREAGPWASLNCTLDPSASTP QMIGDGCDLGLGEEEGGTGLPYPCQFCDKSPIRLSYLKRHEQIH SDKLPFKCTYCSRLFKHKRSRDRHIKLHTGDKKYHCHECEAAFS RSDHLKIHLKTHSSSKPFKCTVCKRGFSSTSLOSHMOAHKKNK	6057			LSGTY
GSLYLVICGODDGPGSEDPERDDHEGOPRPRVPRKRGHISPKS RPMANSTLIGLLAPPGEAWGILGOPPNRPNHSPPSAKVKKIFG WGDFYSNIKTVALLNLUTGKIVDHGNGTFSVHFQHNATGQGNIS ISLVPPSKAVEFHQEQQIFIBAKASKIFNC\RMEWEKVE\RGRR TSLFTHDPAKICSRDHAQSSATWSCSQPFKVVCVYIAFYSTDYR LVQKVCPDYNYHSDTPYYPSG  HPLPSASLGLPSVSLGVSLCVRSALLEAVVPMLPKKRRARVGSP SGDAASSTPPSTRFPGVAITLVEPRMGRSRRAFLTGLARSKGFR VLDACSSEATHVVMEETSAEEAVSWQERRMAAAPPGCTPPALLD ISWLTESLGAQQPVPVECRHRLEVAGPSKGPLSPAWMPAYACQR PTPLTHHNTGLSEALEILAEAAGFEGSEGRLLTFCRAASVLKAL PSPVTTLSQLQGLPHFGEHSSRVVQELLEHGYCEEVERVRRSE/ RLFTQIFGVGVKTADRWYREGLRTLDDLREQPQKLTQQQKAGEP SREAGPWASLNCTLDPSASTP QMIGDGCDLGLGEEEGGTGLPYPCQFCDKSFIRLSYLKRHEQIH SDKLPFKCTYCSRLFKHKRSRDRHIKLHTGDKKYHCHECEAAFS RSDHLKIHLKTHSSSKPFKCTVCKRGFSSTSSLOSHMOAHKKNK		*	853	FVARLKEQEGEGGLGPRKEKGRARGRERRRKMQLTRCCFVFLVO
RPMANSTLIGLLAPPGEAWGILGOPPNRPNHSPPPSAKVKKIFG WGDFYSNIKTVALNILVTGKIUOHGNGTFSVHFQHNATGQGNIS ISLVPPSKAVEFHQEQQIFIEAKASKIFNC\RMEWEKVE\RGRR TSLFTHDPAKICSRDHAQSSATWSCSQPPKVVCVYIAPYSTDYR LVQKVCPDYNYHSDTPYYPSG  6058  1  986  HPLPSASLGLPSVSLGVSLCVRSALLEAVVPMLPKKRRARVGSP SGDAASSTPPSTRPPGVAIYLVEPRMGRSRRAFLTGLARSKGFR VLDACSSEATHVVMEETSAEEAVSWQERRMAAAPPGCTPPALLD ISWLTESLGAQQPVPVECRHRLEVAGPSKGPLSPAWMPAYACQR PTPLTHHNTGLSEALEILAEAAGFEGSEGRLLTFCRAASVLKAL PSPVTTLSQLQGLPHFGEHSSRVVQELLEHGVCEEVERVRRSE/ RLFTQIFGVGVKTADRWYREGLRTLDDLREQPQKLTQQQKAGEP SREAGPWASLNCTLDPSASTP QMIGDGCDLGLGEEEGGTGLPYPCQFCDKSFIRLSYLKRHEQIH SDKLPFKCTYCSRLFKHKRSRDRHIKLHTGDKKYHCHECEAAFS RSDHLKIHLKTHSSSKPFKCTVCKRGFSSTSSLOSHMOAHKKNK		1		GSLYLVICGODDGPPGSEDPERDDHEGOPRPRVPRKRGHISDKG
1SLVPPSKAVEFHQEQQIFIEAKASKIFNC\RMEWEKVE\RGRR TSLFTHDPAKICSRDHAQSSATWSCSQPFKVVCVYIAFYSTDYR LVQKVCPDYNYHSDTPYYPSG  6058 1 986 HPLPSASIGLPSVSLGVSSALLEAVVPMLPKRRRARVGSP SGDAASSTPPSTRFPGVAIYLVEPRMGRSRRAFLITGLARSKGFR VLDACSSEATHVVMEETSAEEAVSWQERRMAAAPPGCTPPALLD ISWLTESLGAGQPVPVECHRLEVAGFSKGPLSPAWMPAYACQR PTPLTHHNTGLSEALEILAEAAGFEGSEGRLTFCRAASVIKAL PSPVTTLSQLQGLPHFGEHSSRVVQELLEHGVCEEVERVRRSE/ RLFTQIFGVGVKTADRWYREGLRTLDDLREQPQKLTQQQKAGEP SREAGPWASLNCTLDPSASTP QMIGDGCDLGLGEEEGGTGLPYPCQFCDKSFIRLSYLKRHEQIH SDKLKJFKCTYCSRLFKHKRSRDRHIKLHTGDKKYHCHECEAAFS RSDHLKIHLKTHSSSKPFKCTVCKRGFSSTSSLOSHMOAHKKNK	1			RPMANSTLLGLLAPPGEAWGILGOPPNRPNHSPPPSAKVKKTEG
1SLVPPSKAVEFHQEQQIFIEAKASKIFNC\RMEWEKVE\RGRR TSLFTHDPAKICSRDHAQSSATWSCSQPFKVVCVYIAFYSTDYR LVQKVCPDYNYHSDTPYYPSG  6058 1 986 HPLPSASIGLPSVSLGVSSALLEAVVPMLPKRRRARVGSP SGDAASSTPPSTRFPGVAIYLVEPRMGRSRRAFLITGLARSKGFR VLDACSSEATHVVMEETSAEEAVSWQERRMAAAPPGCTPPALLD ISWLTESLGAGQPVPVECHRLEVAGFSKGPLSPAWMPAYACQR PTPLTHHNTGLSEALEILAEAAGFEGSEGRLTFCRAASVIKAL PSPVTTLSQLQGLPHFGEHSSRVVQELLEHGVCEEVERVRRSE/ RLFTQIFGVGVKTADRWYREGLRTLDDLREQPQKLTQQQKAGEP SREAGPWASLNCTLDPSASTP QMIGDGCDLGLGEEEGGTGLPYPCQFCDKSFIRLSYLKRHEQIH SDKLKJFKCTYCSRLFKHKRSRDRHIKLHTGDKKYHCHECEAAFS RSDHLKIHLKTHSSSKPFKCTVCKRGFSSTSSLOSHMOAHKKNK	i i			WGDFYSNIKTVALNLLVTGKIVDHGNGTFSVHFQHNATGQGNIS
6058 1 986 HPLPSASLGLPSVSLGVSLCVRSALLEAVVPMLPKRRARVGSP SGDAASSTPPSTRFPGVAIYLVEPRMGRSRRAFLITGLARSKGFR VLDACSSEATHVVMEETSAEEAVSWQERRMAAAPPGCTPPALLD ISWLTESLGAGOPVPVECRHRLEVAGPSKGPLSPAMMPAYACQR PTPLTHHNTGLSEALEILAEAAGFEGSEGRLLITFCRAASVLKAL PSPVTTLSQLQGLPHFGEHSSRVVQELLEHGVCEEVERVRRSE/ RLFTQIFGVGVKTADRWYREGLRTLDDLREQPQKLTQQQKAGEP SREAGPWASLNCTLDPSASTP QMIGDGCDLGLGEEEGGTGLPYPCQFCDKSPIRLSYLKRHEQIH SDKLPFKCTYCSRLFKHKRSRDRHIKLHTGDKKYHCHECEAAFS RSDHLKIHLKTHSSSKPFKCTVCKRGFSSTSSLOSHMOAHKKNK	1		1	ISLVPPSKAVEFHQEQQIFIEAKASKIFNC\RMEWEKVE\RGPP
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SGDAASSTPSTRFPGVAIYLVEPRMGRSRAFLTGLARSKGFR VLDACSSEATHVVMEETSAEEAVSWQERRMAAAPPGCTPPALLD ISWLTESLGAGGPVPVECHRLEVAGPSKGPLSPAWMPAYACQR PTPLTHHNTGLSEALEILAEAAGFEGSEGRLLTFCRAASVLKAL PSPVTTLSQLQGLPHFGEHSSRVVQELLEHGVCEEVERVRRSE/ RLFTQIFGVGVKTADRWYREGLRTLDDLREQPQKLTQQQKAGEP SREAGPWASLNCTLDPSASTP QMGDGCDLGLGEEEGGTGLPYPCQFCDKSPIRLSYLKRHEQIH SDKLPFKCTYCSRLFKKRSRDRHIKLHTGDKKYHCHECEAAFS RSDHLKIHLKTHSSSKPFKCTVCKRGFSSTSSLOSHMOAHKKNK	6058	<del></del> -		
SGDAASSTPPSTRFPGVAIYLVEPRMGRSRRAFLTGLARSKGFR VLDACSSEATHVVMEETSAEEAVSWQERRMAAAPPGCTPPALLD ISWLTESLGAGQPVPVECRHRLEVAGPSKGPLSPAWMPAYACQR PTPLTHHNTGLSEALEILAEAAGFEGSEGRLLTFCRAASVLKAL PSPVTTLSQLGCLPHFGEHSSRVVQELLEHGVCEEVERVRRSE/ RLFTQIFGVGVKTADRWYREGLRTLDDLREQPQKLTQQQKAGEP SREAGPWASLNCTLDPSASTP QMGDGCDLGLGEEEGGTGLPYPCQFCDKSFIRLSYLKRHEQIH SDKLPFKCTYCSRLFKHKRSRDRHIKLHTGDKKYHCHECEAAFS RSDHLKIHLKTHSSSKPFKCTVCKRGFSSTSSLOSHMOAHKKNK		•	986	HPLPSASLGLPSVSLGVSLCVRSALLEAVVPMLPKRRARVGSP
VLDACSSEATHVVMEETSAEEAVSWQERRMAAAPPGCTPPALLD ISWLTESLGAGQPVPVECRHRLEVAGPSKGPLSPAWMPAVACQR PTPLTHHNTGLSEALEILAEAGFEGSEGRLLTFCRAASVLKAL PSPVTTLSQLQGLPHFGEHSSRVVQELLEHGVCEEVERVRSE/ RLFTQIFGVGVKTADRWYREGLRTLDDLREQPQKLTQQQKAGEP SREAGPWASLNCTLDPSASTP QQDFESLADLTDHRAHRCPGDGDDDPQLSWVASSPSSKDVASPT QMIGDGCDLGLGEEEGGTGLPYPCQFCDKSFIRLSYLKRHEQIH SDKLPFKCTVCSRLFKHKRSRDRHIKLHTGDKKYHCHECEAAFS RSDHLKIHLKTHSSSKPFKCTVCKRGFSSTSSLOSHMOAHKKNK	- 1			SGDAASSTPPSTRFPGVAIYLVEPRMGRSRRAFLTGLARSKGFP
ISWLTESLGAGQPVPVECRHRLEVAGPSKGPLSPAWMPAYACQR PTPLTHHNTGLSEALEILAEAAGFEGSEGRLLTFCRAASVLKAL PSPVTTLSQLQGLPHFGEHSSRVVQELLEHGVCEEVERVRRSE/ RLFTQIFGVGVKTADRWYREGLRTLDDLREQPQKLTQQQKAGEP SREAGPWASLNCTLDPSASTP QQDFESLADLTDHRAHRCPGDGDDDPQLSWVASSPSSKDVASPT QMIGDGCDLGLGEEEGGTGLPYPCQFCDKSFIRLSYLKRHEQIH SDKLPFKCTYCSRLFKHKRSRDRHIKLHTGDKKYHCHECEAAFS RSDHLKIHLKTHSSSKPFKCTVCKRGFSSTSSLOSHMOAHKKNK	1	j	1	VLDACSSEATHVVMEETSAERAVSWOERRMAAAPPGCTPDALLD
PTPLTHHNTGLSEALEILAEAAGFEGSEGRLLTFCRAASVLKAL PSPVTTLSQLQGLPHFGEHSRVVQELLEHGVCEEVERVRRSE/ RLFTQIFGVGVKTADRWYREGLRTLDDLREQPQKLTQQQKAGEP SREAGPWASLNCTLDPSASTP QQDFESLADLTDHRAHRCPGDGDDDPQLSWVASSPSSKDVASPT QMIGDGCDLGLGEEEGGTGLPYPCQFCDKSFIRLSYLKRHEQIH SDKLPFKCTYCSRLFKHKRSRDRHIKLHTGDKKYHCHECEAAFS RSDHLKIHLKTHSSSKPFKCTVCKRGFSSTSSLOSHMOAHKKNIK	1	1	1	ISWLTESLGAGQPVPVECRHRLEVAGPSKGPLSPAWMPAYACOP
PSPVTTLSQLQGLPHFGEHSSRVVQELLEHGVCEEVERVRRSE/ RLFTQIFGVGVKTADRWYREGLRTLDDLREQPQKLTQQQKAGEP SREAGPWASLNCTLDPSASTP QQDFESLADLTDHRAHRCPGDGDDDPQLSWVASSPSSKDVASPT QMIGDGCDLGLGEEEGGTGLPYPCQFCDKSPIRLSYLKRHEQIH SDKLPFKCTYCSRLFKHKRSRDRHIKLHTGDKKYHCHECEAAFS RSDHLKIHLKTHSSSKPFKCTVCKRGFSSTSSLOSHMOAHKKNK	1	İ	1	PTPLTHHNTGLSEALEILAEAAGFEGSEGRLLTFCRAASVLKAI.
RLFTQIFGVGVKTADRWYREGLRTLDDLREQPQKLTQQQKAGEP  SREAGPWASLNCTLDPSASTP  QQDFESLADLTDHRAHRCPGDGDDDPQLSWVASSPSSKDVASPT QMIGDGCDLGLGEEEGGTGLPYPCQFCDKSPIRLSYLKRHEQIH SDKLPFKCTYCSRLFKHKRSRDRHIKLHTGDKKYHCHECEAAFS RSDHLKIHLKTHSSSKPFKCTVCKRGFSSTSSLOSHMOAHKKNK	1	İ		PSPVTTLSQLQGLPHFGEHSSRVVOELLEHGVCEEVERVRRSR/
6059 2 3650 QQDFESLADLTDHRAHRCPGDGDDDPQLSWVASSPSSKDVASPT QMIGDGCDLGLGEEEGGTGLPYPCQFCDKSPIRLSYLKRHEQIH SDKLPFKCTYCSRLFKHKRSRDRHIKLHTGDKKYHCHECEAAFS RSDHLKIHLKTHSSSKPFKCTYCKRGFSSTSSLOSHMOAHKKNK	1		į.	RLFTQIFGVGVKTADRWYREGLRTLDDLREOPOKLTOOOKAGRP
QQPFSLADLTDHRAHRCPGDGDDDPQLSWVASSPSSKDVASPT QMIGDGLGGEEEGGTGLPYPCQFCDKSFIRLSYLKRHEQIH SDKLPFKCTYCSRLFKHKRSRDRHIKLHTGDKKYHCHECEAAFS RSDHLKIHLKTHSSSKPFKCTYCKRGFSSTSSLOSHMOAHKKNK	6050			SREAGPWASLNCTLDPSASTP
QMIGDGCDLGLGEEEGGTGLPYPCQFCDKSFIRLSYLKRHEQIH SDKLPFKCTYCSRLFKHKRSRDRHIKLHTGDKKYHCHECEAAFS RSDHLKIHLKTHSSSKPFKCTVCKRGFSSTSSLOSHMOAHKKNK	0033	4	3650	QQDFESLADLTDHRAHRCPGDGDDDPQLSWVASSPSSKDVASPT
SDKLPFKCTYCSRLFKHKRSRDRHIKLHTGDKKYHCHECEAAFS RSDHLKIHLKTHSSSKPFKCTVCKRGFSSTSSLOSHMOAHKKNK		ł	i	QNIGDGCDLGLGEEEGGTGLPYPCOFCDKSFIRLSYLKRHEOIH
RSDHLKIHLKTHSSSKPFKCTVCKRGFSSTSSLOSHMOAHKKNK	[	i	I	SDKLPFKCTYCSRLFKHKRSRDRHIKLHTGDKKYHCHECEAAFS
EHLAKSEKEAKKDDFMCDYCEDTFSOTEBLEKHVI.TBNPOLGBN	1			RSDHLKIHLKTHSSSKPFKCTVCKRGFSSTSSLOSHMOAHKKNK
				ehlaksekeakkddfmcdycedtfsqteblekhvltrhpqlsek

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	U-Wichiding T-To-levelet W T
1	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
-	amino acid	residue of	C-Coming W. When a W. W. D.
İ	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
1	amino acid		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	sequence	Codon, /=possible nucleotide deletion,
ļ	sequence		\=possible nucleotide insertion)
1			ADLQCIHCPEVFVDENTLLAHIHQAHANQKHKCPMCPE\QFSSV
ļ			\EGVYCHLDSHRQPDSSNHSVSPDPVLGSVASMSSATPDSSASV
1	i		RRGSTPDSTLKPLRGQKKMRDDGQGWTKVVYSCPYCSKRDFNSL
İ			AVLEIHLKTIHADKPQQSHTCQICLDSMPTLYNLNEHVRKLHKN
			HAYPVMQFGNISAFHCNYCPEMFADINSLQEHIRVSHCGPNANP
	{		SDGNNAFFCNQCSMGFLTESSLTEHIQ\Q\AHCSVGSAKLESPV
			VQPTQSFMEVYSCPYCTNSPIFGSILKLTKHIKENHKNIPLAHS
1			KKSKAEQSPVSSDVEVSSPKRQRLSASANSISNGEYPCNQCDLK
1			FSNFESFQTHLKLHLELLLRKQACPQCKEDFDSQESLLQHLTVH
1			YMTTSTHYVCESCDKQFSSVDD\LQKH\LLDMPHPLCCTHCT\L
			CQEVFDS\KVSI\QVHLAVKHSNEKKMYRCTACNWDFRKEADLQ
			VHVKHSHLGNPAKAHKCIFCGETFSTEVBLQCHITTHSKKYNCK
1	]		FCSKAFHAIILLEKHLREKHCVFDAATENGTANGVPPMATKKAE
1			PADLQGMLLKNPEAPNSHEASEDDVDASEPMYGCDICGAAYTME
	1		VLLQNHRLRDHNIRPGEDDGSRKKAEFIKGSHKCNVCSRTFFSE
			NGLREHLQTHRGPAKHYMCPICGERFPSLLTLTEHKVTHSKSLD
			TGTCRICKMPLQSEEFFIEHCQMHPDLRNSLTGFRCVVCMQTVT
			STLELKIHGTFHMQKLAGSSAASSPNGQGLQKLYKCALCLKEFR
			SKQDLVKLDVNGLPYGLCAGCMARSANGQVGGLAPPEPADRPCA
			GLRCPECSVKFESAEDLESHMQVDHRDLTPETSGPRKGTQTSPV
			PRKKTYQCIKCQMTFENEREIQIHVANHMIBEGINHECKLCNQM
ł			FDSPAKLLCHLIEHSFRGMGGTFKCPVCFTVFVQANKLQQHIFA
6060	2145	202	VHGQEDKIYDCSQCPQKFFFQTELQNHTMSQHAQ
0000	2143	202	SYEIVGKNKLEVNHSQLKALCKCSLPSRLLPLGENLPLLDRGFR
			KEPRSRGSRERDNMLHLHHSCLCFRSWLPAMLAVLLSLAPSASS
			DISASRPNILLLMADDLGIGDIGCYGNNTMRTPNIDRLAEDGVK
			LTQHISAASLCTPSRAAFLTGRYPVRSGMVSSIGYRVLQWTGAS
			GGLPTNETTFAKILEEKGYATGLIGKWHLGLNCESASDHCHHPL
1.	,		HHGFDHFYGMPFSLMGDCARWELSEKRVNLEQKLNFLPQVLALV ALTLVAGKLTHLIPVSWMPVIWSALSAVLLLASSYFVGALIVHA
			DCFLMRNHTITEQPMCFQRTTPLILQEVASFLKRNKHGPPLLFV SFLHVHIPLITMENFLGKSLHGLYGDNVKEMDWMVGRILDTLDV
			EGLSNSTLIYFTSDHGGSLENQLGNTQYGGWNGIYKGGKGMGGW
1.			EGGIRVPGIFRWPGVLPAGRVIGEPTSLMDVFPTVVRLAGSEVP
			QDRVIDGQDLLPLLLGTAQHSDHEFLMHYCERFLHAARWHQRDR
1.	. }		GTMWKVHFVTPVFQPEGAGACYGRKVCPCFGEKVVHHDPPLLFD
			LSRDPSETHILTPASEPVFYQVMER\VQQAVWEHQRTLSPVPLQ
	1		LDRLGNIWRPWLQPCCGPFPLCWCLREDDPQ
6061	110	1330	MNIHMKRKTIKNINTFENRMLMLDGMPAVRVKTBLLESEOGSPN
			VHNYPDMEAVPLLLNNVKGEPPEDSLSVDHFQTQTEPVDLSINK
	1		ARTSPTAVSSSPVSMTASASSPSSTSTSSSSSRLASSPTVITS
ļ. l			VSSASSSTVLTPGPLVASASGVGGQQFLHIIHPVPPSSPMNLO
	į		SNKLSHVHRIPVVVQSVPVVYTAVRSPGNVNNTIVVPLLEDGRG
	į		HGKAQMDPRGLSPRQSKSDSDDDDLPNVTLDSVNETGSTALSIA
	ļ	•	RAVQEVHPSPVSRVRGNRMNNQKFPCSISPFSIESTRRQRTVLN
1	İ		PPDSRKTAYSTDCDF\EGLQQKLYTKSSSPGRVHRRTHTGEKPY
			KCTWEGCTWKFARSDELTRHYRKHTGVKPFKCADCDRSFSRSDH
] ]			LALHRRHMLV
6062	71	1079	ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT
	ĺ		LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR
			TEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP
1			EFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKI
	. [		LEICDNVTMYW\INPTL\ISGTFAKQLHHNFAFIILVSELQDFE
			EEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELP
			INDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYP
			YPYCYQGGRVICRVIMPCNWWVARMLGRV
6063	71	1079	ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT
		· <b>*</b>	LIVLFNGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR
1	1		TEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP
İ	1	Ì	EFSEPBEEIDENEEITTFFEQSVIWVPAEKPIENRDFLKNSKI
	1		LBICDNVTMYW\INPTL\ISGTFAKQLHHNFAFIILVSELQDFE
<del></del>	<del></del>	··	

Г	SEQ	Predicted	Predicted end	Anino agid come to
- 1	ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
- [		location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
		corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
Į		to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
		amino acid	residue of	S=Serine, T=Threonine, V=Valine,
İ		residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
		amino acid	sequence	Codon, /=possible nucleotide deletion,
		sequence	<u> </u>	\=possible nucleotide insertion)
				EEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELP
J			1	INDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYP
			İ	YPYCYQGGRVICRVIMPCNWWVARMLGRV
	6064	913	311	NLPQSLPRPTEHSPPYSLEKMTDLVAVWDVALSDGVHKIEFEHG
- 1				TTSGKRVVYVDGKEEIRKEWMFKLVGKETFYVGAAKTKATINID
			·	AISGFAYEYTLEINGKSLKKYMEDRSKTTNTWVLHMDGENFRIV
				LEKDAMDVWCNGKKLETAGEFVDDGTETHFSIGTH\ACYIKAV\
1				SSG\KRKEGIHTLIVDNREIPEIAS
	6065	1153	641	MSVRVARVAWVRGLGASYRRGASSFPVPPPGAQGVAELLRDATG
				AEEEAPWAATERRMPGQCSVLLFPGQGSQVVGMGRGLLNYPRVR
	Í	!		BLYAAARRVLGYDLLELSLHGPQETLDRTVHCQPAIFVASLAAV
- 1				EKLHHLQPSVIENCVAAAGFSVGEFAALVFAGAMEFAEG
7	6066	68	3470	VKENMPATRKPMRYGHTEGHTEVCFDDSGSFIVTCGSDGDVRIW
	i			EDLDDDDPKFINVGEKAYSCALKSGKLVTAVSNNTIQVHTFPEG
1	1			VPDGILTRFTTNANHVVFNGDGTKIAAGSSD\FLVKIVDVMDSS
				QQKTFRGHDAPVLSLSFDPKDIFLASASCDGSVRVWQISDQTCA
	i			ISWPLLQKCNDVINAKSICRLAWQPKSGKLLAIPVEKSVKLYRR
	}			ESWSHQFDLSDNFISQTLNIVTWSPCGQYLAAGSINGLIIVWNV
	ł			ETKDCMERVKHEKGYAICGLAWHPTCGRISYTDAEGNLGLLENV
-				CDPSGKTSSSKVSSRVEKDYNDLFDGDDMSNAGDFLNDNAVEIP
				SFSKGIINDDEDDEDLMMASGRPRQRSHILEDDENSVDISMLKT
1	1		•	GSSLLKEEEEDGQEGSIHNLPLVTSQRPFYDGPMPTPRQKPFQS
				GSTPLHLTHRFMVWNSIGIIRCYNDEQDNAIDVEFHDTSIHHAT
1	J			HLSNTLNYTIADLSHEAILLACESTDELASKLHCLHFSSWDSSK
				EWIIDLPQNEDIEAICLGQGWAAAATSALLLRLFTIGGVQKEVF
1	ŀ	}		SLAGPVVSMAGHGEQLFIVYHRGTGFDGDQCLGVQLLELGKKKK
		1		QILHGDPLPLTRKSYLAWIGFSAEGTPCYVDSEGIVRMLNRGLG
	1			NTWTPICNTREHCKGKSDHYWVVGIHENPQQLRCIPCKGSRFPP
	- 1			TLPRPAVAILSFKLPYCQIATEKGQMEEQFWRSVIFHNHLDYLA
1	ł	}		KNGYEYEESTKNOATKEQQELLMKMLALSCKLEREFRCVELADL
1				MTQNAVNLAIKYASRSRKLILAQKLSELAVEKAAELTATQVEEE
1	- 1			EEEEDFRKKLNAGYSNTATEWSQPRFRNQVEEDAEDSGEADDEE
	1	į		KPEIHKPGQNSFSKSTNSSDVSAKSGAVTFSSOGRVNPFKVSAS
1		j		SKEPAMSMNSARSTNILDNMGKSSKKSTALSRTTNNEKSPIJKP
1	l l	1	·	LIPKPKPKQASAASYFQKRNSQTNKTEEVKEENLKNVLSETPAI
1	- 1			CPPQNTENQRPKTGFQMWLEENRSNILSDNPDFSDEADTIKEGM
Ì		j.	}	IRFRVLSTEERKVWANKAKGETASEGTEAKKRKRVVDESDETEN
<u>_</u>	067			QEEKAKENLNLSKKQKPLDFSTNQKLSAFAFKOE
1 0	067	858	321	LPWQRLGVLLSRGKMAVTGWLESLRTAQKTALLODGRRKVHYLF
1				PDGKEMAEEYDEKTSELLVRKWRVKSALGAMGOWOLEVGDPAPI.
1			İ	GAGNIGPELIKESNANPIFMRKDTKMSFOWRIRNLPYPKDVYSV
1	1		1	SVDQKERCIIVRTTNKKYYKKFSIPDLDRHQLPLDDALLSFA\T
-	068	<del></del>		PTAP
۱ "		13	1730	GSKMADLANEEKPAIAPPVFVFQKDKGQKSPAEQKNLSDSGEEP
		1	i	RGEAEAPHHGTGHPESAGEHALEPPAPAGASASTPPPPAPEAQL
l		i		PPFPRELAGRSAGGSSPEGGEDSDREDGNYCPPVKRERTSSLTQ
1	- 1		1	FPPSQSEERSSGFRLKPPTLIHGQAPSAGLPSQKPKEQQRSVLR
]		1		PAVLQAPQPKALSQTVPSSGTNGVSLPADCTGAVPAASPDTAAW
ſ		ł		RSPSEAADEVCALEEKEPQKNESSNASEBEACEKKDPATQQAFV
		1	1	FGQNLRDRVKLINESVDEADMENAGHPSADTPTATNYFLOVISS
1	- 1		1	SLENSTNSADASSNKFVFGQNMSERVLSPPKLNEVSSDANRENA
	ł			AAESGSESSSQEATPEKESLABSAAAYTKATARKCLLEKVEVTT
l			i	GEEAESNVLQMQCKLFVFDKTSQSWVERGRGLLRLNDMASTDDG
l	- 1			TLQSRLSDAGPRGSLR\LILNTKLWAOMOIDKASEK\SIRITAM
	ſ	Í		DNEDQGVKVFLISASSKDTGQVYAALHHRILALRSRVEOEGEAK
l	., I			MPAPEPGAAPSNEEDDSDDDDVLAPSGATAAGAGDEGDGOTTGS
60	69	583		T
"		203	27	PTRPGQAGSSSAMAAQRLGKRVLSKLQSPSRARGPGGSPGGLQK
	1	1		RHARVTVKYDRRELQRRLDVEKWIDGRLEELYRGMEADMPDEIN
				IDELLELESEEERSRKIQGLLKSCGKPVEDFIQELLAKLQGLHR

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, T=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ŀ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
+	sequence	Sequence	\=possible nucleotide insertion)
<u> </u>	bequence	<del>                                     </del>	Q\PGLRQPSPSP\DGQPSAPFQGPGARTASPLTLLALFPGPPER
			RPALLCVLSCI
6070	478	858	IRVTVDGEFLHYIFPLQFLDSPEW/RFTETHRGRHF\QVTLTAE
1 ****	1 -70	656	TROUVICUEDANT TO PROVINCIA FOUR TOORY DAY WAY TO
}	j		TDCRYVSWRRKKLYLLFAQHRYISRLFSVLIGSDIADKLYALND
6071	2	1654	RVYIGKRYHYDIRLPNFYQMSTPEIRRSPLTQHFQNSRRYW
1 00/1	<b>'</b>	1034	HEARTKGNMALARP\VRLFSLVTRLLLAPRRGLTVRSPDEPLPV
			VRIPVALQRQLEQRQSRRRNLPRPVLVRPGPLLVSARRPELNQP
			ARLTLGRWERAPLASQGWKSRRARRDHFSIERAQQEAPAVRKLS
İ			SKGSFADLGAWKPRVLHALQE\AAPEVVQ\PTTVQSSTIPSLLR
i		}	GRHVVCAAETGSGKTLSYLLPLLQRLLG\HPSLDSLPIPAPRGL
	ì	i	VLVPSRELAQQVRAVAQPLGRSLGLLVRDLEGGHGMRRIRLQLS
			ROPSADVLVATPGALWKALKSRLISLEQLSFLVLDEADTLLDES
1	}	Į	FLELVDYILEKSHIAEGPADLEDPFNPKAQLVLVGATFPEGVGQ
1	1		LLNKVASPDAVTTITSSKLHCIMPHVKQTFLRLKGADKVAELVH
1	ļ		ILKHRDRAERTGPSGTVLVFCNSSSTVNWLGYILDDHKIQHLRL
			QGQMPALMRVGIFQSFQKSSRDILLCTDIASRGLDSTGVBLVVN
	•		YDFPFTLQDYIHRAGRVGRVGSEVPGTVISFVTHPWDVSLVQKI
6070			ELAARRRSLPGLASSVKEPLPQAT
6072	1	742	KMERTEMMPTINSQLEPKSKPFPLVSSSRWLVKRGELTAYVEDT
			VLFSRRTSKQQVYFFLFNDVLIITKKKSEESYNVNDYSLRDQLL
			VESCDNEELNSSPGKNSSTMLYSRQSSASHLPTLTVLSNHANEK
	•		VEMLLGAETQSERARWITALGHSSGKPPADRTSLTQVEIVRSFT
4			AKQPDELSLQVADVVLI\YQRVSDGWYEGER\LRDGERGWFPME
			CAKEITCQATIDKNVERMGRLLGLETNV
6073	620	860	PCRRGLARPLSRRPG/SILVHCAVGVSRSATLVLAYLMLYHHLT
<u></u>			LVEAIKKVKDHRGIIPNKGFLRQLLALDRRLRQGLEA
6074	168	1110	PGARCMATELQCPDSMPCHNQQVNSASTPSPEQLRPGDLILDHA
			GGNRASRAKVILLTGYAHSSLPAELDSGACGGSSLNSEGNSGSG
			DSSSYDAPAGNSFLEDCELSRQIGAQLKLLPMNDQIRELQTIIR
			DKTASRGDFMFSADRLIRLVVEEGLNQLPYKECMVTTPTGYKYE
			GVKFEKGNCGVSIMRSGEAMEQGLRDCCRSIRIGKILIQSDEET
1			QRAKVYYAKFPPDIYRRKVLLMYPILQTG\NTVIEAVKVLIEHG
			VQPSVIILLSLFSTPHGAKSIIQEFPEITILTTEVHPVAPTHFG
			QKYFGTD
6075	320	1091	PPTCQPQEVEHH\YGYVPILGNKTLPSRCHQCVIVSSSSHLLGT
1			KLGPEIERAECTIRMNDAPTTGYSADVGNKTTYRVVAHSSVFRV
]			LRRPQEFVNRTPETVFIFWGPPSKMQKPQGSLVRVIQRAGLVFP
			NMEAYAVSPGRMRQFDDLFRGETGKDREKSHSWLSTGWFTMVIA
] .			VELCDHVHVYGMVPPNYCSQRPRLQRMPYHYYEPKGPDECVTYI
<b> </b>			QNEHSRKGNHHRFITEKRVFSSWAQLYGITFSHPSWT
6076	1721	107	HPSPTEAPRVQHLTMDCTWRILFLVAAATGTHAQVQLVQSGAEV
j [			KKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGAFDPBD
1 1			GETIYAQKFQGRVTMTEDTSTDTAYMELSSLRSEDTAVYYCATD
į l			HGDYAFDIWGQGTMVTVSSAPTKAPDVFPIISGCRHPKDNSPVV
1 1			LACLITGYHPTSV\TVTWYMGTQSQA\QRTFPEIQRRDSYYMTS
1			SQLSTPLQQWRQGEYKCVVQHTASKSKKEIFRWPESPKAQASSV
1			PTAQPQAEGSLAKATTAPATTRNTGRGGEEKKKEKEKEEQEERE
1			TKTPECPSHTQPLGVYLLTPAVQDLWLRDKATFTCFVVGSDLKD
1 1			AHLTWEVAGKVPTGGVEEGLLERHSNGSQSQHSRLTLPRSLWNA
/	j		GTSVTCTLNHPSLPPQRLMALREPAAQAPVKLSLNLLASSDPPE
	}		A\ASWLLCEVSGFSPPNILLMWLEDHGEVNTSGFAPARPLPKP\
			RSTTFWA\WSVLRVPAPPSPQPATYTCVVSHEDSRTLLNASRSL
L			BVSYVTDHGPMK
6077	3687	1268	LLPDMNLQPIFWIGLISSVCCVFAQTDENRCLXANAKSCGECIQ
	1	-	AGPNCGWCTNSTFLQEGMPTSARCDDLEALKKKGCPPDDIENPR
1	ļ		GSKDIKKNKNVTNRSKGTAEKLKPEDITQIQPQQLVLRLRSGEP
1 1			QTFTLKFKRAEDYPIDLYYLM\DLSYSMKDDLENVKSLGTDLMN
, !			EMRRITSDFRIGFGSFVEKTVMPYISTTPAKLRNPCTSEQNCTS
[	1		PFSYKNVLSLTNKGEVFNELVGKQRISGNLDSPEGGFDAIMQVA
]	1		VCGSLIGWRNVTRLLVFSTDAGFHFAGDGKLGGIVLPNDGQCHL

SEO	Predicted	Predicted end	
ID	beginning		Amino acid segment containing signal peptide
NO:	nucleotide	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	location	Glutamic Acid, F-Phenylalanine, G-Glycine,
j		corresponding	H=H1Stidine, I=Isoleucine, K=Lvsine
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
- 1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine
	amino acid	residue of	S=Serine, T=Threonine, V=Valine.
ļ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown *=Stop
i	amino acid	sequence	Codon, /=possible nucleotide deletion
	sequence		\=possible nucleotide insertion)
		·	ENNMYTMSHYYDYPSIAHLVQKLSENNIQTIFAVTEEFQPVYKE
	1		LKNLIPKSAVGTLSANSSNVIQLIIDAYNSLSSEVILENGKLSE
ļ			GVTISYQSY\CKNGVNGTGENGRKCSNISIGDEVQFEISITSNK
1	ſ		CPKYDEDSEKIEDI GERGENGKACSNISIGDEVQFEISITSNK
i			CPKKDSDSFKIRPLGFTEEVEVILQYICECECQSEGIPESPKCH
1		Į.	EGNGTFECGACRCNEGRVGRHCECSTDEVNSEDIGCFTARKENQ
ı	Į.	}	FQKSASNHGRVPSAGQCVCRKRDNTNBIYSGKFCECDNFNCDRS
	1		NGLICGGNGVCKCRVCECNPNYTGSACDCSLDTSTCEASNGQIC
1	1	j	NGRGICECGVCKCTDPKFQGQTCEMCQTCLGVCAEHKECVQCRA
1		<b>!</b>	FNKGEKKDTCTQECSYFNITKVESRDKLPOPVOPDPVSHCKEKD
ŀ	1		VDDCWFYPTYSVNGNNEVMVHVVENPECPTGPDIIPIVAGVVAG
1	1	Í	IVLIGLALLLIWKLLMIIHDRREFAKFEKEKMNAKWDTGENPIY
			KSAVTTVVNPKYEGK
6078	1426	180	BTEDVMELLEEDLTCPICCSLFDDPRVLPCSHNFCKKCLEGILE
1	1		GSVRNSLWRPVPFKCPTCRKKTFSYWELIPLQVNYSLKGIVEKY
ł	1		NKIKISPKMPVCKGH\LGQPLNIF\CL\TDMQLDL/CGIC\ATR
		İ	GEHTKHVFCSIEDAYAQERDAFESLFQSFETWRRGDALSRLDTL
1		:	ETSKRKSLQLLTKDSDKVKEFFEKLQHTLDQKKNEILSDFETMK
ı			LAVMON YORK TAKET ORODAY DOWN TO THE TAKET IS DEED WE THE TAKET IS DEED WE THE TAKET IS DEED WE THE TAKET IS DEED WE THE TAKET IS DEED WE THE TAKET IS DEED WE THE TAKET IS DEED WE THE TAKET IS DEED WE THE TAKET IS DEED WE THE TAKET IS DEED WE THE TAKET IS DEED WE THE TAKET IS DEED WE THE TAKET IS DEED WE THE TAKET IS DEED WE THE TAKET IS DEED WE THE TAKET IS DEED WE THE TAKET IS DEED WE THE TAKET IS DEED WE THE TAKET IS DEED WE THE TAKET IS DEED WE THE TAKET IS DEED WE THE TAKET IS DEED WE THE TAKET IS DEED WE THE TAKET IS DEED WE THE TAKET IS DEED WE THE TAKET IS DEED WE THE TAKET IS DEED WE THE TAKET IS DEED WE THE TAKET IS DEED WE THE TAKET IS DEED WE THE TAKET IS DEED WE THE TAKET IS DEED WE THE TAKET IS DEED WE THE TAKET IS DEED WE THE TAKET IS DEED WE THE TAKET IS DEED WE THE TAKET IS DEED WE THE TAKET IS DEED WE THE TAKET IS DEED WE THE TAKET IS DEED WE THE TAKET IS DEED WE THE TAKET IS DEED WE THE TAKET IS DEED WE THE TAKET IS DEED WE THE TAKET IS DEED WE THE TAKET IS DEED WE THE TAKET IS DEED WE THE TAKET IS DEED WE THE TAKET IS DEED WE THE TAKET IS DEED WE THE TAKET IS DEED WE THE TAKET IS DEED WE THE TAKET IS DEED WE THE TAKET IS DEED WE THE TAKET IS DEED WE THE TAKET IS DEED WE THE TAKET IS DEED WE THE TAKET IS DEED WE THE TAKET IS DEED WE THE TAKET IS DEED WE THE TAKET IS DEED WE THE TAKET IS DEED WE THE TAKET IS DEED WE THE TAKET IS DEED WE THE TAKET IS DEED WE THE TAKET IS DEED WE THE TAKET IS DEED WE THE TAKET IS DEED WE THE TAKET IS DECENTRANCE IN THE TAKET IS DECENTRANCE IN THE TAKET IS DECENTRANCE IN THE TAKET IS DECENTRANCE IN THE TAKET IS DECENTRANCE IN THE TAKET IS DECENTRANCE IN THE TAKET IS DECENTRANCE IN THE TAKET IS DECENTRANCE IN THE TAKET IN THE TAKET IN THE TAKET IN THE TAK
			LAVMQAYDPEINKLNTILQEQRMAFNIABAFKDVSEPIVFLQQM
1			QEFREKIKVIKETPLPPSNLPASPLMKNFDTSQWEDIKLVDVDK
i	1 · ·		LSLPQDTGTFISKIPWSFYKLFLLILLLGLVIVFGPTMFLEWSL
1			FDDLATWKGCLSNFSSYLTKTADFIEQSVFYWEQVTDGFFIFNE
6079	1586		RFKNFTLVVLNNVAEFVCKYKLL
1 80.3	1 1286	141	ATARDLGCARRIDRVVMESTPSRGLNRVHLQCRNLQEFLGGLSP
1	. 1		GVLDRLYGHPATCLAVFRELPSLAKNWVMRMLFLEOPLPODAVA
i	1		LWVKKEFSKAQEESTGLLSGLRIWHTQLLPGGLOGLTLNPTFRO
i	i .		NLRIALLGGGKAWSDDTSQLGPDKHARDVPSLDKYAEERWEVVL
1	1	•	HFMVGSPSAAVSQDLAQLLSQAGLMKSTEPGEPPCTTSAGFOFT.
İ			LLDTPAQLWYFMLQYLQTAQSRGMDLVEILSFLFQLSFSTLGKD
	1		YSVEGMSDSLLNFLQHLREFGLVFQRKRKSRRYYPT/RALAINL
ľ	i i		SSGVSGAGGTVHQPGFIV\VETNYRLYAYTBSELQIALIALFSE
1			MLYPFP\NMVV\ARVTR\ESVQQAIASGITAQQIIHFLRTRAHP
1	1 1		VMLKQTPVLPPTITDQIRLWELERDRLRFTEGVLYNQFLSQVDF
		·	ELL\LAHAPKLGVLVFB/NTPAKRLMVVTPAGHSDVKRFWKRQK
	ľ		HSS
6080	1	1199	
ĺ	- 1	1139	TETIDHVGEFAMAAQAAGVSRQRAATQGLGSNQNALKYLGQDFK
i I			TLRQQCLDSGVLFKDPEFPACPSALGYKDLGPG8PQTQGIIWKR
, l		}	PTELCPSPQFIVGGATRTDICQGGLGDCWLLAAIASLTLNEELL
} [			YRVVPRDQDFQENYAGIFHFQPLCPPSP\FWQYGEWVEVVIDDR
<b>!</b>		j	LPTKNGQLLFLHSEQGNEFWSALLEKAYAKLNGCYEALAGGSTV
1 1	'		EGFEDFTGGISEFYDLKKPPANLYQIIRKALCAGSLLGCSIDVY
) 1		1	SAAEAEAITSQKLVKSHAYSVTGVEEVNFOGHPEKLIRLRNDWG
ļ. ļ	ŀ		EVEKSGAWSDDAPEWNHIDPRRKEELDKKVEDGEFWMSLSDEVP
). I	ì	ļ	QFSRLEICNLSPDSLSSEEVHKWNLVLFNGHWTRGSTAGGCQNY
	<u> </u>		PGSS
6081	3	865	EMLPLLLPLPLLWA/GALAQDARFRLEMPESVTVQEGLCIFVHC
	1	į.	SVFYLEYGWKDSTPAYGHWFREGVSVDQETPVATNNSTQKVQKE
	1	j	TOGRPHLLGDPSRNNCSLSIRDARRRDNGSYFFWVARGRTKFSY
	ł	1	KYSPLSVYVTALTHRPDILIPEFLKSGHPSNLTCSVPWVCEQGT
i			PPIFSWMSAADTSLGDDTLUCGUTTTTDDOORGET
1			PPIFSWMSAAPTSLGPRTLHSSVLTIIPRPQDHGTNLICQVTPP
	ļ	,	GAGVTTERTIQLSVSWKSGTVEEVVVLAVGVVAVKILLLCLCLI
6082	283	1288	ILSFHKKKAVRAVEVEENVYAVMG
		1208	EARSPGPTQTRTAPGLAAPGLAQPAALRLLLSRPPSAAMDGDGD
- 1	1		PESVGQPEEASPEEQPEEASAEEERPEDQQEEEAAAAA\Y\LDE
l			LPEPLLA/LRVLAALPRHE\LVQACR\LVCLRWKELVDGAPT.WT.
- 1		1	LKCQQEGLVPEGGVEEERDHWQQFYFLSKRRRNLLRNPCGEEDI.
1		i	EGWCDVEHGGDGWRVEELPGDSGVEFTHDESVKKYFASSFEWCR
ſ	į	ł	KAQVIDLQAEGYWEELLDTTQPAIVVKDWYSGRSDAGCLYELTV
ļ	ŀ	1.	KLLSEHENVLAEFSSGQVAVPQDSDGGGWMEISHTFTDYGPGVR
		ļ	FVRFEHGGQDSVYWKGWFGARVTNSSVWVEP
6083	1865	309	KOWCAERRGLGMSLADELLADLEEAAEEEEGGSYGEEEEEPAIE

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
ĺ	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
ļ	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
-	amino acid	h .	P=Proline, Q=Glutamine, R=Arginine,
	residue of	residue of	S=Serine, T=Threonine, V=Valine,
	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1		sequence	Codon, /=possible nucleotide deletion
	sequence		\=possible nucleotide insertion)
			DVQEETQLDLSGDSVKTIAKLWDSKMFAEIMMKIERVISKOAVA
1			SEVMGPVEAAPEYRVIVDANNLTVEIENELNITHKEIDDKVCVB
1	<b>{</b>		FPBLESLVPNALDYIRTVKELGNSLDKCKNNENLQQILTNATIM
1		ļ	VVSVTASTTOGOOLSEEELERLEEACDMALELNASKHRIYEYVE
1			SRMSFIAPNLSIIIGASTAAKIMGVAGGLTNLSKMPACNIMLLG
			AQRKTLSGFSSTSVLPHTGYIYHSDIVQSLPPIPPPFSVAP\DL
i	1		RRKAARLVAAKCTLAARVDSFHESTEGKVGYELKDEIERKFDKW
i	1		QEPPPVKQVKPLPAPLDGQRKKRGGRRYRKMKERLGLTEIR\KQ
1 .	1		ANRMSFGEIEEDAYQEDLGFSLGHLGKSGSGRVRQTQVNEATKA
			RISKTLORTLOKOSVVYGGKSTIRDRSSGTASSVAPTPLOGLEI
İ	}		VNPQAAEKKVAEANQKYFSSMAEFLKVKGEKSGLMST
6084	1865	309	KOWCAPPRCI CMCLADRI Y DOLLAR TOKOK GEKSGLMST
Į	i		KQWCAERRGLGMSLADELLADLEEAAEEEEGGSYGEEEEEPAIE
Í			DVQEETQLDLSGDSVKTIAKLWDSKMFAEIMMKIEEYISKQAKA
1 1			SEVMGPVEAAPEYRVIVDANNLTVEIENELNIIHKFIRDKYSKR
1			FPELESLVPNALDYIRTVKELGNSLDKCKNNENLQQILTNATIM
			VVSVTASTTQGQQLSEELERLEEACDMALELNASKHRIYEYVE
			SRMSFIAPNLSIIIGASTAAKIMGVAGGLTNLSKMPACNIMLLG
1			AQRKTLSGFSSTSVLPHTGYIYHSDIVQSLPPIPPPFSVAP\DL
1 1	' . I		RRKAARLVAAKCTLAARVDSFHESTEGKVGYELKDEIERKFDKW
1 1	)		QEPPPVKQVKPLPAPLDGQRKKRGGRRYRKMKERLGLTEIR\KQ
	t t		ANRMSFGEIEEDAYQEDLGFSLGHLGKSGSGRVRQTQVNEATKA
1 1	1		RISKTLORTLOKOSVVYGGKSTIRDRSSGTASSVAFTPLOGLEI
6085	2	1455	VNPQAAEKKVAEANQKYFSSMAEFLKVKGEKSGLMST
	•	1456	SGPRSFQGNRAVGRISLGGKRNPEVTLLPGVSSERVRRWRRARV
1			GVARVKPGNPWKPSPATQVPR/VPAQVYLPGRGPPLREGEELVM
1 1			DEEAYVLYHRAQTGAPCLSFDIVRDHLGDNRTELPLTLVLCDGT
1 1	-		QAESAQSNRLMMLRMHNLHGTKPPPSEGSDEREEEEDERDERE
} [			KPQLELAMVPHYGGINRVRVSWLGEEPVAGVWSEKGOVEVENIE
f t			RLLQVVEEPQALAAFLRDEQAOMKPIFSFAGHMGEGFALDUSDB
	1		VIGRULTGDCQKNIHLWTPTDGGSWHVDORPFVGHTRSVEDI OW
1 1	i		SPIENTVFASCSADASIRIWDIRAAPSKACMLTTATAHDGDVANA
1		i	ISWSRREPFLLSGGDDGALKIWDLROFKSGSPVATEKOHVADUT
1 1		İ	SVEWHPQDSGVFAASGADHOITOWDLG/IVERDPEAGDURADDG
] . [	i		LADLPQQLLFVHQGETELKELHWHPQCPGLLVSTALSGFTIFRT
6086			ISV
1 8008 1	2419	1357	GAATQHGGAMNLLPCNPHGNGLLYAGFNQDHGCFACGMENGFRV
1		i	YNTDPLKEKEKQEFLEGGVGHVEMLFRCNYLALVGGGKKEKVDD
1		ļ	NKVMIWDDLKKKTVIEIEFSTEVKAVKLRR\DKTVVVI.DGMTVV
j j			FTFTHNP\HQLHVFE\TCYNPKGLCVLCPNSNNSI.I.A FPGTHTG
			HVQLVDLASTEKPPVDIPAHEGVLSCIALNLOGTRIATASRKCT
]		Í	LIRIFDTSSGHLIQELRRGSQAANIYCINFNODASLICVSSDHG
	i		TVHIFAAEDPKRNKQSSLASASFLPKYFSSKWSFSKFOVDSGED
1	j	1	CICAFGTEPNAVIAICADGSYYKFLFNPKGECIRDVYAQFLEMT
			DDKT (
6087	476	1877	QNSQRTGLPITIFSRSFPLLTGSDLCBNMPCTCTWRNWRQWIRP
}	.	. 1	LVAVIYLVSIVVAVPLCVWELQKLEVGIHTKAWFIAGIFLLLTI
ļ	1	1	PISLWVILQHLVHYTQPELQKPIIRILWMVPIYSLDSWIALKYP
ĺ	1	ł	GIAIYVDTCRECYEAYVIYNFMGFLTNYLTNRYPNLVLILEAKD
1		1	QQKHFPPLCCCPPWAMGEVLLFRCKLGVLQYTVVRPFTTIVALI
- 1	1		CELLGIYDEGNFSPSNAWTYLVIINNMSQLFAMYCLLLFYKVLK
1			EELSPIQPVGKFLCVKLVVFVSFWQAVVIALLVKVGVISEKHTW
J		į.	EWQTVEAVATGLQDFIICIEMFLAAIA\HHYTFSYKPYVQEARE
1		1.7	GSCFDSFLAMWDVSDIRDDISEQVRHVGRTVRGHPRKKLFPEDQ
ļ		1	DQNEHTSLLSSSSQDAISIASSMPPSPMGHYQGFGHTVTPQTTP
		;	TTAKISDEILSDTIGEKKEPSDKSVDS
6088	1684	689	GASGLVRLLQQGHRCLLAPVAPKLVPPVRGVKKGFRAAFRFOKE
·	l		LEROSLIBCODDODODOSEVOTO TO THE TAKE OF THE TAKE
1	1	Ji	LERQRLLRCPPPPVRRSEKPNWDYHAEIQAFGHRLQENFSLDLL
ſ	į	[ ;	KTAFVNSCYIKSEBAKRQQLGIEKEAVLLNLKSNQELSEQGTSF
ŀ	ŀ	12	SOTCLTOFLEDEYPOMPTEGIKNLVDFLTGEEVVCHVARNLAVE
		1 %	QLTLSEEPPVPPAVLQQTFFAVIGALLQSSGPERTALFIRDFLI
		<del> 1</del>	romtgkelfemwkiinpmgllvbelkkrnvsapesrltrosg\a

	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
	ID	beginning	nuclectide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	NO:	nucleotide	location	Glutamic Acid, F-Phenylalanine, G-Glycine,
		location	corresponding	H=Histidine, I=Isoleucine, K=Lysine.
		corresponding	to first	L-Leucine, M-Methionine, N-Asparagine
		to first	amino acid	P=Proline, Q=Glutamine, R=Arginine
		residue of	residue of amino acid	S=Serine, T=Threonine, V=Valine,
i		amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
		sequence	sequence	Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
		- <del> </del>	<del> </del>	PTALPLYFVGLYCDKKLIAEGPGETVLVAEEEAARVALRKLYGF
l		_		TENRRPWNYSKPKETLRAEKSITAS
[	6089	3	3054	TRLGIPGSTISSRPRLCALAAEGHFLGHSWTGSRAGAHTGAPAW
		1		PSRRLRDLPAGGMWRLRRAAVACEVCQSLVKHSSGIKGSLPLQK
- 1		İ	1	LHLVSRSIYHSHHPTLKLQRPQLRTSFOOFSSLTNLDIDKIKES
		1		PIKYGYQPRRNFWPARLATRLLKLRYLILGSAVGGGYTAXKTED
ı				QWKDMIPDLSEYKWIVPDIVWEIDEYIDFEKIRKALPSSEDLVK
ı				LAPDFDKIVESLSLLKDFFTSGSPEETAFRATDRGSESDKHFRK
- 1				VSDKEKIDQLQEELLHTQLKYQRILERLEKENKELRKLVLQKDD
ļ				KGIPFIBSLRKSLIDMYSEVLDVLSDYDASYNTQDHLPRVVVVG
		,		DQSAGKTSVLEMIAQARIFPRGSGEMMTRSPVKVTLSEGPHHVA LFKDSSREFDLTKEEDLAALRHEIELRMRKNVKEGCTVSPETIS
- 1			•	LNVKGPGLQRMVLVDLPGVINTVTSGMAPDTKETIFSISKAYMQ
- 1				DPNAIILCIQDGSVDAERSIVTDLVSQMDPHGRRTIFVLTKVDL
-1		· I		AEKNVASPSRIQQIIEGKLFPMKALGYFAVVTGKGNSSRSIEDI
- 1		1.		REYEEEFFQNSKLLKTSMLKAFQVTTRNLSLAVSDCFWKMVRES
- [		e.		VEQQADSFKATRFNLETEWKNNYPRLRELDRNELFEKAKNETLD
				EVISLSQVTPKHWEEILQQSLWERVSTHVIENIYLPAAQTMNSG
				TFNTTVDIKLKQWTDKQLPNKAVEVAWETLQEEFSRFMTEPKGK
				EHDDIFDKLKEAVKEESIKRHKWNDFAEDSLRVIQHNALEDRSI SDKQQWDAAIYFMEEALQARLKDTENAIENMVGPD\WKKRWLYW
1				KNRTQEQCVHNETKNELEKMLKCNEEHPAYLASDEITTVRKNLE
				SRGVEVDPSLIXDTWHQVYRRHFLKTALNHCNLCRRGFYYYQRH
				FVDSELECNDVVLFWRIQRMLAITANTLROOLTNTEVRRIEKMV
		1		KEVLEDFAEDGEKKIKLLTGKRVQLAEDLKKVREIQEKLDAFIE
H	6090	194	1560	ALHQEK
-	****	134	1560	PVFVPAPGAVLEQAS/ASPPLATQTVVPLQHCKIPELPVQASIL
1				FELQLFFCQLIALFVHYINIYKTVWWYPPSHPPSHTSLNFHLID
1	•			FNLLMVTTIVLGRRFIGSIVKEASQRGKVSLFRSILLFLTRFTV LTATGWSLCRSLIHLFRTYSFLNLL/FPLLSVWDVHSVFAAELR
		İ		P\RKTSLFNHMASMGPREAVSGLAKSRDYLLTLR\RRGSSTQDS
ı			ı	CMARTPCP/PHACCLSPSLIRSEVEFLKMDFNWRMKEVI.VSSMI.
1				SAYYVAFVPVWFVKNTHYYDKRWSCELFLLVSISTSVTLMOHT.
				PASYCOLLHKAAAHLGCWQKVDPALCSNVLOHPWTEECMWPOGV
				LVKESKNVYKAVGHYNVAIPSDVSHFRFHFFFSKDI.RTI.NTT.L.
			i	LEGAVIVYQLYSLMSSEKWHQTISLALILFSNYYAFFKLLRDRL VLGKAYSYSASPQRDLDHRFS
Г	6091	3279	412	SSRTREMEEKEILRRQIRLLQGLIDDYKTLHGNAPAPGTPAASG
1				WQPPTYHSGRAFSARYPRPSRRGYSSHHGPSWRKKYSLVNRPPG
1			Ì	PSDFPADHAVRPLHGARGGQPPVPQQHVLERQVQLSQGQNVVIK
				VKPPSKSGSASASGAQRGSLEEFEDTPWSDORPRRGEGEPPRGO
1			i	LQPSRPTRARGTCSVEDPLLVCQKEPGKPRMVKSVGSVGDSPRE
			1	PRRTVSESVIAVKASFPSSALPPRTGVALGRKIGSHSVASCADO
		1	1	LLGDRRVDAGHTDQPVPSGSVGGPARPASGPRQAREASLVVTCR
l				TNKFRKNNYKWVAASSKSPRVARRALSPRVAAENVCKASAGMAN
1	ı			KVEKPQLIADPEPKPRKPATSSKPGSAPSKYKNKASSPSASSS SFRWQSEAGSKDHASQLSPVLSRSPSGD\RPAVGHSGLKPLSGE
	ļ			TPLSAYKVKSRTKIIRRRGSTSLPGDKKSGTSPAATAKSHLSLR
Į	i		i	RRQALRGKSSPVLKKTPNKGLVQVTTHRLCRLPPSRAHLPTKEA
l	- 1		;	SSLHAVRTAPTSKVIKTRYRIVKKTPASPLSAPPFPLSLDSWDA
	ļ	,	1	RRLSLSRSLVLNRLRPVASGGGKAOPGSPWWRSKGYRCIGGVLY
l	ļ			KVSANKLSKTSGQPSDAGSRPLLRTGRLDPAGSCSRSLASDAVO
	l	1		RSLAIIRQARQRREKRKEYCMYYNRFGRCNRGERCPYIHDPEKV
	İ			AVCTRFVRGTCKKTDGTCPFSHHVSKEKMPVCSYFLKGICSNSN
l	]		1	CPYSHVYVSRKAEVCSDFLKGYCPLGAKCKKKHTLLCPDFARRG ACPRGAQCQLLHRTQKRHSRRAATSPAPGPSDATARSRVSASHG
	- 1			PRKPSASQRPTRQTPSSAALTAAAVAAPPHCPGGSASPSSSKAS
		!	1	SSSSSSSPPASLDHEAPSLOEAALAAACSNRLCKLPSFISLOS
١	5092			SPSPGAQPRVRAPRAPLTKDSGKPLHIKPRL
'	.032	143	3190	AKAPPTGESSEPEAKVLHTKRLYRAVVEAVHRIDITLCNKTAVO
-				EVFKPENISLRNKLRELCVKLMFLHPVDYGRKAEELLWRKVYYE

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
}	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ł	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ļ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
į	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ł	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ĺ	amino acid	sequence	Codon, /=possible nucleotide deletion,
ł	sequence	Sequence	\=possible nucleotide insertion)
<b> </b>	sequence	ļ	VIOLIKTNKKHIHSRSTLECAYRTHLVAGIGFYOHLLLYIQSHY
ļ		ì	OLELOCCIDWTHVTDPLIGCKKPVSASGKEMDWAOMACHRCLVY
ţ	<u> </u>	ļ	1
}			LGDLSRYQNELAGVDTELLAERFYYQALSVAPQIGMPFNQLGTL
ł		i	AGSKYYNVEAMYCYLRCIQSEVSFEGAYGNLKRLYDKAAKMYHQ
1		}	LKKCETRKLSPGKKRCKDIKRLLVNFMYLQSLLQPKSSSVDSEL
ł			TSLCQSVLEDFNLCLFYLPSSPNLSLASEDEREYESGYAFLPDL
ļ	<b>∫</b> ·	<b>}</b>	LIFQMVIICLMCVHSLERAGSKQYSAAIAFTLALFSHLVNHVNI
	1		RLQAELEEGENPVPAFQSDGTDEPESKEPVEKEEEPDPEPPPVT
ļ	†	Ì	PQVGEGRKSRKFSRLSCLRRRRHPPKVGDDSDLSEGFESDSSHD
ł			SARASEGSDSGSDKSLEGGGTAFDAETDSEMNSQESRSDLEDME
1			EEEGTRSPTLEPPRGRSEAPDSLNGPLGPSEASIASNLQAMSTQ
ł	}	1	MFQTKRCFRLAPTFSNLLLQPTTNPHTSASHRPCVNGDVDKPSE
ł	1	ì	PASEEGSESEGSESSGRSCRNERSIQEKLQVLMAEGLLPAVKVF
J	1	1	LDWLRTNPDLIIVCAQSSQSLWNRLSVLLNLLPAAGELQESGLA
l		1	LCPEVQDLLEGCELPDLPSSLLLPEDMALRNLPPLRAAHRRFNF
}	}	İ	DTDRPLLSTLEESVVRICCIRSFGHFIARLQGSILQFNPEVGIF
ł		}	VSIAQSEQESLLQQAQAQFRMAQEEARRNRLMRDMAQLRLQLEV
}		}	SQLEGSLQQPKAQSAMSPYLVPDTQALCHHLPVIRQLATSGRFI
}	]		VIIPRTVIDGLDLLKKEHPGARDGIRYLEAEFKKGNRYIRCQKE
1		i e	VGKSFERHKLKRQDADAWTLYKILDSCKQLT\LAQGAGEEDPSG
}	1	ľ	MVTIITGLPLDNPSLLSGPMQAALQAAAHASVDIKNVLDFYKQW
ł	Ì	1	KEIG
6093	76	1002	ACGRRAMLALRVART/SRWGAL\RGAVWAPGTRPSKRRACWALL
ł		•	PPVPCCLGCLAERWRLRPAALGLRLFGIGQRNHCSGAGKAAPR\
ì		}	PAAGAGAAAEAPGGQWGPASTPSLYENPWTIPNMLSMTRIGLAP
ł	}	1	VLGYLIIEEDFNIALGVFALAGLTDLLDGFIARNWANQRSALGS
}		}	ALDPLADKILISILYVSLTYADLIPVPLTYMIISRDVMLIAAVF
}	)	}	YVRYRTLPTPRTLAKYFNPCYATARLKPTFISKVNTAVQLILVA
i .		1	ASLAAPVFNYADSIYLQILWCFTAFTTAASAYSYYHYGRKTVQV
1	}		IKD
6094	23	1010	PFLRCLRGDQKAKMSERKVLNKYYPPDFDPSKIPKLKLPKDRQY
}		1	VVRLMAPFNMRCKTCGEYIYKGKKFNARKETVQNEVYLGLPIFR
	1	1	FYIKCTRCLAEITFKTDPENTDYTMEHGATRNFQAEKLLEEEEK
{ ·	}	}	RVQKEREDEELNNPMKVLENRTKDSKLEMEVLENLQELKDLNQR
1		<b>j</b>	QAHVDFEAMLROHRLSEEERRRQQQEEDEQETAALLEEARKRRL
}			LEDSDSEDEAAPSPLQPALRPNPTAILDEAPKPKRKVEVWEQSV
}	[	[	GSLGSRPPLSRLVVVKKAKADPDCSNGQPQA/APHPRSPAEQEG
1	}	}	GOPYTPDAWRVLPEPTGCIPGO
6095	1	1599	TRGRAAERSRGRGHGFLGGGFA\SVVDYFPSEDFYRCGYCKNES
2000	1	1555	GSRSNGMWAHSMTVQDYQDLIDRGWRRSGKYVYKPVMNQTCCPQ
	1	[	YTIRCRPLOFOPSKSHKKVLKKMLKFLAKGEVPKGSCE\DEPMD
1		ļ	
1		1	STMDDAVAGDFALINKLDIQCDLKTLSDDIKESLESEGKNSKKE
	l	L	EPQELLQSQDFVGEKLGSGEPSHS

TRADOCS:1416257.1(%CSH011.DOC)

	SEO	Predicted	Predicted end	
Ì	ID	beginning	nucleotide	Amino acid segment containing signal peptide
- 1	NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
		location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
		corresponding	to first	
ı		to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
- 1		amino acid		P=Proline, Q=Glutamine, R=Arginine,
- 1		residue of	residue of	S=Serine, T=Threonine, V=Valine,
- 1		amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
- [			sequence	Codon, /=possible nucleotide deletion
ŀ		sequence		\=possible nucleotide insertion)
- 1				VKVHTVPKPGKGADLSKPPCRKAKE I RKRRKRI KI MOONDAGET
- 1				EGFQAQGHPPSLFPPKAKSNOPKSLEDLIPESI.DENA SUKT.EUD
				VVRSSPPSSQFKATLLESYOVYKRYOMVIHKNDDDTDTDCCDTD
- 1				FLCSSPLEAETPPNGPDCGYGSFHOOYWLDGKTTAVGYTDTLDN
		,		CVSSVYLYYDPDYSFLSLGVYSALREIAFTROLHEKTSOLSVVV
- [				MGFYIHSCPKMKYKGQYRPSDLLCPETYVWVPIEQCLPSLENSK
			•	YCRFNQDPEAVDEDRSTEPDRLQVFHKRAIMPYGVYKKQQKDPS
Ļ				EEAAVLQYASLVGQKCSERMLLFRN
- 1	6096	2277	575	QRVRAALLSSAMEDSEALGFEHMGLDPRLLQAVTDLGWSRPTLI
ł		. }		QEKAIPLALEGKOLLARARTGSGKTAAYAIPMLQLLLHRKATGP
ı				VVEQAVRGLVLVPTKELARQAQSMIQQLATYCARDVRVANVSAA
J				EDSVSQRAVLMEKPDVVVGTPSRILSHLQQDSLKLRDSLELLVV
	1			DEADLLFSFGFEEELKSLLCHLPRIYQAFLMSATFNEDVQALKE
ı	l	j		LILHNPVTLKLQESQLPGPDQLQQFQVVCETEEDKFLLLYALLK
- [	Ţ	i		LSLIRGKSLLFVNTLERSYRLRLFLEQFSIPTCVLNGELPLRSR
-	- 1			CHIISQPNQGFYDCVIATDAEVLGAPVKGKRRGRGPKGDKASDP
	1	1		EAGVARGIDFHHVSAVLNFDLPPTPEAYIHRAGRTARANNPGIV
1				LTFVLPTEQFHLGKIEBLLSGENRGPILLPYQFRMEEIEGFRYR
1		j		CRDAMRSVTKQAIREARLKEIKEBLLHSEKLKTYFEDNPR\DLQ
	1	i		LLRHDLPLHPAVVKPHLGHVPDYLVPPALRGLVRPHKK\GRSCL
L		1		PLVGRPREQSPRTHCAASSTKERNSDPQPSPPEVVGPLWS
Г	6097	1673	192	APGTMSGGKKKSSFQITSVTTDYEGPGSPGASDPPTPQPPTGPP
	ł	1		PRLPNGEPSPDPGGKGTPRNGSPPPGAPSSRFRVVKLPHGLGEP
				YRRGRWTCVDVYERDLEPHSFGGLLEGIRGASGASGRSLDSRL
		1		ELASLGLGAPTPPSGLSQGPTSWLRPPPTSPGPQARSFTGGLGQ
1	- 1	*		LVVPSKAKAEKPPLSASSPQQRPPEPETGESAGTSRAATPLPSL
1	ľ	İ		RVEAEAGGSGARTPPLSRRKAVDMRLRMELGAPEEMGQVPPLDS
1.	ŀ	1		RPSSPALYFTHDASLVHKSPDPFGAVAAQKFSLAHSMLAISGHL
	[			DSDDDSGSGSLVGIDNKIEQAMDLVKSHLMFAVREEVEVLKEQI
	f			RELAERNAALEQENGLLRALA\SPEQLGSAGPPRGVPR\LGPPA
1	]			PNGPFVLSLPSLTIVPLGLPGLASAAWPPLPMPALIVPVFPGVG
ì		į.		VQALSNGPWSPGPLPHLLIIPSLDGGEGFRTGRQQGAPFGEET
L		1		QPPPSLPGTPQQ
[	6098	168	1074	NYCLRHRSPLEKDSSPGSSSTSLLIKKQRETSDTFIMRALKELD
1			}	EGKIFKNWGTQTEKEDTSNINPRQTETSVNASRSPEKCAQQRQK
ł	}	ì		RLNSASQRSSSLPPSNRKSSTPTKREIMLTPVTVAYSPKRSPKE
ı				NLSPGFSHLLSKNESSPIRFDILLDDLDTVPVSTLQRTNPRKQL
	1			\QFLPLDDSEEK\TYSEKAT\DNIVNHSSCPBPVPNGVKKVSVR
1	1	}	ŀ	TAWEKNKSVSYEQCKPVSVTPQGNDFEYTAKIRTLAETERFF\D
L		_ 1	Ì	ELTKEKDQIEAALSRMPSFGGRITLQTRLNQEAFGRSFGKD
1	6099	168	1074	NYCLRHRSPLEKDSSPGSSSTSLLIKKQRETSDTPIMRALKELD
1	1			EGKTEVNWGTOTEVEDTONINDS
ı	i			EGKIFKNWGTQTEKEDTSNINPRQTETSVNASRSPEKCAQQRQK
l				RLNSASQRSSSLPPSNRKSSTPTKREIMLTPVTVAYSPKRSPKE
ı	l			NLSPGFSHLLSKNESSPIRFDILLDDLDTVPVSTLQRTNPRKQL
	- 1		1	\QFLPLDDSEEK\TYSEKAT\DNIVNHSSCPEPVPNGVKKVSVR
L	Ī	1	1	TANEKNKSVSYEQCKPVSVTPQGNDFEYTAKIRTLAETERFF\D
	6100	2	713	ELTKEKDQIEAALSRMPSPGGRITLQTRLNQEAFGRSFGKD
		j	' '- '	FVEVSGYRSRADPEPRGRDTMTYAYLFKYIIIGDTGVGKSCLLL
	1		] ]	QFTDKRFQPVHDLTIGVEFGARMVNIDGKQIKLQIWDTAGQESF
	J	1	1:	RSITRSYYRGAAGALLVYDITRRETFNHLTSWLEDARQHSSSNM
	Ì		1 '	VIMLIGNKSDLESRRDVKREEGEAPARE\HGLTFMFTSAVTACNI
	J	1	1 '	VEEAFINTAKEIYRKIQQGLFDVHNEANGIKIGPOOSISTSVGP
E	5101	1	13	SASQKNSRDIGSNSGCC
		- <u>-</u>	1333	FRGRAWPLREVSHWLGCRRVCSWSASWGRLPALSARLSPLLAFR
	ļ		1.0	JKMYFPLSCAVQQYAWGKMGSNSEVARLLASSDPLAGTAEDKDV
_				AELWMGTHPRGDAKILDNRISQKTLSQWIAENQDSLGSKVKDTF

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
Į.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	scquence	Codon, /=possible nucleotide deletion,
L	sequence	•	\=possible nucleotide insertion)
			NGNLPFLFKVLSVETPLSIQAHPNKELAEKLHLQAPQHYPDANH
-			KPEMAIALTPFQGLCGFRPVEEIVTFLKKVPEFQFLIGDEAATH
1	ļ		LKQTMSHDSQAVASSLQSCFSHLMKSEKKVVVEQLNLLVKRISQ
1	1		QAAAGNNMEDIFGELLLQLHQQYPGDIGCFAIYFLNLLTLKPGE
j			AMFLEANVPHAYLKGDCVECMACSDNTVRAGLTPKFIDVPTLCE
			MLSYTPSSSKDRLFLPTRSQEDPYLSIYDPPVPDFTIMKA\EVP
	!		G\SVTEYKDLALDSASILLMVQGTVIASTPTTQTPIPLQRGGVL
L			FIGANESVSLKLTEPKDLLIFRACCLL
6102	70	2415	QTPQATLAANGAEDSRGGEMLPAGEIGASPAAPCCSESGDERKN
			LEEKSDINVTVLIGSKQVSEGTDNGDLPSYVSAFIEKEVGNDLK
			SLKKLDKLIEQRTVSKMQLEEQVLTISSEIPKRIRSALKNAEES
1			KOPLNOFLEGETHLFSAINSHLLTAQPWMDDLGTMISQIEEIER
			HLAYLKWISQIEELSDNIQQYLMTNNVPBAASTLVSMAELDIKL
1	1		QESSCTHLLGFMRATVKFWHKILKDKLTSDFEEILAQLHWPFIA
			PPQSQTVGLSRPASAPEIYSYLETLFCQLLKLQTSHELLTEPK\
]			HSQKNTLFLPPLLSS/WPIQVMLTPLOKRFRYHFRGNROTMULS
! !	[		KPEWYLAQVLMWIGNHTEFLDEKIQPILDKVGSLVNARLEFSRG
1 1			LMMLVLEKLATDIPCLLYDDNLFCHLVDEVLLFERELHSVHGYP
			GTFASCMHILSEETCFQRWLTVERKFALOKMDSMLSSEAAWVSO
			YKDITDVDEMKVPDCAETFMTLLLVITDRYKNLPTASRKLOFLE
1 1			LQKDLVDDFRIRLTQVMKEETRASLGFRYCAILNAVNYISTVLA
1			DWADNVFFLQLQQAALEVFAENNTLSKLQLGQLASMESSVFDDM
1			INLLERLKHDMLTRQVDHVFREVKDAAKLYKKERWLSLPSOSEO
1 1			AVMSLSSSACPLLLTLRDHLLQLEQOLCFSLEKIFWOMLVEKLD
1 1	•		VYIYQEIILANHFNEGGAAQLQFDMTRNLFPLFSHYCKRPENYF
6103			KHIKEACIVLNLNVGSALTAGKDVLPVQLQGSFPAT
1 6203	207	2523	ESNSTMTTYLEFIQQNEERDGVRFSWNVWPSSRLEATRMVVPVA
1 1	'	•	ALFTPLKERPDLPPIQYEPVLCSRTTCRAVLNPLCQVDYRAKLW
1			ACNFCYQRNQFPPSYAGISELNQPAELLPQFSSIEYVVLRGPQM
1 1	1		PLIFLYVVDTCMEDEDLQALKESMQMSLSLLPPTALVGLITFGR
1 1			MVQVHELGCEGISKSYVFRGTKDLSAKQLQEMLGLSKVPVTQAT
1 1			RGPQVQQPPPSNRFLQPVQKIDMNLTDLLGELQRDPWPVPQGKR
1	ŀ	!	PLRSSGVALSIAVGLLECTFPNTGARIMMFIGGPATQGPGMVVG
1	}		DELKTPIRSWHDIDKDNAKYVKKGTKHFEALANRAATTGHVIDI
	ļ		YACALDQTGLLEMKCCPNLTGGYMVMGDSFNTSLFKQTFQRVFT
j	ŀ		KDMHGQFKMGFGGTLEIKTPR\EIKISGAIGPCVSLNSKGPCVS
[ [			ENEIGTGGTCQWKICGLSPTTTLAIYFEVVNQHNAPIPQGG\RG
, 1			A\IQFVTQY\QHSSGQRRIRVTTIARN\WADAQTQIQNIAASFD
1 1	1	ľ	QEAAAILMARLAIYRAETEEGPDVLRWLDRQLIRLCCKFGEYHK DDPSSFRFSETFSLYPQFMFHLRRSSFLQVFNNSPDESSYYRHH
[	1		FMRQDLTQSLIMIQPILYAYSFSGPPEPVLLDSSSILADRILLM
[ [	1	l	DTFFQILIYHGETIAQWRKSGYQDMPEYENFRHLLQAPVDDAQE
j		1	ILHSRFPMPRYIDTEHGGSQARFLLSKVNPSQTHNNMYAWGQES
(	}	}	GAPILTDDVSLQVFMDHLKKLAVSSAA
6104	124	732	KVSEYIILSKDKILFHALAMLVLVVSPWSAARGVLRNYWERLLR
			KLPQSRPGFPSPPWGPALAVQ\AQPCLQSQQMIPVEVKRI/RSL
	ĺ		LDSIFWMAAPKNRRTIEVNRCRRRNPQKLIKVKNNIDVCPECGH
1	1	J	LKQKHVLCAYCYEKVCKETAEIRRQIGKQEGGPFKAPTIETVVL
			YTGETPSEQDQGKRIIERDRKRPSWFTQN
6105	3	989	PLHGACTSLVLQRFCHRRPRPCAPARPEDMRRPAAVPLLLLLCF
	ŀ		GSQRAKAATACGRPRMLNRMVGGQDTQEGEWPWQVSIQRNGSHF
[ [			CGGSLIAEQWVLTAAHCFRNTSETSLYQVLLGARQLVQPGPHAM
	ľ		YARVRQVESNPLYQGTASSADVALVELEAPVPFTNYILPVCLPD
			PSVIFETGMNCWVTGWGSPSEEDLLPEPRILQKLAVPIIDT\PR
i		1	CNLLYSKDTEFGYQPKTIKNDMLCAGFEEGKKDACKGDSAGPLV
_	1		CLVGQSWLQAGVISWGEGCARQNRPGVYIRVTAHHNWIHRIIPK

SEQ	Predicted	Predicted end	Amino agid gogmant contact
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
İ	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
ł	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid		P=Proline, Q=Glutamine, R=Arginine,
ì	residue of	residue of	S=Serine, T=Threonine, V=Valine,
		amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, +=Stop
i	amino acid	sequence	Codon, /=possible nucleotide deletion,
<u> </u>	sequence		\=possible nucleotide insertion)
			LQVQPSEVGRPEVTPPGPGAP
6106	3	1302	GRPPTAPHTGRPPTANRGDPRLDLKRGCARLLTSIESRGRPAAS
1			AGLRRDRCALRRWPLRRAPLARATRRRAGSPRRCAPRPRACPOG
ı			WSRARHQPGGLCLLLLLCQFMEDRSAQAGNCWLRQAKNGRCQV
1			LYKTELSKEECCSTGRLSTSWTEEDVNDNTLFKWMIFNGGAPNC
i	1		IPCKETCENVDCGPGKKCRMNKKNKPRCVCAPDCSNITWKGPVC
			GLDGKTYRNECALLKARCKEQPELEVQYQGRCKKTCRDVFCPGS
1	1		STCV\VDQTNNAYCVTCNRICPEPASSEQYLCGNDGVTYS\SAC
1			HLRKATCLLGRSIGLAYEGKCIKAKSCEDIQCTGGKKCLWDFKV
]	1		GRGRCSLCDELCPDSKSDEPVCASDNATYASECAMKRAACSSGV
1	1		LIFUYUCCCONCICEDTERREPREDED DODA DO CONTROL
6107	623	168	LLEVKHSGSCNSISEDTEEEEEDEDQDYSFPISSILEW
1		700	SRCSSPRPEPGRGRGK/LSPSEHRKWVEVFKACDEDHKGYLSRE
1			DFKTAVVMLFGYKPSKIEVDSVMSSINPNTSGILLEGFLNIVRK
I			KKEAQRYRNEVRHIFTAFDTYYRGFLTLEDFKKAFRQVAPKLPE
6108	3		RTVLEVFREV\DRDS\DGHVSF
0200	1 3 1	1348	GGSLRFSPPRVPSCSRVFCPVPPGGCGLPSPMSASRPQSPTTPW
			CLPRRYMKHKRDDGPEKQEDEAVDVTPVMTCVFVVMCCSMLVLL
	1		YYFYDLLVYVVIGIFCLASATGLYSCLAPCVRRLP\SASAGESA
1	1 1		LLAPTIPNNSLPYFHKRPQARMLLLALFCVAVSVVWGVFRNEDQ
	1		WAWVLQDALGIAFCLYMLKTIRLPTFKACTLLLLVLFLYDIFFV
ŀ	1		FITPFLTKSGSSIMVEVATGPSDSATREKLPMVLKVPRLNSSPL
ł			ALCDRPFSLLGFGDILVPGLLVAYCHRFDIQVQSSRVYFVACTI
1			AYGVGLLVTFVALALMQRGQPALLYLVPCTLVTSCAVALWRREL
1	1		GVFWTGSGFAKVLPPSPWAPAPADGPQPPKDSATPLSPOPPSEE
Į	] [		PATSPWPAEQSPKSRTSEEMGAGAPMREPGSPAESEGRDQAQPS
<u> </u>	1		PVTQPGASA
6109	1	1381	CRSRAGAASGGAILEGTKLRRQRVDTNKPLDPLVPSALRAAMLY
			LEDYLEMIEQLPMDLRDRFTEMREMDLQVQNAMDQLEQRVSEFF
1	1		MNAKKNKPEWREEQMASIKKDYYKALEDADEKVQLANQIYDLVO
	1		RHLRKLDQELAKFKMELEADNAGITEILERRSLELDTPSQPVNN
1	1 1		HHAHSHTPVEKRKYNPTSHHTTTDHIPEKKFKSEALLSTLTSDA
ſ	<u> </u>		SKENTLGCRNNNSTASSNNAYNVNSSQPLGSYNIGSLSSGTGAG
í	1 1		GI\TMAAAQAVQATAQMKEGRRTSSLKASYEAFKNNDFQLGKEF
	1		SMARETVGYSSSSALMTTLTQNASSSAADSRSGRKSKNNNKSSS
			QQSSSSSSSSLSSGSSSSTVVQEISQQTTVVPESDSNSQVDWT
1			YDPNBPRYCICNQVSYGEMVGCDTQDCPIEWFHYGCVGLTEAPK
			GKWYCPQCT\AAMKRRGSRHK
6110	77	2464	ACPSAATMSDQDHSMDEMTAVVKIEKGVGGNNGGNGNGGGAFSQ
			ARSSTGSSSTGGGGQESQPSPLALIAATCSRIESPNENSNNS
		ľ	QGPSQSGGTGELDLTATQLSQGANGWQIISSSSGATPTSKEQSG
}	• .		SSTNGSNGSESSKNRTVSGGQYVVAAAPNLQNQQVLTGLPGVMP
1			NIQYQVIPQFQTVDGQQLQFAATGAQVQQDGSGQIQIIPGANQQ
[		ľ	IITNRGSGGNIIAAMPNLLQQAVPLQGLANNVLSGQTQYVTNVP
1 1	· [		VALNGNITLLPVNSVSAATLTPSSQAVTISSSGSQESGSQPVTS
	]	1	GTTISSASLVSSQASSSSFFTNANSYSTTTTTSNMGIMNFTTSG
j l	·	1	SSGTNSQGQTPQRVSGLQGSDALNIQQNQTSGGSLQAGQQKEGE
		1	O/NOCLOYFICE CABOLTOOC/ 021 0/ 2 202 2 22 COCCAS
			Q\NQQTQAAPKSI.SRPQLVQGG\QALQ\AFQAAPLSGQTFTTQA
	ĺ	i	ISQETLQNLQLQAVPNSGPIIIRTPTVGPNGQVSWQTLQLQNLQ
		ľ	VQNPQAQTITLAPMQGVSLGQTSSSNTTLTPIASAASIPAGTVT
	j	·	VNAAQLSSMPGLQTINLSALGTSGIQVHPIQGLPLAIANAPGDH
į i	l		GAQLGLHGAGGDGIHDDTAGGEEGENSPDAQPQAGRRTREACT
		ł	CPYCKDSEGRGSGDPGKKKQHICHIQGCGKVYGKTSHLRAHLRW
1	Ì	1	HTGERPFMCTWSYCGKRFTRSDELQRHKRTHTGEKKFACPECPK
l i		1	RFMRSDHLSKHIKTHONKKGGPGVALSVGTLPLDSGAGSEGSGT
		1	ATPSALITTNMVAMEAICPEGIARLANSGINVKEGGQFCSPINT
	<u> </u>		SANGF

Deginning   notleotide   location   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   corresponding   correspo	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Mo:	ID	beginning	1	(Azalanine C-Cysteins D Asserbis 3
Corresponding to first tamino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid acid amino acid amino acid amino acid acid acid acid acid acid acid acid	NO:	nucleotide	location	Giutamic Acid F-Phenylala-i-a C-Cli-
Leleucine, Memethionine, Neapsaragine, amino acid residue of amino acid sequence   Secrite, TeThreonine, VeValine, amino acid sequence   Secrite, TeThreonine, VeValine, Seguence   Sequence   Secrite, TeThreonine, VeValine, Seguence   Sequence   Secrite, TeThreonine, VeValine, Memorial   Sequence   Secrite, TeThreonine, VeValine, Memorial   Sequence   Secrite, TeThreonine, VeValine, Seguence   Secrite, TeThreonine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeValine, VeVali		location		H=Hisridine T=Tsoleucine V=Tusine
amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid	Į	corresponding		LaLeucine Mamethionine Nationaline
residue of amino acid sequence solvence control and acid sequence sequence sequence sequence sequence control and acid sequence control acid sequence control acid sequence control acid sequence control acid sequence control acid sequence control acid sequence control acid sequence control acid sequence control acid sequence control acid sequence control acid sequence control acid sequence control acid sequence control acid sequence control acid sequence control acid sequence control acid sequence control acid sequence control acid sequence control acid sequence control acid sequence control acid sequence control acid sequence control acid sequence control acid sequence control acid sequence control acid sequence control acid sequence control acid sequence control acid sequence control acid sequence control acid sequence control acid sequence control acid sequence control acid sequence control acid sequence control acid sequence control acid sequence control acid sequence control acid sequence control acid sequence control acid sequence control acid sequence control acid sequence control acid sequence control acid sequence control acid sequence control acid sequence control acid sequence control acid sequence control acid sequence control acid sequence control acid sequence control acid sequence control acid sequence control acid sequence control acid sequence control acid sequence control acid sequence control acid sequence control acid sequence control acid sequence control acid sequence control acid sequence control acid sequence control acid sequence control acid sequence control acid sequence control acid sequence control acid sequence control acid sequence control acid sequence control acid sequence control acid sequence			amino acid	P=Proline, O=Glutamine, N=Argining
### ### ### ### ### ### ### ### ### ##	1	amino acid	residue of	S=Serine T=Threonine V-Valina
Sequence sequence sequence sequence sequence sequence sequence 111 1637 797 RUDPRUKGMAPPRIKILAGYGRVLLDISGUTYDSGGGGTAIAG SVERVARLKRSIKVEKTENSSGKRREKIVGOLDGISGUTYDSGG SVERVARLKRSIKVEKTENSSGKRREKIVGOLDGISGUTYSGTENG VIVIADAGSSFSVORNNAFGVULKEKGULFYLLIHGGYVASEFDOLDTS; STENG VIVIADAGSSFSVORNNAFGVULKEKGULFYLLIHGGYVASEFDOLDTS; STENG LMLDVGFVWKALEVACGIKAEVGGKSPSPFYKSALGAIGVEAHO AVMIGDIVIGUNGAGGGGRANGLKEKVULTSGVYKYETSG LMLDVGFVWKALEVACGIKAEVGGKSPSPFYKSALGAIGVEAHO AVMIGDIVIGUNGAGGGGRANGLKEKVULTSGVYKYETSG LMLDVGFVWKALEVACGIKAEVGGKSPSPFYKSALGAIGVEAHO AVMIGDIVIGUNGAGGGGRANGLKEKVULTSGVYKYETSG LMLDVGFVWKALEVACGIKAEVGKSPSFILOWILKTGVKKERPWK  6112 77 196 MSSKSFKSKSFTALKKEKPWRSTLOWILKTGVKKERPWK SKSSSNAGGVPLOGANGERSGVRASEASSFGKRADVSWWSRQL ETWODILAMTS INTENDILLVINGS ULKKRKKYSKYSKITEPWK WEGESSNAGGVPLOGANGERSGVRASEASSFGKRADVSWWSRQL LELLPETUQAKRRWNIKTAKKSFVVSAASATERGESTISHIEDEV LELLPETUQAKRRWNIKTAKKSFVVSAASATERGESTISHIEDEV RUGCKKCKVVVGAESSRGFFLIFRLSFKPVRVUSLCYRRLAAGOKT REGERGAGVPASHABAR PICGRATDICKTGTUGKTGTRSALTERG RUGCKRATVVGAESSRGFFLIFRLSFKPVRVUSLCYRRLAAGOKT EBERGGAGVPASHABAR PICGRATDICKTGTUGKTGRAPPER RUGCKRATVVGAESSRGFFLIFRLSFKPVRVUSLCYRRLAAGOKT EBERGGAGVPASHABARAFICGRATDICKTGTAGARPER RUGCKRATVVGAESSRGFFLIFRLSFKPVRVUSLCYRRLAAGOKT EBERGGAVTPASPCTLAAATETTSRHCHRATTERAAGCATT PAANSSTFRAGGSTAKSMASACVSAAPSSSWPASSSWPGCPFRCCTTR RRRGSFRCGLAAGSMCSCSFSWRCTEVSACWSSPPPP PAREPVGC GHDEPPHARPRARIAFDVAARAKGGOMPHAGPAGFAGTATGAGSGVT GROWFLERGULVFISH GROWPTURPSCHIPVAARAGKGGOGGREPPELLLAATETPASF HIGGGRFTVFAPPCTLIAATETPSRHCHRATTERAAGCATT ARVONFRGWRAAGATTSTALTTSBHAWAATAGACATTAGACATT GROWPTGRWAATTSBHAWAATAGACATTAGACATTAGACATT ARVONFRGWRAAGATTSBAATTAGACATTAGACATTAGACATTAGACATTAGACATTAGACATTAGACATTAGACATTAGACATTAGACATTAGACATTAGACATTAGACATTAGACATTAGACATTAGACATTAGACATTAGACATTAGACATTAGACATTAGACATTAGACATTAGACATTAGACATTAGACATTAGACATTAGACATTAGACATTAGACATTAGACATTAGACATTAGACATTAGACATTAGACATTAGACATTAGACATTAGACATTAGACATTAGACATTAGACATTAGACATTAGACATTAGACATTAGACATTAGACATTAGACATTAGACATTAGACATTAGACATTAGACATTAGACATTAGACATTAGACATTAGACATTAGACATTAGACATTAGACATTAGACATTAGACATTAGACATT		residue of	amino acid	W=Tryotophan Y=Tyrosine Y=thknown + 0+
Toposable nucleotide insertion		amino acid	sequence	Codon. /=possible nucleotide deletion
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TRECREKCAKPRIFFERDILUYGSIULMKRKYRSGHIPLEEUT LELLPETLOAKRWMINTAKKSFUVSASTERQEWISHIEECU RROLRATGRPA\STEHAAPMIPDKATDICMRCTQTRFSALTRH HCRKCRVVVCAECSRQRFLLPRLSPKVVRVCSLCTRELAAQQKK EEABEQCAGVPRAASHLARPICGRVEWINTPTRTRRAGCATO PAAMSSTPRGWFGLPSTADPRAPELLSPSQLHCPGPOEGSSRSC PGLRDIPIPMQVQKRGUALSGLPVPFCMTLCPYGFTAGNAFPFR KPONTHRSW 6114 818 246 PTSSPRPSPGSPAMSWSACVSAAPSSSWPASSSWPCGFRCCTR RRCSPRCGLAAGSMCSCSPSWRCTPVPACWSPPPP\PABGVQC GHLPPHADDRRALRLPVAAPAROPGFGHPAGPPARPTPPASP HGPORPTVPAPPCPLLAATEPTSPRPHQWTREDRULGRGSQVT GRQWFLRGLVLIFSL 6115 324 71 DVCGRVCAAPHLYTHIMMICAHAC\ITHAQLC/ITASHALAH SHLYTCMVMLTASHTPSHTHPHTAVHEERADVLRGTLTLR 6116 595 1430 TGWWPGRRHAAJISSSGVPFGGRAA\LQTVKREEEDBSYTFVQ AARQCILMRCQGLFTAGLPRQLRYHBSGEDSYTFVQ AARQCILMRCQGLFTAGLPRGLRYHBSGETTSLRELCRW LRPDVLSKAQILBLUVLEGFLSILDFGLRYWOLHNPSGEEVL WPCMRSCRGTMMGPGGTAALP\SPCRCLWHSEEDBSYTFVQ AARQCILMRCQGLFTAGLPRGLRYBGGGTTSLLCRW LRPDVLSKAQILBLUVLEGFLSILDFGLRYWSCHEEDBSYTFVQ AARQCILMRCQGLFTAGLPRGCLTTAGGGSTPAAQMPALFPRE GCCGGQVTPTRSLTAGLGETMTFKDVEVTFSGUBWGLDSAQRN LYRDWMLSWRYNNASSLEL WPCMRSCRGTMAHPGGTAALP\SPCRCLWAGSDTLDAAQRN LYRDWMLSWRYNNASSLEL GCLSLFPPAAMPHAAPTPLEVVVAAVLWAAAPTRGLIRATSDHNA SMDFADLPALFGATLSQGGGGWTGLLKEGGGGRTFLLLLATRTE GLLSLFPPAAMPHAAPTPLEVVVAAVLWAAAPTRGLIRATSDHNA SMDFADLPALFGATLSQGGLQGPLVBAHPDNACSPIAPPPAPV NGSVFIALLRRFDCHPDLKVLNAAQKAGYGAAVVUMNSNELLNM VMSBEJQQJWIFSVFIGESSSYLRALAFVYEKGRGVLVYDDN TFFLGYYLIPTGIVGLLVLAMAQAVMARCQHRRRQCRNLTK \CDLKQILPTDVKAGDQDVCAICLDSPEGDELRRLDCANAY HSRCUDPMLOTRETCPJCKQPWRGGPGDEDEETQCGEGDB GCPPDHPASETTPLLGSSPTLPTSFGSLAPAPLVFPGPSTDPPL SPPSSPVILV  6116 1044 247 STISCRACTSGATPGAQSHRSAKGHAAGKBTAALGMERGKVKK KEKETGKKKCTGKKKGEKEKVKKEVEGKKOEKOKGKCKGKRKKK KEKETGKKKGEGEKGREKVKKEVEGKKOEKOKGKOKGKGKGKKKK KEKETGKKKGEGEKGREKVKKEVEGKKOEKOKGKOKGKGRKGK KEKEKTTGKKKTGKKGTANTKCHSCOGFFGGEKGENKDSTLTTTPLEPLEK NKGLLTVAKKKYLHQLLAANPVLELVVYANKQDLEAAYHITDIHEALA 111  6119 1217 462 DPRFVIENTKAPAGERTTOPRSSRGGTLRSTMEYLSALNPSDL LRSVSNISSEFGRRWTSSVLONGOLGAGRAFTUVKROUDPG TIWKAKYLHQLLAANPVLELVVYANKGDLEFGUTKGNATAT QELLAKARSTLLLANGVTLILLEEDGTAVGCDFOLKGKKERENGDFOLKGRONGONG DLAGLL				ETMVDHLANTEINSORIAAVESCEGASGOPLAT.PGPVII.GEGUT
LELLPETLQAKRIMMIKTAKKSPVGAASATERQEMISHIEECU RRQCRATGRPA STEHAPWIPDKATURCRTQTTFSALTIRRI HCRKCRVVVCASCSRQFPLLPRISPKDVRVCSLCYRELAAQORK EEABEQGAGVPRAASHLARPICGRYVEMINTETIRRAGTATG PAAWSSTPRGWEGLPSTADPRAPHLESPSQLHCPGPQEGSSRSC BGLRDFIPMKQVQRWGVALSGLPVPFCNTLCPYGFTAGNAFPPR KPONTIRSW  6114 818 246 PTSSPRPSGSSAMSWGACVSAAPSSSWPGGSRRCCTR RRCSPRCCTRACLAGSWGACSPSWRCTWADSPPP\PAEQVQC GHLPPHADDRALRLPVAAPARGPGPHPAGFAFPPARTPPASP HGPGRPTVPAPPPPLLAATEPTSGRPHQRWTREDRIMLGRGSQVT GRQWBLRGLVLFSL 6115 324 71 DVCGRYCAHPHLYTHIMMICAHAC\THTAQLC\TTASHALAH SHLYTCMWALTASHTSPHTPHTAWHARDVLRGTLTDLR GRQWBLRGLVLFSL ASPQLRSSSSALDHLEPTSFFHRHTAVHARDVLRGTLTDLR COMMPPORRHAAJTGSGGVPFGGRAA\LQTVKKBEEDESYTFVQ AARQCILANPOQELFRQLFRQLRYHESSGPLSTBLRELCRWW LRPDVLSKAQILELLVLRGFLSILPGELKWWQLHNESSGESL LWPCWMSCRSTLMGHPGGTBALP\SPRCALDGYS\LKSAQIMSL ASPLRSSSALDHLEPTYPTIERAPPLERBVURGTLTBLRELCRWW LRPDVLSKAQILELLVLRGFLSILPGELKWWQUHNPESGESLL LYRDWLBLWYNNASIGK GCGGQVYPTTSSLTAQLGFTWTFKDVEVTFSQDEWGWLDSAQRN LYRDWLBWYNNASIGK GCGCGQVYPTTSSLTAQLGFTWTFKDVEVTFSQDEWGWLDSAQRN LYRDWLBWYNNASIGK GCGCGGQVYPTTSSLTAQLGFTWTFKDVEVTFSQDEWGLLATTRC GLLSLFPPAAMPHAAFPLFVVVAAVLWGAAPTRGLIRATSDINA SWDFADLPAHFGATLSGGELGGFLVARAFDVARGFLIRATSDINA WNNSEIGQOTWTFSVTGERSSFYLRALFYYERGARVLLVDDN TFFLGYYLLIPTGIVGLLVLAMAQAVALARCIGHEKRLQRNRLTK \CDLKQI JPTTDVGCGGQGWTFGILCBCEFTGGGEGG GFPRHPARSERTPLLGSSPTLPTFGSLAPAPLVFFGGSTDPL HSRCVDPWLTQTRTCTPTCKQPVHRGFGGBDGGEETCGGEGGB GFPRHPARSERTPLLGSSPTLPTFFGSLAPAPLVFFGGSTDPL HSRCVDPWLTQTRTCTPTCTCKQPVHRGFGGBDGGEETCGGEGGB GFPRHPARSERTPLLGSSPTLPTFFGSLAPAPLVFFGGSTDPL HSRCVDPWLTQTRTCTPTCTCKQPVHRGFGGBGGGTRAVCTITE DSQMFFLEIGGSKPPRSYWMYLSVLOKGKQEKGRKGK KEEECTKQGKETNKEKEQFKGGEEKGKNDSTLTTTPLEPLEK NGQILVIJGLGGGAPRSTWMYLSVLOKGKGGEKGKKGNF LRSVSNISSEFGRRWTSAPPCGFFRYCHKKTGGTATAT GLLAKAKYLHQLIAANPVLPLVVPANKQDLEAAYHITDIHEALA II  DPRFYTENTTKARAGGERTTOPRSSREGTLRSTMEYLSALNPSDL LRSVSNISSEFGRRWTSAPPCPCKRKTRIKGGTATAT GLLAKAKSTLULNGCTUTLULBEDGTADDFFOLLEBDPTCLM VUQSGGSWSPTRSGVLSFGGGFKKKKENDIARFTTGVYKGNPE DLJGSLAWAKSTCDGGLAGFKGUKKELLGRATTTO	ſ			TKECRKKAKPRIFFLFNDILVYGSIVLNKRKYRSOHIIPLEEUT
RRQLRATGERA STEHAAPHTPIKATDICMRCTOTRESALTREH HCRKCRVVCAESCREILBERISVEWCGLCYBLAAQORK EEREEQGAGVBRASHLARPICGR PVEMIMITPIRTRRAAGTATG PAAWSTPRGWPGLPSTADERPAEHLSPSQLHCGPOEGGSSRSC PGERDPIPWKQVQRWGWALSGLPVPFCWTLCPYGFTAGNAFPFR KPONTHRSW  6114 818 246 PTSRPFSPSSSAMSWSACVSAAPSSSWPAGSSWPCGFRRCCTR RRRGSPRCGLAAGSWCSCSPWRCTPVPACWPSPPPVPACWPSPPPVPACWPSPPPVPACWPSPPPVPACWPSPPPVPACWPSPPPVPACWPSPPPVPACWPSPPPVPACWPSPPPVPACWPSPPPVPACWPSPPPVPACWPSPPPVPACWPSPPPVPACWPSPPPVPACWPSPPPVPACWPSPPPVPACWPSPPPVPACWPSPPPVPACWPSPPPVPACWPSPPPVPACWPSPPPVPACWPSPPPPPPSSPPPCWARPALLIFETHIMHYCAHACVIHTHAQLC/ITASHILAH 6116 595 1430 TOVMPPGRWHAA/ISSSGPVFEGARA\LQTVKKBEEDESYTPVQ AARPOTLNRPOGELFRQLPFRQLRYWCHMPESGEEVL WPCMRSCRGTLMGHPGGTRAPLVPGSPPLETSKREICKWW LRPDVLSKAQILELLVLEQPLSILPGELRYWVQLHNPESGEEVL WPCMRSCRGTLMGHPGGTRAPLVPGCHOWSYNS\LRSAQINSL ASPLRSSSALGHHLEPPYELEARDFLAGGSDTPAAQMPALFPRE GCRGDVTFTRSLTAQLQETMTFKDVEVTFSGDEWGWLDSAQRN LYRDVMLENYRNMASLGK  6117 1433 222 VGVPSBAPPCSWEUGPGGGWTFGILKEGGGGRRTPLLLLATETR GLLSFPPPAAMHPARTPLPVVAAVAUWAAPTGGLIRATSDENA SMDFADLPALFGATLSQEGLQGFLVEAHPDNACSPIAPPPPAPV NGSVFIALLRRFPCNFDLKVLNAQKAGYGEBGGWRTPLLLLATETR GLLSFPPAAHPBAFFLPVVAAVAUWANVENNELILMN VWNSEEIQQOIWIFSVFIGERSSFYLRALFVVEKKGRVLLVPDM TFFLGYYLIPFTGIVCLLVLAMGAWMARGIORKKLULVDM TFFLGYYLIPFTGIVCLLVLAMGAWMARGIORKKLULVDM HSRCVDPMLTOTRRTCPICKQPVHRGPGDBDGETGGGEBGB GEPRDHPASETPTLLGSSFTLBYSFGSLAPAPLVFPGPSTDPPL SPPSSPVILV 5TISCRACTSGATFGAGSHRSARGHAAGGKETAALGMERGKVKK KEKEETCKKIGEKGREKVKREVEKKKUSKKOBKGEKGKKKK KEKEETCKKIGEKGREKVKREVEKKKIGSKGERGKVKK KEKEETCKKEIGEKGREKVKREVEKKKIGSKGERGKVKK KEKEETCKKEIGEKGREKVKREVEKKKIGSKGERGKVKK KEKEETCKKEIGEKGREKVKREVEKKIKGSKGERGKCH KEKEETCKKEIGEKGREKVKREVEKKIKGSKGERGKVKK KEKEETCKKEIGEKGREKVKREVEKKIKGSKGERGKCH KEKEETCKKEIGEKGREKVKREVEKKIKGSKGERGKCH KEKEETCKKEIGEKGEREKVKREVEKKIKGSKGERGKCH KEKEETCKKEIGEKGEREKVKREVEKKIKGSKGERGKCH KEKEETCKKEIGEKGEREKVKREVEKKIKGSKGERGKCH KEKEETCKKEIGEKGEREKVKREVEKKIKGSKGERGKCH KEKEETCKKEIGEKGEREKVKREVEKKIKGSKGERGKCH KEKEETCKKEIGEKGEREKVKREVEKKIKGITAATR DSQMEFLBIGGSKPRSTWEMISIN/ADSLARSFEVGFKODSPP TIWKAKKYLHQUIANGSCHICHTPUT	1	1		LELLPETLQAKNRWMIKTAKKSFVVSAASATEROEWISHTEECV
HCRCRCVVCAECSRORFLLPRISPROPVENTMTPTRTRAAGCATO EARSCQAGUPRAABHLARPICGRPVENTMTPTRTRAAGCATO PAAMSSTPROWPGLPSTADPRPAHLSPSQLHCGGOEGSSRSC PGLRDPIPMKQVQRKGVALSGLPVPFCWTLCPYGFTAGNAFPPR KPQMTHRSW  6114 818 246 PTSRPRPSPSSPAMSWSACVSAPSSSWPASSSWPCGPRRCCTR RRCSPRCGLAAGSNCCSSPSWRCTPVPACNSPSPPP\PAGQUCC GHLPPHADRRALRLPVAAPARGPGPGHPAGFAGFRPARTTPASP HGGGRTVVPAPPCPLLAATEPTSRPHQRWTREDRHLGRGSQVT GRQWFLRGLULFSI 6115 324 71 DVCGRVCAMPHLYTHIMMH CAMAC\IHTHQLC/ITASHALAH SHLYTMWWLTASHTPSHTWHTAWHKERADVLRGTLTPLY AARPQTLNRICQGLFTQLFRQLRYHESSGPLETISRIRGLCRW LRPVLSKAQILELLVLEOFLSILFDGELTSKRIRGLCRW LRPVLSKAQILELLVLEOFLSILFDGELTSKRIRGLCRW LRPVLSKAQILELLVLEOFLSILFDGELTSKRIRGLCRW LRPVLSKAQILELLVLEOFLSILFDGELTSKRIRGLCRW LRPVLSKAQILELLVLEOFLSILFDGELTSKRIRGLCRW LRPVLSKAQILELLVLEOFLSILFDGELTSKRIRGLTRW ASPLRSSSALGHLEPPYEIEARDFLAGGSDTPAGMPALFPRE GCGGQVTPTRSLTAGLQETMTFKDVEVTFSQDEWGMLDSAQRN LYRDVMLENYRMASLCK VGVSSPAPPCSWWEGPGGGWTFGILKEGGGGRRTPLLLLATTT GLLSI_PPDAMHDAAFPLPVVVAAVLWGAAPTRGLTRATSDINA SMDFADLPALFGATLSGCGLQGFLVBAHPDNACSPIAPPPPAPV NGSVEIALLRRFDCNPLKVLHAQKGAAVVHNNTSELLNM VNNSEEIQQQIWIFSVFIGERSSEVLRALFYYEKGARVLLVPDN TFFLGYVIJFPTGIVGLULLARGAWHARCIQHRKRLQRNRLTK LOOLKQI\PTHDYQKGDQVDVCAICLDEYBGGBKTQLCCAHAY HSRCVDPWILTDTRKTCPICKQVHRGFGDBDGEETQGGBEBDB GSPRHHPASERTPILLSSSFTLPTSFGSLAPPLYFFGPSTDPPL SPPSSPVILV SPSSPVILV STISCRACTSGATPGAQSHRSARGHAAGKETAALGMERGKVKK KXEKETQKEXIGEKGREKVKREVGKKKOBKQEKGERRKGK KKEKERTKQGKETNKEKGPKVGGEKGENTHTFTPLEPLEK NGQILVLGLDAGKGTSVHSLSLANSVCHSVAPTQGFHAVCINTE BQMFFLEIGGSKPFRSYMEMYLSN/ADSLARSFSVGFKODSOP ITWKAKKYLHQLIAANPVLPLVVPANKQDLEAAVHITDHEALA 11 1217 462 DPRFVIENTTKAPAGERTTOPRSSREGTLRSTMEVLSALMPSDL LRSVSNISSEPGGRVWTSAPPPQRFFKVCDKKRIKGKGFKVKRETSTLIO QELLAKALETLLINGVLTLVLEEBOTAVDSBDFFCLLEDDTCLM VLGSGSWSPTRSGVLSVSGLORGERPKHSKDIARTFTDVYKQNRR DLFGSLWKATFFGLVKASSCOPPOOLGGRKKYKRETSTLIO DLFGSLWKATFFGLVKASSCOPPOOLGGRKKYKRETSTLIO DLFGSLWKATFFGLVKASSCOPPOOLGGRKKYKRETSTLIO DLFGSLWKATFFGLVKASSCOPPOOLGGRKKYKRETSTLIO DLFGSLWKATFFGLVKASSCOPPOOLGGRKKYKRETSTLIO DLFGSLWKATFFGLVKASSCOPPOOLGGRKTGTSTTTPLDFORD	1			RRQLRATGRPA\STEHAAPWIPDKATDICMRCTOTRFSALTERH
EEAEEQCAGVPRAASHLARPICGRPVEMMTFTRTRRAAGTAG PAAMSSTPRGWEGLESTADRPRAHESSGLHCEOPGGSSRSC PGLRDFIPWRQVQRWGVALSGLPVPPCWTLCPYGFTAGNAFPPR RCQNTHRSW  6114 818 246 PTSRPRPSGSPAMSWSACVSAAPSESWPASSSWPCGPRRCCTR RRRCSPRCGLAAGSNCSCSPSWRCTPVPACWPSPPP, PASGVQC GHLPPHADRRAIRLPVAAPAARGEDHPAGPAGPRPATPPASP HGPGRPTVPAPPCPLLAATEPTPSRPHQRWTREDRILGRGSQVT GRPQWFLRGLVLFSL 6115 324 71 DVCGRVCAHPHLYTHIMMTCAHAC\\ 1HTHAQLC\\ 1TASHALAH SHLYTCMVALITASHTPSHTHPHAVUKERRADVLRGTLTPLR 6116 595 1430 TGWPPGRWHAA\\ 158SGPYPEGARL, QTVKKEEEDESYTPVQ AARQQTLNRRCQELFRQLFRQLFRQLFRULGYRS\LSELGERWW LRPDVLSKAQLIELLVLEGFLSILDGELRVWVQLHNPESGEE\\ L WPCMRSCRGTLMGHPEGTTARL\\ PECALDGYRS\LKSAQLISLL ASPLRSSSALGHHLPPYEISARDFLAGGSDTPAAGMPALFPRE GCEGDUYTTRSLTADLQETWTKKDUEVTFSQDEWGWLDSAQRN LYRDWALRNYRMASLCK  6117 1433 222 VGVSPDAPPGSWRVGPGGGWTPGILKEGGGGRRTPLLLTATTR GLISLFPPAAMHPAAFFLEVVVAAUMAAPTRGLIRATTSDHNA SMDFADLPALFGATLSGEGLGGFLVBAHPDNACSPTAPPPAPV NGSVITALIRRFCORPHLKVLHANGKVGAVVHNVNNSHLLNM VMNSEEIQQQIWIFSVFIGERSSEYLRALFVYEKGARVLLVPDIN TFPLGYYLIFFTGIVCLLVLLANGAVMIARCIGRKRLQRNRLITK \CGLKGI\PTHDVGKGQDVCACLGVBEDGKLKEVLCCHAVY HSRCVDPWLTGTRTCPICKQVHRGPGDBDGEETCQCBEBGB GGFPGHPASERTPLLGSSFTLPTSFGSLAPALVFPGPSTDPPL SPPSSPVILV  6118 1044 247 STISCRACTSGATPGAQSHRSARGHAAGGETTQFBROKEYKK KEKERTKRGKETNLESGRIFGKGGEKKERKEVERKEVERKKIGSKGEKGRKKK KEKERTKRGKETNLESGRIFGKGGEKKERNEVARTEVENGTHAUCHTPLEFLEK NKGLIVLGLDGAGKTSVLHSLASNRVQHSVAPTGGFHAVCINTE DSQMEFLBIGGSKPFRSYWEMYLSN\DSGLARAFSFEVGRODSQP ITWKAKKYLHQLIDAGKTSVHISLASNRVQHSVAPTGGFHAVCINTE DSQMEFLBIGGSKPFRSYWEMYLSN\DSGLARAFSFEVGRODSQP ITWKAKKYLHQLIDAGKTSVHISLASNRVQHSVAPTGGFHAVCINTE DSQMEFLBIGGSKPFRSYWEMYLSN\DSGLARAFSFEVGRODSQP ITWKAKKYLHQLIDAGKTSVHISLASNRVQHSAPTGFHAVCINTE DSQMEFLBIGGSKPFRSYWEMYLSN\DSGLARAFFTEVLSALNPSDL LRSVNISSEFGRRVWTSAPPPQRFFRVCCHKRTIRKGLTAATR QELLAKABRILLINGVLTIVLEEDGOTAVDSRFFFGLEDDTCLM VLQSGSWSFTRSGVLSYGLOGERPKHSKDIARTTRKGLTAATR QELLAKABRILLINGVLTIVLEEDGOTAVDSBFFFGLEDDTCLM VLQSGSSSFTRSGVLSYGLOGERPKHSKDIARTTRKGLTAATR	1	ŀ		HCRKCRVVVCAECSRQRFLLPRLSPKPVRVCSLCYRELAAOORK
PARMSSTPRGWPGLPSTADPRPACHLSPSGLHCCGPCDESSRSC PGLEDPTPMGVORGVALSGLPVPFCWTLCPYGFTAGNAFPER KPQMTHRSW PGREDPTPWGVORGVALSGLPVPFCWTLCPYGFTAGNAFPER RPGCSPRCSPAMSWSACVSADPSSSWPASSSWPGGPRRCCTR RRRCSPRCGLAAGSMCSCSPSWCTPVPACWBSPPVPAGWGOVC GHLPPHADRRALRLPVAADPAGGPGPGPAGFPPARTPPASP HGPGRPTVPAPPCPLLAATEPTPSRPHQRWTREDRILGRGSQVT GRPQWFLRGLVLFSL 6115 324 71 DVCGRVCAHPHLYTHIHMICAHAC\ITHTHQLC/ITASHALAH SHLYTCMVALITASHTPSITHPHATAVHKEHRADVLRGTLPPLR SHLYTCMVALITASHTSHTHPHATAVHKEHRADVLRGTLPPLR SHLYTCMVALITASHTPSITHPHATAVHKEHRADVLRGTLPPLR LRPDVLSKAQILELLULLEQFLSLIPGELRWWQLHNPESGES\L RPDVLSKAQILELLULLEQFLSLIPGELRWWQLHNPESGES\L RPDVLSKAQILELLULLEQFLSLIPGELRWWQLHNPESGES\L RPDVLSKAQILELLULLEQFLSLIPGELRWWQLHNPESGES\L RPDVLSKAQILELLULLEQFLSLIPGELRWWQLHNPESGES\L RPDVLSKAQILELLULLEQFLSLIPGELRWWQLHNPESGES\L RPDVLSKAQILELLULLEQFLSLIPGELRWWQLHNPESGES\L RPCMRSCRGTLMGHGGTRALP\RPCALDGYRS\LRSGAQMPALFPRE GCPGQVTPTRSLTAQLQETMTFKDVEVTFSQDEMGWLDSAQRN LYRDVMLRNYRNMASLGK GCPGQVTPTRSLTAQLQETMTFKDVEVTFSQDEMGWLDSAQRN LYRDVMLRNYRNMASLGK GLISLFPPAAMHPAAFPLPVVVAAVLWGAAPTGLIRATSDHNA SMDFADLPALFGATLSQEGLQGFLVEAHPTVEKGARVLLUPDN NGSVFIALLRRFDCNFDLKVLNAQKAGYGAAVVHNVNSNELLNM VWNSEEIQQQTWIPSVFIGERSSEYLRALFVYEKGARVLLUPDN TFFLGYYLIFFTGTVGLULLAMGWLARCIGHRRRLQRNLTK \SQLKQILYTHDYQKGDQYDVCAICLDEYEDGDKLRVLPCHANY HSRCVDPWLTGTRRTCPICKQPVHRGFGBBDGEETGQGEEGBB GEPRHPASERTPLUGSFTLPTSFGSLAPAPLVFPGPSTDPPL SPPSSPVILV STISCRACTSGATPGAQSHSARGHAAGGKETAALGMERGKVKK KEXEKETQKEXIGEKGRENKVRKSVECKIKGSKQERGERGKVK KEXEKETQKEXIGEKGRENKVRKSVECKIKGSKQERGRRKKK EKEKERTXGGETMKEKEGPKGGEEKGRNKNSTLTRTFLEPLEK NQLIJULGLDGAGKTSVIHSLAGNVGHSVAPTGGFHAVCINTE BSQMSFLBIGGSKPFRSYMMYLSN/ADSLARSPSVGFKQDSP ITWKAKKYLHQLIAANPVLPLVVFANKQDLEAAYHITDHEALA 111 1217 462 DPRFVIENTTKAPAGERTTOPRSSREGTLRSTMEYLSALMPSDL LRSVSNISSERGRRVWSSAPPPQRPFCOCHKRTIRKGLTAATR QELLAKALETLLLNGUITLVLEEDGTAVDSBDFFQLLEDDTCLM VLQSGGSSPTRGGUSNSCHOLGKRRKKKBILDRTTFTVYKQNPR DLFGSLAWNATFYGFLXSMSCDPCJGKKKKBILDRTTFTDVXKQNPR DLFGSLAWNATFYGFLXSMSCDPCJGKKKKBILDRTTFTDVXKQNPR DLFGSLAWNATFGFGLXSMSCDPCJGKKKKBLERTSTTILLO	1		•	EEAEEQGAGVPRAASHLARPICGRPVEMTMTPTRTRRAAGTATC
FIGUR DE PERMOVORMOVALSGLPVPFCMTLCPYGFTAGNAFPFR KPONTHRSW PTSRPRPSGSPAMSWSACVSAAPSSSWPASSSWPCGPRRCCTR RRGCSRCGLAGGSMCSCSPSWRCTPVPACMPSPPP\PAGQVGC GHLPPHADRRAILERVAAPARSGPGGHPAGPAGPPARTPPASP HGPGRPTVPAPPCPLLAATEPTPSRPHQRWTREDRULGRGSQVT GRPQWFLRGLVLFSL 6115 324 71 DVGGRVCAHPHLYTHIHMHICAHAC\\ITHAQLC\/ITASHALAH SHLYTCMVMLTASHTPSHTHPHTAVHKEHRADVLAGGTLPLR 6116 595 1430 TGWMPPGRWHAA\/ISSSGPVPGGARA\\QTVKKEEEDESYTFVQ ARRQTLNRPQGLFRQLFRGLARGHLSGTLSRLRGLCRWW LRPDVLSKAQILELLVLEOFLSILPGELRWVQLHNPESGEE\L WPCMRSCRGTLMGHGGTRALP\/PSPCALDGYRS\LRSAQIWSL ASPLRSSSALGDHLEPPYEIEARDFLAGGSDTPAAQMPALFPRE GCPGQVTPTRSLTAQLQETMTFKDVEVTFSQDEMGWLDSAQRN LYEDVUSKAQILELLVLEOFLSILPGELGGSGRTFLLLLATATR GLLSLFPPAAMHPAAFPLFVVVAAVUNGAAPTRGLIRATSCHNA SMDFADLPALFGATLSQGGLQGFLVERHPDNACSTJAPPPPAPV NGSVFIALLRRDCOMFDLKVLNAQKAGYGAAVHNVNSNELLNM VNNSESIQQOTHIPSVTIGERSSEYLRALFVYEKGARVLLVPDN TFPLGYYLIPFTGIVGLLVLAMAGVMIARCIGHRRRLQRNNLTK \SQLKQI\PTHDYQKGDQYDVCAICLDEVEDDKLRVLPCAHAY HGRCVDPMLTQTRKTCFICKQPHGGDENGGEETQGDEEGDE GEPRDHPASERTPLLGSSPTLPTSFGSLAPAPLVFPGPSTDPPL SPPSSPVILV 6118 1044 247 STISCRACTSGATFGAQSHRSARGHAAGGKETAALGMRGKVKK KKEKETQKEXIGEKGREEKVKRKEVBQKIKQEKQEKQEKKKK KKEKETQKEXIGEKGREEKVKRKEVBGKIKGEKQEKGK KKEKETQKEXIGEKGREEKVKRKEVBGKIKGEKQEKKKK KKEKETQKEXIGEKGREEKVRKEVBGKIKGEKQEKGKK KKEKETGKEXIGEKGREEKVRKEVBGKIKGEKQEKGCHAQCHAQ III DPRFVTENTTKAPAQERTTOPRSSREGTLRSTMEYLSALNPSDL LKSVSNISSEFGRRVWTSAPPPQRFFRVCDEKKRTIRKGLTAATR QELLAKALETLLINGVLTLVLLEEDGTAVDSDEFFQLLEDDTCLM VLQSGGSWSFRSGRUSYSCLGGERPKHSKDIARFTEPVYKQNPR DLFGSLAWNATFYGLKSMSCDCDG/GKKVLKELLERTSTTLIQ DLFGSLAWNATFYGLKSMSCDCDG/GKKVLKELLERTSTTLIQ	1			PAAWSSTPRGWPGLPSTADPRPAEHLSPSOLHCPGPOEGSSRSC
6114  818  246  PTSRPRPSGSPAMSWSACVSAAPSSSWPASSSWPCGPRRCCTR RRRCSPRCGLAAGSMCSCSPSWRCTSPACWBSPPP) PAGOVGC GHLPPHADRRALRLPVAAPARGFGPGHPAGPAPPARTPPASP HGPGRPTVPAPCPCLLAATEPTPSRPHQRWTREDRULGRGSQVT GRPQWFLRGLVLFSL  6115  324  71  DVCGRVCABPHLYTH HMHICAHAC\IHTHAQLC/ITASHALAH SHLYTCMVMLTASHTPSHTHPHTAVHKERRADVLRGTLTPLR  6116  595  1430  TGWMPFGRWHAA/IESSGPVFEGARA\LQTVKKEEEDESYTFVO ARRPQTLNRRCGELFAQLFRQURYHESSGPLETLSFLRELCRWW LRPDVLSKAQILELLVLEQFLSILPGELRVWOOLHNPESGEE\L WPCKRSCRGTLMHPHGGTRALPEPPSLLTALGGSTPPAAQMPALFFRE GCEGQVTPTRSLTAQLQSTMTFKDVEVTFSQDEWGWLDSAQRN LYEDVMLENYRMASLGK  6117  1433  222  VGVPSPAPPSSWSVGFGGWTFGILKEGGGGRRTFLLLLATTR GLLSLFPPAAMHPAAFFLDVVVAAVLWAAAFTRGLIRRTSCHNA SMDFADLPALFGATLSQEGLQGFLVEAHPDMACSPIAPPPPAPV NGSVFIALLRRFDCHFDLKVLNAQKAGGAAVVINVNSNELLNM VWNSESIQQOIWLFSVFIGERSSFYLRALFVYEKGARVLLVPDN TFPLGYYLIPFTGIVGLLVLAMGAVMIARCIQHKKRLQRNRLTK \SQLKQI\PTHDYQKGDQYDVCAICLDSFEGDGKLRVHCCHAY HGRCVDPWLTOTRKCTPICKGVPURGPGBDDGEETCGQEEGDB GGPRDHPASERTPLLGSSPTLPTSFGSLAPAPLVFFGPSTDPPL SPPSSPVLIV  6116  1044  247  STISCRACTSGATFGAQSHRSARGHAAGGKETAALGMERGKVKK KEKEKETQKEKIGKEKIGKEKGPKKQGEKGERNDSTLTRTPLEPPLEK NKQILVLGLDGAGKTSVLHSLASMRVCHSVAPTGGFHAVCINTE DSQMFFLBIGGSKPFRSYWENYLSN/ADSLARSFSVGFKQDSQP TTWKAKKYLHQLIAANPVLPLVVFAKKQDLEAAYHTTDHEALA  6119  1217  462  DPRFVTENTTKAPAQGRTTQPFSSREGITKSTMEYLSALMPSDL LKSVSNISSEFGRRWYMSAPPQRPFRVCHKRTIRKGLTAATR QELLAKALETLLLMGVLTLVLEEDGTAVDSBDFFQLLEDDTCLM VLQSGGSWSPCRSSULSYGLGRERFKKSNIARFTTEDVYKQNPR DLFGSLNVKATFYGLISSMSCHGOLGPRKELRWTSTLIJO	1			PGLRDPIPWWQVQRWGVALSGLPVPFCWTLCPYGFTAGNAFPFR
RRRGSPRCGLAGSMCGGSPSSWRCTSPPACWSPGPRCCTR RRRGSPRCGLAGSMCGGSPSWRCTPVPACWSPGPPQVCC GHLPPHADRALRLPVAADARGGGPGHPAGPAGPARTPPASP HGPGRPTVPAPPCPLLAATEPTSSRHCWTREDRHLGRGSQVT GRPQWFLRGLVLFSL  6115 324 71 DVCGRVCARIPHLYTH HMHTCARAC\IHTHAGLC/ITASHALAH SHLYTCWMITASHTPSHTHPHTAVHKEHRADVLGRGTUPLR SHLYTCWMITASHTPSHTHPHTAVHKEHRADVLGRTUPLR ARROTLNRCGSLF3QLFRQLRYHESGGPLETLSRLRSLCRWW LRPDVJSKAQILBLLVLEGFLSILPGELRVWVQLHNPESGEE\L WPCWRSCRGTLMGHPGGTRALP\EBFCRLDGYRS\LRSQLWSL ASPLRSSSALGDHLEPPYSIBARDFLAGGSDTPAAQMPALPPRE GCPGQVTPTRSLTAQLQERTHFOUVAVINGAGGSDTPAAQMPALPPRE GCPGQVTPTRSLTAQLQERTHFOUVAVINGAGAPAVINIVNSNELLART GLLSLFPPAAMHPAAPFLEVVVAAVINGAAPTRGLIRATSDHNA SMDFADLPALFGATLSQEGLQGFLVEAHPDNACSPIAPPPPAPV NGSVFIALLRRFDCHFDLKVLNAQKAGGAAVVINIVNSNELLANM VWNSEEIQQUIHPSVFIGERSSEVLRALFVYEKGARVLLVPON TFPLGYYLIPFTGIVGLLVLAMGAWMIARCIQHRKRLQRNRLTK \EQLKQI\PTHDYQKGDQVDVCALCLDEYEGGBGBB GEPRHPASERTPLLGSSPTLPTSFGSLAPAPLVFPGSTDPPL SPPSSFVILV 6118 1044 247 STISCRACTSGATPGAQSHRSARGHAAGGKETAALGMERGKVKK KEKERETQKEKIGEKGREKVKRKEVEGKIKGEKGEKGEKKK KEKERETQKEKIGEKGREKVKRKEVEGKIKGEKGEKVKK KEKERETOKEKIGEKGREKVKREVEGKIKGEKGEKORERKGK KEKERTTOKEKIGEKGREKVKREVEGKIKGEKGEKGEKKKK KEKERTOKEKIGEKGREKVKREVEGKIKGEKGEKGEKGEK KEERTKIGGEKTIKKEKEGYPEGEKGENDSTLTRTPLEPLEK NGQILVLGLDGAGKTSVLHSLASHRVCHSVAPTQGFHAVCINTE DSQMSFLBIGGSKPFRSYWEMYLSN/ADSLARSFSVCPKGDSQ- TIWKAKKVLHQLIAANPVLPLVVPANKQDLEAAYHITDIHEALA II 6119 1217 462 DPRFVTIENTTKAPAGERTTOPRSSREGTLRSTMEYLSALMPSDL LKSVSNISSEFGRRWWTSAPPQGREFFCLEDDTCLM VLQSGGSWSPTRSCVLSYGLGREFFKIKSINARFTETUVKQNPR DELLAKALETLLLMGVLTLVLEEDGTAVDSBDFFQLLEDDTCLM VLQSGGSWSPTRSCVLSYGLGREFFKIKSKIARFTETUVKQNPR DLLAKALETLLLMGVLTLVLEEDGTAVDSBDFFQLLEDDTCLM VLQSGGSWSPTRSCVLSYGLGGREFFKIKSLIARFTTUVKQNPR DLLAKALETLLLLMGVLTLVLEEDGTAVDSBDFFQLLEDDTCLM VLQSGGSWSPTRSCVLSYGLGGREFFKINSLIARFTTETUVKQNPR	6114	0.7.0		
GHLPPHADRRALRIPVAAPAGGGGFBPAGFAGFRARTPPASP HGGGRPTVPAPPCPLLAATEPTPSRPHQRWTREDRULGGGGVT GRPQWFLEGULFSL  T1 DVCGRVCAHPPLYTHIMHICANAC\THTHAQLC\TTASHALAH SHLYTCHWMLTASHTPSHTHPHATVHKERRADVLRGTLTPLR GTGMPFGRWHAA\TSSSGPVFGGRAV\QTVKKBEEDSSYTPVQ AARPOTLNRICQELFRQLFRQLFRQLRYHESGGPLETLGRLRELCRWW LRPDVLSKAQILELLVLEQFLSTUPGBLRWWCQUHNPESGEE\L WPCWRSCRGTLMGHPGGTRALP\BPBCRLDGYRS\LRSAQIWSL ASPLRSSALGDHLEPPYEIEARDPLAGQSDTPAAQMPALFPRE GCPGDQVTPTRSLTAQLQETMTKKDVEVTFSQDEWGWLDSAQRN LYRDVMLENYRNASLGK  LYRDVMLENYRNASLGK  G117 1433 222 VGVSSPAPPCSWBVGGGGWTFGILKEGQGGRRTPLLLLATRTR GLLSLFPPAAMHPAAFPLEVVVAAVUMGAAPTRGLIRATSDHNA SMDFADLPALFGATLSGGEGLGGFLVEAHPDNACSPILAPPPAPV NGSVFIALLRRFDCNFDLKVLNAQKAGYGAAVVHNVNSNELLNM VWNSEBIQQQIMIPSVFIGERSSEVIRALFVYEKGRVULVPDN TFFLGYYLIPFTGIVGLIVLAMGAVMIARGIQBKRKLQRRRLTK \EQUKQI\PTHDYQKGDQYDVCAICLDEYEDGDKLRVLPCAHAY HSRCVDPWHTQTRKTCPICKQVVHRGPGDEDGEETGGGEGBG GEPRDHPASERTPLLGSSPTLPTSFGSLAPAPLVFFPGSTDPPL SPPSSPVILV  6118 1044 247 STISCRACTSGAFFGAQSHRSARGHAAGKETAALGMERGKVKK KEKETQKEKIGEKGREEKVKRKEVEQKIKQBKQEKQERRKGK KEKETQKEKIGEKGREEKVKRKEVEQKIKQBKQEKQERRKGK KEKETQKEKIGEKGREEKVKRKEVEGKIKGBKQEKQERRKGK KEKEKTOKEKIGLGARSVLHSLASNRVOHSVAPTOGFHAVCIJTTE DSQMFFLBIGGSKPFRSYWEMYLSN\ADSLARSFSVGFKQDSQP ITWKAKKVLHQLIAANPVLPLVVFANKQDLEAAYHITDHHEALA II  DPRFVTENTTKAPAQERTTQPRSSREGTLASTMEYLSALNPSDL LRSVSNISSEFGRRWTSAPPPQRFFRVCDHKRTIRKGLTAATR QELLAKAUETLLLNGVLTLVLEEDGTAVDSBOFFQLLEDDTCLM VLQSGQSWSPTRSGVLSVGLGRERFKHSKDIARFFTPDVYKQNPR DLFGSLNVKATFYGLYSNSCOPOOLOGLOGK/KKKRLELLEWTSTLLO	0.13	070	246	PTSRPRPSPGSPAMSWSACVSAAPSSSWPASSSWPCGPRRCCTR
HGGGRPTYPAPPCCLLAATEPTSRPHQRWTREDRMLGRGSQVT GRQWFURGLUFSL  515 324 71 DVCGRVCAHFHLYTH IHMHICAHAC\ITHAQLC/ITASHALAH SHLYTCMVMLTASHTPSHTHPHTAVKEHRADVLRGTLTPLR 516 595 1430 TGWMPGGWHAA/ISSGPVFTGARA\LQTVKKEEEDESYTPVQ AARPQTLNRPQGELFRQLFRQLRYHESSGPLETLSRLRELCRWW LRPDVLSKAQILELLVLEQFLSILPGELRWWQLHNPESGEE\L WPCWRSCRGTLMGHPGGTRALP\EPPETLARDFLAGQSDTPAQQWPALPPRE GCCEDQVTPTRSITAQLQETMTFKDVEVTFSQDEWGWLDSAQRN LYRDVMLNNYRMASLGK  6117 1433 222 VGVPSPAPPCSWBVGPGGGWTFGILKEGQGGRTFLLLLATRTR GLLSLFPPAAMHPAAFPLPVVVAAVWGAAPTRGLIRATSDHNA SMDFADLPALFGATLSQEGLQFLVEAHPDNACSPIAPPPPAPV NGSVFIALLRRPDCNPDLKVLNAQKAGYGAAVVHNVNSNELLNM VWNSEBIQQQINIPSVFIGERSSEYLRALFVYEKGARVLLVPDN TFPLGYYLIPFTGIVGLLVLAMGAVMIARCIQHRKRLTK \CQLKQI\PTHDYQKGDQVDVCAICLDEVEDGDKLRVLPCAHAY HERCVDPWHTQTRKTCPICKQPVHRGGGBEDGEETQGGEEGDB GEPRDHASERTPLLGSSPTLPTSGLAPAPLVFFGPSTDPPL SPPSSPVILV  6118 1044 247 STISCRACTSGATPGAQSHRSARGHAAGGKETAALGMERGKVKK KEKEKETQKEKIGGKGREKVKRKEVEQKIKGEKQERKKKK EKEKETQKEKIGGKGREKVKRKEVEQKIKGEKQERKKKK EKEKETQKEKIGGKSTNKEKEQFKCQEEKGERKDSTLTHTPLEPLEK NQQILVLGLDGAGKTSVLHSLASNRVQHSVAPTQGFHAVCINTE DSQMEFLBIGGSKPFRSYWEMYLIN/ADSLARSFSVGFKQDSQP ITWKAKKVLHQLIAANPVLPLVVFANKQDLEAAYHITD HEALA II  DPRFVTENTTKAPAQERTTQPRSSREGTLRSTMEYLSALNPSDL LRSVSNISSEFGRRWWTSAPPPQRFFVCDHKRTIRKGLTAATR GELLAKALETLLLMGVLTLVLEEDGTAVDSBDFFQLLEDDTCLM VLQSGQSWSPTRSGVLSVGLGRERPKHSKDIARFFTPDVYKQNPR				RRRCSPRCGLAAGSMCSCSPSWRCTPVPACWPSPPP\PAROVOC
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6115  324  71  DVCGRVCAHFHLYTHIMMICAHAC\IHTHAQLC/ITASHALAH SHLYTCHVMLTASHTPSHTHPHTAVHKERRADVLRGTLTPLR 6116  595  1430  TGWMPPGWHAA/ISSGPVFEGARA\LQTVKKEEEDESYTFVQ AARPQTLNRPCQELFRQLFRQLFRCLFSKERELCRWW LRPDVLSKAQILELLVLEQFLSILPGELRVWVQLHNPESGEE\L WPCWRSCRGTLMGHPGGTERALP\EDPRCALDGYRS\LRSAQIWSL ASPLRSSSALGDHLEPPYEIEARDFLAGGSDTPAAQMPALFPRE GCEGDQVTPTRSLTAQLQETMTFKDVEVTFSQDEWGWLDSAQRN LYRDVMLENYRNASLGK  6117  1433  222  VGVPSPAPPCSWEVGPGGGWTTGILKEGQGGRRTPLLLLATETR GLLSLFPPAAMHPAAFPLPVVVAAVLWGAAPTRGLIRATSDHNA SMDFADLPALFGATLSQEGLQGFLVEAHDDNACSPIAPPPPAPV NGSVFIALLRRFDCNFDLKVLNAQKAGYGAAVVHNVNSHELLMM VNNSEBIQQQIWIPSVFIGERSSEYLRALFYVEKGRVVLLVPDN TFPLGYYLIPFTGIVGLLVLAMGAVMIARCIQHRKRLQRNRLTK \EQLKQI\PTHDYQKGDQYDVCAICLDEYEDGDKLRVLPCAHAY HERCVDPWLTQTRKTCTJCKQPVHRGFGDEQGEEETQGQEEGDB GEPRDHPASERTPLLGSSFTLPTSFGSLAPAPLVPFGPSTDPPL SPPSSFVILV  6118  1044  247  STISCRACTSGATFGAQSHRSARGHAAGGKETAALGMERGKVKK KEKEKETQKEKIGEKGREEKVKRKEVEKKI KQEKQEKQERKKKK EKEKERTKKGGKETNKE KEQFKGQEEKGENKDSTLTRTPLEPLEK NKQILVLGLDGAGKTSVLHSLASNRVCHSVAPTQGFHAVCINTE DSQMFFLBIGGSKPFRSYWEMYLSN/ADSLARSFSVGFKODSQP ITWKAKKYLHQLIAANPVLPLVVFANKQDLEAAYHITDIHEALA II  6119  1217  462  DPRFVTENTTKAPAQERTTQPRSSREGTLRSTMEYLSALNPSDL LRSVSNISSEFGRRWTSAPPPQRPFFVCCHKRTIRKGLTAATR QELLAKALETLLLINGVLTJVLEEDGTAVDSBDFFQLLEDDTCLM VLQSGQSWSPTRSGVLSYGLIGERPKHSKDIARFTFDVYKRNPR DLFGSLNVKATFYGLYSMSCDPGOL\QPKKVLRELLRWTSTILO				HGPGRPTVPAPPCPLLAATEPTPSRPHQRWTREDRMLGRGSQVT
SHYTCHWINTASHIPSHTHPHTAVHKERADULGGTLTPLR  SHYTCHWINTASHIPSHTHPHTAVHKERADULGGTLTPLR  TGWMPPGRWHAA/ISSSGPVFEGARA\LQTVKKEEEDESYTFVQ AARPQTLNRICQELFRQLFRQLKYHESSGPLETLSRIRELCRWW LRRPAVLSKAQILELLVLEGFLSILDEELRVWVQLHNPESGEE\L WPCWRSCRGTLMGHPGGTRALP\EPPCALDGYRS\LRSAQIWSL ASPLRSSALGDHLEPPYEIEARDFLAGGSDTPAAQMPALPPRE GCCDQVTPTRSLTAQLGETMTFKDUEVTFSQDEWGWLDSAQRN LYRDVMLENYRNMASLGK  GLISTPPAAMHPAAFPLPVVVAAVLWGAAPTRGLIRATTSDHNA SMDFADLPALFGATLSGEGLGGFLVEAHFDNACSPILAPPPAPV NGSVFIALLRFFCNFOLKVLNAQKAGYGAAVVHNVNSNELLNM VWNSEBIQQQIWIPSVFIGERSSEYLRALFVYEKGARVLLVPDN TFPLGYYLIPFTGIVGLLVLAMGAVMIARCIQHRKRLQRNRLTK \SQLKQI\PPHDVQKGDQYDVCAICLDEYEDGDKLRVLPCAHAY HSRCVDPWLTQTRKTCPICKQPWIRGPGDEDGEETQGGEEGBE GEPRHPASERTPLLGSSFTLPTSFGSLAPAPLVFFGPSTDPPL SPPSSPVILV  6118  1044  247  STISCRACTSGATFGAQSHRSARGHAAGGKETAALGMERGKVKK KKKEKETQKEKIGEKGREEKVKRKEVEGKIKQEKQEKQERRGK EKEKERTKQGKETNKEKEQFKGQEEKGENKDSTLTRTPLEPLEK NKQILVIGLDGAGKTSVLHSLASNRVQHSVAPTQGFHAVCINTE DSQMFFLBIGGSKPPRSYWEMYLSN/ADSLARSFSVGPKQDSQP ITWKAKKYLHQLIAANPVLPLVVFANKQDLEAAVHITDIHEALA II  6119  1217  462  DPFFVTENTTKAPAQERTTQPRSSREGTLRSTMEYLSALNPSDL LRSVSNISSEFGRRVWTSAPPPQRPFFVCDHKRTIRKGLTAATR QELLAKAUETLLLINGVLTLVLEEDGTAVDSBDFFQLLEDDTCLM VLQSGQSWSPTRSGVLSYGLGEERPKHSKNIARFTFDVYKONPR DLFSSLNVKATFYGLYSMSCDPGOL\QPKKVLRELLRRTSTILO	6115	324	71	
TGMPPGRWHAA/ISSGPVPEGARA\LQTVKKEEEDESYTFVQ AARPQTLNRPQQELFRQLRYHESSGPLETLSRLRELCRWW LRPDVLSKAQILELLVLEQFLSILPGELRVWQULNPESGEE\L WPCWRSCRGTLMGHPGGTRALP\EPPRCALDGYRS\LRSAQIWSL ASPLRSSSALGDHLEPPYBIEARDFLAGGSDTPAAQMPALFPRE GCPCDQVTPTRSLTAQLQETMTFKDVEVTFSQDEWGWLDSAQRN LYRDVMLENYRNMASLGK  6117 1433 222 VGVSPAPPCSWEVGFGGWTFGILKEGQGGRRTFLLLLATRTR GLLSLFPPAAMHPAAFFLEVVVANVLWGAAPTRGLIRATSCHNA SMDFADLPALFGATLSQEGLQGFLVEAHPDNACSPIAPPPAPV NGSVFIALLRRFDCNFDLKVLNAQKAGYGAAVVHNVNSKELLMM VWNSEBIQQQIWIPSVFIGERSSEYLRALFYYEKGARVLLVPDN TFPLGYYLIPFTGIVGLLVLAMGAVMIARCIQHRKRLQRNRITK \COLKQI\PTHDYQKGDQYDVCAICLDEYBCDGKLRVLPCAHAY HSRCVDPWLTQTRKTCPICKQPVHRGPGDEDGEETGQGEEGDB GEPRDHPASERTPLLGSSFTLPTSFGSLAPAPLVFPGPSTDPPL SPPSSPULV  6118 1044 247 STISCRACTSGATPGAQSHRSARGHAAGGKETAALGMERGKVKK KEKEKETQKEKIGEKGREEKVKRKEVEQKIKQEKQEKQERKGK KEKEKETQKEKIGEKGREEKVKRKEVEQKIKQEKQEKQERKGK KEKEKTTKGGKETNKEKCFFKQGEEEGBNDSTLTRTPLEPLEK NKQILVIGLDGAGKTSVLHSLASNRVOHSVAPTQGFHAVCINTE DSQMEFLEIGGSKPFRSYWEMYLSI/ADSLARSFSVGFKODSQP ITWKAKKYLHQLIAANPVLPLVVFANKQDLEAAYHITDIHEALA 11 6119 1217 462 DPRFVTENTTKAPAQERTTQPRSSREGTLRSTMEYLSALNPSDL LRSVSNISSEFGRRVWTSAPPPQRPFRVCDHKRTIRKGLTAATR QELLAKALETLLLNGVLTLVLEEDGTAVDSBDFFQLLEDDTCLM VLQSGQSWSPTRSGVLSYGLERFFRHYKSKDIARFTEDVYKQNPR DLFGSLNVKATFYGLYSMSCDFOOL\GPKKVLELRWTSTLLD		72.	/1	DVCGRVCAHPHLYTHIHMHICAHAC\IHTHAQLC/ITASHALAH
AARPOTINRPCGELFRQLFRQLFRQLERYBESGPLETLSRLRELCRWW LRPDVLSKAQILELLVLEQFLSILPGELRVWVQLHNPESGEE\L WPCWRSCRGTIMGHPGGTRALP\BPRCALDGYRS\LRSAQIWSL ASPLRSSALGDHLEPPFEIEARDFLAGQSDTPAAQMPALFPRE GCPGDQVTPTRSLTAQLQETMTFKDVEVTFSQDEWGWLDSAQRN LYRDVMLENYRMASLGK  6117 1433 222 VGVPSPAPPCSWEVOPGGGWTFGILKEGQGGRTFLLLLATRTR GLLSLFPPAAMHPAAFPLPVVVAAVLWGAAPTRGLIRATSDHNA SMDFADLPALFGATLSQEGLQGFLVEAHPDNACSPIAPPPPAPV NGSVFIALLRRFDCNFDLKVLNAQKAGYGAAVVHNVNSNELLNM VWNSEEIQQQIWIPSVFIGERSEYLRALFVYEKGARVLLVPDN TTFPLGYVLIPFTGIVGLLVLAMGAVMIARCIQHRKRLQRNRLTK \EQLKQI\PTHDYQKGDQYDVCAICLDEYBDGDKLRVLPCAHAY HSRCVDPWLTQTRKTCPICKQPVHRGPGDBDQEEETQGEEGDB GEPRDHPASERTPLLGSSPTLPTSFGSLAPAPLVFPGPSTDPPL SPPSSPVILV  6118 1044 247 STISCRACTSGATPGAQSHRSARGHAAGGKETAALGMERGKVKK KEKEKETQKEKIGEKGREEKVKRKEVEQKIKQEKGEKGEKVKK KEKEKETQKEKIGEKGREEKVKRKEVEQKIKQEKGEKGEKKOK KEKEKETQKEKIGEKGREEKVKRKEVEQKIKQEKGEKGEKKOK NKQILVIGLDGAGKTSVLHSLASNRVQHSVAPTQGFHAVCINTE DSQMEFLEIGGSKPFRSYWEMYLSN/ADSLARSFSVGFKODSQP ITWKAKKYLHQLIAANPVLPLVVFANKQDLEAAYHITDIHEALA III  6119 1217 462 DPRFVTENTTKAPAQERTTQPRSSREGTLRSTMEYLSALNPSDL LRSVSNISSEFGRRVWTSAPPPQRPFRVCDHKRTIRRGLTAATR QELLAKALETLLLNGVLTLVLEEDGTAVDSBDFFQLLEDDTCLM VLQSGGSWSPTRSGVLSYGLERFFKHSKDIAFTFDVYKQNPR DLFGSLNVKATFYGLYSMSCDFQGL\GPKKVLRLERFTSTILD	6116	595	1430	TOWN DODGE AND A CONSTRUCTION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY
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SMDFADLPALFGATLSQEGLQFLVEAHPDNACSPIAPPPPAPV  NGSVFIALLREFDCHFDLKVLNAQKAGYGAAVVHNVNSNELLNM  VWNSEEIQQQIWIPSVFIGERSSEYLRALFYYEKGARVLLVPDN  TFPLGYYLIPFTGIVGLLVLAMGAVMIARCIQHRKRLQRNRLTK  \EQLKQI\PTHDYQKGDQYDVCAICLDEYEDGDKLRVLPCAHAY  HSRCVDPWLTQTRKTCPICKQPVHRGPGDBDQEEETQGQEEGDB  GEPRDHPASERTPLLGSSPTLPTSFGSLAPAPLVFPGPSTDPPL  SPPSSPVILV  6118 1044 247 STISCRACTSGATPGAQSHRSARGHAAGGKETAALGMERGKVKK  KEKEKETQKEKIGEKGREEKVKRKEVEQKIKQEKQERQERRKGK  KEKEKETQKEKIGEKGREEKVKRKEVEQKIKQEKQERQERRKGK  KKEKEKTKQGKETNKEKEQFKGQEEKGENKDSTLTRTPLEPLEK  NKQILVIGLDGAGKTSVLHSLASNRVQHSVAPTOGFHAVCINTE  DSQMEFLBIGGSKPFRSYWEMYLSN/ADSLARSFSVGFKQDSQP  ITWKAKKYLHQLIAANPVLPLVVFANKQDLEAAYHITDIHEALA  II  6119 1217 462 DPRFVTENTTKAPAQERTTQPRSSREGTLRSTMEYLSALNPSDL  LRSVSNISSEFGRRVWTSAPPPQRPFRVCDHKRTIRKGLTAATR  QELLAKALETLLUNGVLTLVLEEDGTAVDSBDFFQLLEDDTCLM  VLQSGQSWSPTRSGVLSYGLGRERPKHSKDIARFTFDVYKQNPR  DLFGSLNVKATFYGLYSMSCDFOGL\GPKKVLRELLRWTSTLLO				GLLSLFPPAAMHPAAFPLPVVVAAVLWGAADTRGLTDATGDUNA
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GEPRDHPASERTPLLGSSPTLPTSFGSLAPAPLVFPGPSTDPPL SPPSSPVILV  STISCRACTSGATPGAQSHRSARGHAAGGKETAALGMERGKVKK KEKEKETQKEKIGEKGREEKVKRKEVEQKIKQEKQEKQERGKGK EKEEKRTKQGKETNKEKEQFKGQEEKGENKDSTLTRTPLEPLEK NKQILVIGLDGAGKTSVLHSLASNRVQHSVAPTQGFHAVCINTE DSQMEFLEIGGSKPFRSYWEMYLSN/ADSLARSFSVGFKQDSQP ITWKAKKYLHQLIAANPVLPLVVFANKQDLEAAYHITDIHEALA II  DPRFVTENTTKAPAQERTTOPRSSREGTLRSTMEYLSALNPSDL LRSVSNISSEFGRRVWTSAPPPQRPFRVCDHKRTIRKGLTAATR QELLAKALETLLINGVLTLVLEEDGTAVDSEDFFQLLEDDTCLM VLQSGQSWSPTRSGVLSYGLGRERPKHSKDIARFTFDVYKQNPR DLFGSLNVKATFYGLYSMSCDFOGL\GFKKVLRELLRWTSTLLO				HSRCVDPWLTQTRKTCPICKOPVHRGPGDRDOEEETOGOEEGDR
6118 1044 247 STISCRACTSGATPGAQSHRSARGHAAGGKETAALGMERGKVKK KEKEKETQKEKIGEKGREEKVKRKEVEQKIKQEKQERGKRGK EKEEKRTKKGGKETNKEKEQFKGQEEKGENKDSTLTRTPLEPLEK NKQILVIGLDGAGKTSVLHSLASNRVQHSVAPTQGFHAVCINTE DSQMEFLEIGGSKPFRSYWEMYLSN/ADSLARSFSVGPKQDSQP ITWKAKKYLHQLIAANPVLPLVVFANKQDLEAAYHITDIHEALA II  6119 1217 462 DPRFVTENTTKAPAQERTTQPRSSREGTLRSTMEYLSALNPSDL LRSVSNISSEFGRRWTSAPPPQRPFRVCDHKRTIRKGLTAATR QELLAKALETLLLNGVLTLVLEEDGTAVDSEDFFQLLEDDTCLM VLQSGQSWSPTRSGVLSYGLGRERPKHSKDIARFTFDVYKQNPR DLFGSLNVKATFYGLYSMSCDFOGL\GPKKVLRELLRWTSTLLO	1 1	1		GEPROHPASERTPLLGSSPTLPTSFGSLAPAPLVFPGPSTDPPL
STISCRACTSGATFGAQSHRSARGHAAGGKETAALGMERGKVKK KEKEKETQKEKIGEKGREEKVKRKEVEQKIKQEKQERQERRKGK EKEEKETKGKETIGKEKGGEEKGERKDSTLTRTPLEPLEK MKQILVIGLDGAGKTSVLHSLASNRVQHSVAPTQGFHAVCINTE DSQMEFLEIGGSKPFRSYWEMYLSN/ADSLARSFSVGPKQDSQP ITWKAKKYLHQLIAANPVLPLVVFANKQDLEAAYHITDIHEALA II  DPRFVTENTTKAPAQERTTOPRSSREGTLRSTMEYLSALNPSDL LRSVSNISSEFGRRVWTSAPPQRPFRVCDHKRTIRKGLTAATR QELLAKALETLLLNGVLTLVLEEDGTAVDSEDFFQLLEDDTCLM VLQSGQSWSPTRSGVLSYGLGRERPKHSKDIARFTFDVYKQNPR DLFGSLNVKATFYGLYSMSCDFOGL\GPKKVLRELLRWTSTLLO	6110	1044		SPPSSPVILV
KEKEKETOKEKIGEKGREEKVRRKEVEQKIKQEKQEKQERREKK EKEEKRTKQGKETINKEKEQFKGQEEKGENKDSTLTRITPLEPLEK NKQILVIGLDGAGKTSVLHSLASNRVQHSVAPTQGFHAVCINTE DSQMEFLBIGGSKPFRSYWEMYLSN/ADSLARSFSVGPKQDSQP ITWKAKKYLHQLIAANPVLPLVVFANKQDLEAAYHITDIHEALA II  6119 1217 462 DPRFVTENTTKAPAQERTTQPRSSREGTLRSTMEYLSALNPSDL LRSVSNISSEFGRRVWTSAPPPQRFRVCDHKRTIRKGLTAATR QELLAKALETLLLNGVLTLVLEEDGTAVDSEDFFQLLEDDTCLM VLQSGQSWSPTRSGVLSYGLGREPKHSKDIARFTFDVYKQNPR DLFGSLNVKATFYGLYSMSCDFOGL\GPKKVLRELLRWTSTLLO	0218	1044	247	STISCRACTSGATPGAQSHRSARGHAAGGKETAALGMERGKVKK
EKEEKRTKQGKETNKEKEQFKGQEEKGENKDSTLTRTPLEPLEK NKQILVLGLDGAGKTSVLHSLASNRVQHSVAPTQGFHAVCINTE DSQMEFLBIGGSKPFRSYWEMYLSN/ADSLARSFSVGFKQDSQP ITWKAKKYLHQLIAANPVLPLVVFANKQDLEAAYHITDIHEALA II  6119 1217 462 DPRFVTENTTKAPAQERTTQPRSSREGTLRSTMEYLSALNPSDL LRSVSNISSEFGRRVWTSAPPPQRPFRVCDHKRTIRKGLTAATR QELLAKALETLLLNGVLTLVLEEDGTAVDSEDFFQLLEDDTCLM VLQSGQSWSPTRSGVLSYGLGRERPKHSKDIARFTFDVYKQNPR DLFGSLNVKATFYGLYSMSCDFOGL\GPKKVLRELLRWTSTLLO	] ]	]	,	KEKEKETQKEKIGEKGREEKVKRKEVEOKIKOEKOEKOERRKGK
NKQILVIGLDGAGKTSVLHSLASNRVQHSVAPTQGFHAVCINTE DSQMEFLBIGGSKPFRSYWEMYLSN/ADSLARSFSVGFKQDSQP ITWKAKKYLHQLIAANPVLPLVVFANKQDLEAAYHITDIHEALA II DPRFVTENTTKAPAQERTTQPRSSREGTLRSTMEYLSALNPSDL LRSVSNISSEFGRRVWTSAPPPQRPFRVCDHKRTIRKGLTAATR QELLAKALETLLLNGVLTLVLEEDGTAVDSBDFFQLLEDDTCLM VLQSGQSWSPTRSGVLSYGLGRERPKHSKDIARFTFDVYKQNPR DLFGSLNVKATFYGLYSMSCDFOGL\GPKKVLRELLRWTSTLLO	[	•	1	EKEEKRTKQGKETNKEKEQFKGQEEKGENKDSTLTRTPLEDLEK
DSQMEFLBIGGSKPFRSYWEMYLSN/ADSLARSFSVGPKQDSQP ITWKAKKYLHQLIAANPVLPLVVFANKQDLEAAYHITDIHEALA II  DPRFVTENTTKAPAQERTTQPRSSREGTLRSTMEYLSALNPSDL LRSVSNISSEFGRRVWTSAPPPQRPFRVCDHKRTIRKGLTAATR QELLAKALETLLLNGVLTLVLEEDGTAVDSEDFFQLLEDDTCLM VLQSGQSWSPTRSGVLSYGLGRERPKHSKDIARFTFDVYKQNPR DLFGSLNVKATFYGLYSMSCDFOGL\GPKKVLRELLRWTSTLLO	1			NKQILVLGLDGAGKTSVLHSLASNRVQHSVAPTOGFHAVCINTR
ITWKAKKYLHQLIAANPVLPLVVFANKQDLEAAYHITDIHEALA  II  DPRFVTENTTKAPAQERTTOPRSSREGTLRSTMEYLSALNPSDL LRSVSNISSEFGRRVWTSAPPQRPFRVCDHKRTIRKGLTAATR QELLAKALETLLLNGVLTLVLEEDGTAVDSEDFFQLLEDDTCLM VLQSGQSWSPTRSGVLSYGLGRERPKHSKDIARFTFDVYKQNPR DLFGSLNVKATFYGLYSMSCDFOGL\GPKKVLRELLRWTSTLLO	]			DSQMEFLEIGGSKPFRSYWEMYLSN/ADSLARSFSVGFKODSOP
6119  1217  462  DPRFVTENTTKAPAQERTTQPRSSREGTLRSTMEYLSALNPSDL  LRSVSNISSEFGRRVWTSAPPPQRPFRVCDHKRTIRKGLTAATR  QELLAKALETLLINGVLTLVLEEDGTAVDSBDFFQLLEDDTCLM  VLQSGQSWSPTRSGVLSYGLGRERPKHSKDIARFTFDVYKQNPR  DLFGSLNVKATFYGLYSMSCDFQGL\GPKKVLRELLRWTSTLLO	1			TTWKAKKYLHQLIAANPVLPLVVFANKQDLEAAYHITDIHEALA
DPRFVIENTKAPAQERTTOPRSSREGTLRSTMEYLSALNPSDL  LRSVSNISSEFGRRVWTSAPPPQRPFRVCDHKRTIRKGLTAATR  QELLAKALETLLLNGVLTLVLEEDGTAVDSEDFFQLLEDDTCLM  VLQSGQSWSPTRSGVLSYGLGRERPKHSKDIARFTFDVYKQNPR  DLFGSLNVKATFYGLYSMSCDFOGL\GPKKVLRELLRWTSTLLO	6119	1217		II
LRSVSNISSEFGRRVWTSAPPPQRPFRVCDHKRTIRKGLTAATR QELLAKALETLLLNGVLTLVLEEDGTAVDSEDFFQLLEDDTCLM VLQSGQSWSPTRSGVLSYGLGRERPKHSKDIARFTFDVYKQNPR DLFGSLNVKATFYGLYSMSCDFOGL\GPKKVLRELLRWTSTLLO		/		DPRFVTENTTKAPAQERTTQPRSSREGTLRSTMEYLSALNPSDL
QELLAKALETLLLNGVLTLVLEEDGTAVDSEDFFQLLEDDTCLM VLQSGQSWSPTRSGVLSYGLGRERPKHSKDIARFTFDVYKQNPR DLFGSLNVKATFYGLYSMSCDFOGL\GPKKVLRELLRWTSTLLO	<b>!</b>	ľ	į	LRSVSNISSEFGRRVWTSAPPPORPFRVCDHKRTIRKGLTAATP
VLQSGQSWSPTRSGVLSYGLGRERPKHSKDIARFTFDVYKQNPR DLFGSLNVKATFYGLYSMSCDFOGL\GPKKVLRELLRWTSTLLO	1 1		1	QELLAKALETLLLNGVLTLVLEEDGTAVDSRDFFOLLEDDTCLM
DLFGSLNVKATFYGLYSMSCDFQGL\GPKKVLRELLRWTSTLLQ GLGHMLLGISSTLRHAVEGAEQWQQKGRLHSY			1	VLQSGQSWSPTRSGVLSYGLGRERPKHSKDIARFTFDVYKONPR
GLGHMLLGISSTLRHAVEGAEQWQQKGRLHSY	1			DLFGSLNVKATFYGLYSMSCDFQGL\GPKKVLRELLRWTSTLLQ
				GLGHULLGISSTLRHAVEGAEQWQQKGRLHSY

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine.
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
[	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ĺ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
6120	sequence		\=possible nucleotide insertion)
6120	785	179	LERAGGGGLSSRALVGSGACLSLVARANGKGLPRGRKEFVBAVR
		İ	VRYVAFRYRTPRAVCLRLWSCRREVIMSGRGKQGGKVRAKAKSR
i	1		SSRAGLQFPVGRVHRLLRKGNYAERVGAGAPVYLAAVLEYLTAE
			ILELAGNAARDNKKTRIIPRHLQLAIRNDEELNKLLGKVTIAQG G\VLPNIQAVLLPKKTESQKDEGANDP
6121	1612	107	FVRAQARGSRQPVRRPLLGAGSRLRCRSCGRMEPLKVEKFATAN
}	]	/	RGNGLRAVTPLRPGELLFRSDPLAYTVCKGSRGVVCDRCLLGKE
1			KLMRCSQCRVAKYCSAKCQKKAWPDHKRECKCLKSCKPRYPPDS
			VRLLGRVVFKLMDGAPSESEKLYSFYDLESNINKLTEDKKEGLR
1	İ		QLVMTFQHFMREEIQDASQLPPAFDLFEAFAKVICNSFTICNAE
1			MQEVGVGLYPSISLLNHSCDPNCSIVFNGPHLLLRAVRDIEVGE
1			ELTICYLDMLMTSEERRKQLRDQYCFECD\CFRCQTQDKDADML
1			TGDEQVWKEVQESLKKIEELKAHWKWEQVLAMCQAIISSNSERL
ŀ			PDINIYQLKVLDCAMDACINLGLLEEALFYGTRTMEPYRIFFPG
[	ł		SHPVRGVQVMKVGKLQLHQGMFPQAMKNLRLAFDIMRVTHGREH
1			SLIEDLILLLE/AMRRQHQSILRERSQREIRRVSLLNALLRSHT LCFVSCVNLSYWKFCSVFV
6122	2	2324	RFRKMADGGAASQDESSAAAAAAADSRMNNPSETSKPSMESGDG
1	_	2324	NTGTQTNGLDFQKQPVPVGGAISTAQAQAFLGHLHQVQLAGTSL
ĺ			QAAAQSLNVQSKSNEESGDSQQPSQPSQQPSVQAAIPOTQLMLA
l			GGQITGLTLTPAQQQLLLQQAQAQAQLLAAAVQQHSASQQHSAA
			GATISASAATPMTQIPLSQPIQIAQDLQQLQQLQQQNLNLQQFV
1			LVHPTTNLQPA\QFIISQTPQGQQGLLQA\QNLLTQLPROSOAN
1			LLQSQPRI\TLTSQPATPTCTIAATPIQTLPQSQSTPKRIDTPS
			LEEP\SDLEELEQFAKTFKQRRIKLGFT\QGDAGLAMVKLYGND
			FSPTTIFRFRALNLSPKNMCKLKPLLEKWLNDAENLSSDSSLSS
	1		PSALNSPGIEGLSRRRKKRTSIEA\NIRVALEKSPLEN\QKPTS
1			EEITMIADQLNMEKGVIRVWFCNRRQKEKRINPPSSGG\TSSSP
			IKAIFPSPTSLVATTPSLVTSSAATTLTVSPVLPLTSAAVTNLS
			VTGTSDTTSNNTATVISTAPPASSAVTSPSLSPSPSASASTSEA SSASETSTTGTTSTPLSSPLGTSQVMVTASGLQTA/AQLLPFKG
1 1			AAQLPANASLAAMAAAAGLNPSLMAPSQFAAGGALLSLNPGTLS
1			GALSPALMSNSTLATIQALASGGSLPITSLDATGNLVFANAGGA
i ]			PNIVTAPLFLNPONLSLLTSNPVSLVSAAAASAGNSAPVASLHA
			TSTSAESIQNSLFTVASASGAASTTTTASKAQ
6123	3	2944	HLLHRWFGTDMQMINFTTGEFQLTEACPYLGTHSEESRFGILHL
1 1			HLQPLEMKRVGVVFTPADYGKVTSLILIRNNLTVIDMIGVEGFG
	1		ARELLKVGGRLPGAGGSLRFKVPESTLMDCRRQLKDSKQILSIT
	Į.		KNFKVENIGPLPITVSSLKINGYNCQGYGFEVLDCHQFSLDPNT
	Į.		SRDISIVFTPDFTSSWVIRDLSLVTAADLEFRFTLNVTLPHHLL PLCADVVPGPSWEESFWRLTVFFVSLSLLGVILIAFQQAQYILM
	1		EFMKTRQRQNASSSQQNNGPMDVISPHSYKSNCKNFLDTYGPS
		i	DKGRGKNCLPVNTPQSRIQNAAKRSPATYGHSQKKHKCSVYYSK
		•	HKTSTAAASSTSTTTEEKQTSPLGSSLPAAKEDICTDAMRENWI
ļi	}		SLRYASGINVNLQKNLTLPKNLLNKEENTLKNTIVFSNPSSECS
			MKEGIQTCMFPKETDIKTSENTAEFKERELCPLKTSKKLPENHL
		İ	PRNSPQYHQPDLPEISRKNNGNNQQVPVKNEVDHCENLKKVDTK
	ſ	ſ	PSSEKKIHKTSREDMFSEKQDIPFVEQEDPYRKKKLQEKREGNL
			QNLNWSKSRTCRKNKKRGVAPVSRPPEQSDLKLVCSDFERSELS
			SDINVRSWCIQESTREVCKADAEIASSLPAAQREAEGYYQKPEK
			KCVDKFCSDSSSDCGSSSGSVRASRGSWGSWSSTSSSDGDKKPM
1			VDAQHFLPAGDSVSQNDFPSBAPISLNLSHNICNPMTGNSLPQY
	ì	,	AEPSCPSLPAGPTGVEEDKGLYSPGDLWPTPPVCVTSSLNCTLE
J			NGVPCVIQESAPVHNSFIDWSATCEGQFSSAYCPLBLNDYNAFP
1	1		EENMYANGFPCPADVQTDFIDHNSQSTWNTPP\NMPAS\WGNA QFPSSSRPYLKSTPKACLPMSGLFGPI\WAP\QSDVYENCCPIN
			W. TOOGHT THE TENACHPHOODEGET WAY QUOVYENCEPIN

SEQ	Predicted	Predicted end	Dmine sold
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine
ł	amino acid	residue of	S=Serine, T=Threonine, V=Valine.
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Imknown *-Stop
}	amino acid sequence	sequence	Codon, /=possible nucleotide deletion
<b>———</b>	sequence		\-possible nucleotide insertion)
	ĺ		PTTEHSD/THMENQA\VVCKEYYPGF\NPFRAYMNLDIWTTT\A
6124	1573	236	NRNANFPLSRDSSYCGNV
İ	ļ	250	SDEALRLAGERGMGRVQLFEISLSHGRVVYSPGEPLAGTVRVRL
1	ļ.		GAPLPFRAIRVTCIGSCGVSNKANDTAWVVEEGYFNSSLSLADK
ļ			GSLPAGEHSFPFQFLLPATAPTSFEGPFGKIVHQVRAAIHTPRF SKDHKCSLVFYILSPLNLNSIPDIEQPNVASATKKFSYKLVKTG
			SVVLTASTDLRGYVVGQALQLHADVENQSGKDTSPVVASLLQKV
}	1		SYKAKRWIHDVRTIAEVEGAGVKAWRRAQWHEQILVPALPQSAL
			PGCSLIHIDYYLQVSLKAPEATVTLPVFIGNIAV/NPCPSEPPA
1			RPGAASWGPTPGG\PSAPPOEEAEAAAGGPHPLDPUFT.crkg
1		•	HSQRQPLLATLSSVPGAPEPCPODGSPASHPLHPPLCTSTGATT
1	]		PYFAEGSGGPVPTTSTLILPPEYSSWGYPYEAPPSYEOSCGGVE
6125	1	904	PSLTPES
1	1 -	904	KTCPKLTCAFTVSVPDSCCRVCRGDGELSWEHSDGDIFRQPANR
1	! !		EARHSYHRSHYDPPPSRQAGGLSRFPGARSHRGALMDSQQASGT
ŀ	i l		IVQIVINNKHKHGQVCVSNGKTYSHGESWHPNLRAFGIVECVLC
ł			TCNVTKQECKKIHCPNRYPCKYPQKIDGKCCKVCPG/KKAKEBL PGQSFDNKGYFCGBETMPVYESVFMEDGETTRKIALETERPPQV
			EVHVWTIRKGILQHPHIEKISKRMFEELPHFKLVTRTTLSQWKI
			PTEGEAQISQMCSSRVCRTELEDLVKVLYLERSEKGHC
6126	1224	389	RLLSEAPCPRSRRRFOMNPEWGOAFVHVAVAGGLCAVAVETGIF
1			DSVSVQVGYEHYAEAPVAGLPAFLAMPPNSI,VNMAVTI.T.CI.CWI.
1 .			HRGGAMGLGPRYLKDVFAAMALLYGPVOWLRLWTOWRRAAVT.DO
1			WLTLPIFAWPVAWCLYLDRGWRP\WLFLSLECVSLASVGLALLU
	ĺ		PQGFEVALGAHVVPAVGOALRT\HRHYG/SATPSATVTALCUTE
	ľ		CLGFVVLKLCDHQLARWRLFQCLTGHFWSKVCDVLQFHFAFLFL
6127	1335	463	THENTHPREHPSGGKTR
			VLPRRCLVFVVNTMDSSREPTLGRLDAAGFWQVWQRFDADEKGY IEEKELDAFFLHMLMKLGTDDTVMKANLHKVKQQFMTTQDASKD
1 1			GRIRMKELAGMFLSEDENFLLLFRRENPLDSSVEFMQIWRKYDA
1 1	' I		DSSGFISAABLRNFLRDLFLHHKKAISEAKLEEYTGTMMKIFDR
			NKDGRLDLNDLARILALQENFLLOFKMDACSTRKRKGDFEKIEA
1 1			YYDVSKTGALEGP\EVDGFVKDMMELVOPSISGVDLDKFREILL.
6128	253.		RHCDVNKDGKIQKSELALCLGLKINP
"12"	2511	843	TCRMSRRQLERWVWSSQQVQARGRNVRAPRLGKIAMGLEMSSKD
i			SPGSLDGRAWEDAOKPOSAWCGGRKTRVYATSSRRADDSFCTDD
[ ]	ſ		GGAARPEKTABEGPPAAPGSLRHSGPLGPHACPTALPEPQVTSA
]			MSSQVVGIEPLYIKAEPASPDSPKGSSETETEPPVALAPG\PAP
]			TRCLPGHKEEEDGEGAGPGEQGGKLVLSSLPKRLCLVCGDVAS GYHYGVASCEACKAFFKRTIQGSIEYSCPASNECEITKRRKAC
	1	1	QACRFTKCLRVGMLKEGVRLDRVRGGRQKYKRRPEVDPLPFPGP
1 1			FPAGPLAVAGGPRKTAAPVNALVSHLLVVEPEKLYAMPDPAGPD
! [		ļ	GHLPAVATLCDLFDREIVVTISWAKSIPGFSSLSLSDQMSVLQS
1 1		Ì	VWMEVLVLGVAQRSLTLQDELAFAEYLVLDEEGARPAGIGEIG\
] [			AALLQLVRRLQALRLEREKYVLLKALALANSDSVHIEDEDDING
[ ]		1	SCEKLLHEALLEYEAGRAGPGGGAERRRAGRILLTI.DILDOTAG
6129	1764	222	KVLAHFYGVKLEGKVPMHKLFLEMLRAMMD
/	1/04	771	ARFARSAHEGKMPKKKTGARKKAENRREREKQLRASRSTIDLAK
			HPCNASMECDKCQRRQKNRAFCYFCNSVOKLPICAOCGKTKCMM
			KSSDCVIKHAGVYSTGLAMVGAICDFCEAWVCHGRKCLSTHACA
,			CPLTDAEC\VECERGVWDHGGRIFSCSFCHNFLCEDDQFEHQAS
	ſ	<u>†</u>	CQVLEAETFKCVSCNRLGQHSCLRCKACFCDDHTRSKVFKQEKG
	İ	1	KQPPCPKCGHETQETKDLSMSTRSLKFGRQTGGEEGDGASGYDA YWKNLSSDXYGDTSYHDEEEDEYEAEDDEEEEDEGRKDSDTESS
		Į	DLFTNLNLGRTYASGYAHYEEQEN
6130	3	577	GRGGTMREYKVVVLGSG\GVGKSALTV\QFVTCTFIEKYDPTIE
			TOOG (G.O.CHILA (GEALCIE IEKIDELIE

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
i	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	corresponding	to first	Halistidine, IaIsoleucine, Kalysine,
i	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
}	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
- 1	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
i	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
- [	sequence	bequence	Codon, /=possible nucleotide deletion,
			\=possible nucleotide insertion)
1	ŀ		DFYRKEIEV\DSSPSVAGISWTQQGTEQF\ASMRDLYIKKGQGC
İ	]	ļ	ILVYSLVNQQSFQ\DIKPMRDQIIRVKVSEKVPVI\LVGN\SVD
		1	LESEREVSSSEGRALAEEWGCPFMETSAKSKTMVDELFAEIVRQ
6131	3	1811	MNYAAQPDKDDPCCSACNIQ
		1011	SSPREKTSDSSHRPSRHGFLFLRLVGLSPFSYLCVPPSRPVPGS
J	Ì	ļ	PRSLSAMRLLPLAPGRLRRGSPRHLPSCSPALLLLVLGGCLGVF
			GVAAGTRRPNVVLLLTDDQDEVLGGMTPLKKTKALIGEMGMTFS
			SAYVPSALCCPSRASILTGKYPHNHHVVNNTLEGNCSSKSWQKI
1	1		QEPNTFPAILRSMCGYQTFF\AGKYLNEYGAPDAGGLEHVPLGW
-			SYWYALBKNSKYYNYTLSINGKARKHGENYSVDYLTDVLANVSL
	1		DFLDYKSNFEPFFMMTATP\APHSPWTAAPQYQKAFQNVFAPRN
			KNFNIHGTNKHWLIRQAKTPMTNSSIQFLDNAFRKRWQTLLSVD
1			DLVEKLVKRLEFTGELNNTYIFYTSDNGYHTGQFSLPIDKRQLY
			EFDIKVPLLVRGPGIKPNQTSKMLVANIDLGPTILDIAGYDLNK
			TQMDGMSLLPILRGASNLTWRSDVLVEYOGEGRNVTDPTCPSLS
1	1		PGVSQCFPDCVCEDAYNNTYACVRTMSALWNLQYCEFDDQEVFV
[	[		EVYNLTADPDQITNIAKTIDPELLGKMNYRLMMLOSCSGPTCRT
6132	96	1011	PGVFDPGYRFDPRLMFSNRGSVRTRRFSKHLL
0132	30	1241	AAGLLPPGLVPEDPRRTRNLLPFGIQGPPFALSRPLFSCVESGW
İ			AWEAMEPEFLYDLLQLPKGVEPPAEEELSKGGKKKYI.PDTSPKD
1			PKFEELQKPA\VLMEWINATLLPEHIVVRSLEEDMFDGLILHHL
Ĭ			FQRLAALKLEAEDIALTATSQKHKLTVVLEAVNRS\CSWRSGRP
	1		SGA/WESIFNKDLLSTLHLLVALAKRFQPDLSLPTNVQVEVITI
1	i .		ESTKSGLKSEKLVEQLTEYSTDKDEPPKDVFDELFKLAPEKVNA
· I	]		VKEAIVNFVNQKLDRLGLSVQNLDTQFADGVILLLLIGQLEGFF
Į.			LHLKEFYLTPNSPAEMLHNVTLALELL/IGRGPAQLPC/LALK/
6133	2	4256	TIVNKDAKSTLRVLYGLFCKHTQKAHRDRTPHGAPN
1		4236	FVHGSMADTDLFMECEEEELEPWQKISDVIEDSVVEDYNSVDKT
	·		TTVSVSQQPVSAPVPIAAHASVAGHLSTSTTVSSSGAQNSDSTK
			KTLVTLIANNNAGNPLVQQGGQPLILTQNPAPGLGTMVTQPVLR
1			PVQVMQNANHVTSSPVASQPIFITTQGFPVRNVRPVQNAMNQVG
1 1			IVLNVQQGQTVRPITLVPAPGTQFVKPTVGVPQVFSQMTPVRPG
1 1		1	STMPVRPTTNTFTTVIPATLTIRSTVPQSQSQQTKSTPSTSTTP
			TATOPTSLGQLAVQSPGQSNQTTNPKLAPSFPSPPAVSLASFVT
	,		VKRPGVTGENSNEVAKLVNTLNTIPSLGQSPGPVVVSNNSSAH\
			GSQRTSGPESSMKVTSSIPVFDLQDGGRKICPRCNAQFRVTEAL
1 1	1		RGHMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSPEKTAPVAS
1 1		]	/THPSSTPIPALSPPY/TKVPEPNENVGDAVQTKLIMLVDDFYY
1 1		ļ	GRDGGKVAQLTNFPKVATSFRCPHCTKRLKNNIRFMNHMKHHVE
1		1	LDQQNGEVDGHTICQHCYRQFSTPFQLQCHLENVHSPYESTTKC
] }		ł	KICEWAFESEPLFLQHMKDTHKPGEMPYVCQVCQYRSSLYSEVD
1		I	VHFRMIHEDTRHLLCPYCLKVFKNGNAFQQHYMRHQKR\NVYH\ CNKCRVQFLFAKDKIEHKLQHHKTFRKPKQLEGLKPGTKVTIRA
1 1	1		SPECOPPTY DISCOURTED BY A STATE OF THE SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND A SPECIFIC AND
j	[	ļ	SRGQPRTVPVSSNDTPPSALQEAPLTSSMDPLPVFLYPPVQRS
[ [	1	ł	IQKRAVRKMSVMGRQTCLECSFEIPDFPNHFPTYVHCSLCRYST
Į l	1		CCSRAYANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT
		}	SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGQTRDRVHDR
1			NVKNMYPPPSFPTNKAATVKSAGATPAEPEELLTPLAPALPSPA
1			STATPPPTPTHPQALALPPLATEGAECLNVDDQDEGSPVTQEPE
1 1	i	1	LASGGGSGGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ
j l			RRIRRWLRRFQASQGENLEGKYLSFEABEKLAEWVLTQREQQLP
j	1		VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHLTPHARRA
]		1	VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL
, ,		•	DTEVLSSDDRKENALQTVGTGBPWCDVVLAILADGTVLPTLVFY
1 1	1	1:	RGQMDQPANMPDSILLEAKESGYSDDEIMELWSTRVWQKHTACQ
			RSKGMLVMDCHRTHLSEEVLAMLSASSTLPAVVPAGCSSKIQPL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ļ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
j	amino acid	residue of	
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
1	amino acid		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
}		sequence	Codon, /-possible nucleotide deletion,
ļ	sequence		\=possible nucleotide insertion)
j i	i		DVCIKRTVKNFLHKKWKEQAREMADTACDSDVLLQLVLVWLGEV
	1		LGVIGDCPELVQRSFLVASVLPGPDGNINSPTRNADMQEELIAS
1	i		LEEQLKLSGEHSESSTPRPRSSPEETIEPESLHQLFEGESETES
	<u> </u>		PYGFEEADLDLMEI
6134	2	4256	PVHGSMADTDLFMECEEEELEPWQKISDVIEDSVVEDYNSVDKT
Î	1	1	TTVSVSQQPVSAPVPIAAHASVAGHLSTSTTVSSSGAQNSDSTK
ſ			KTLVTLIANNNAGNPLVQQGGQPLILTQNPAPGLGTMVTQPVLR
			PVQVMQNANHVTSSPVASQPIFITTQGFPVRNVRPVQNAMNQVG
]			IVLNVQQGQTVRPITLVPAPGTQFVKPTVGVPQVFSQMTPVRPG
	1		STMPVRPTTNTFTTVIPATLTIRSTVPQSQSQQTKSTPSTSTTP
			TATOPTSLGQLAVQSPGQSNQTTNPKLAPSFPSPPAVSIASPVT
1			VKRPGVTGENSNEVAKLVNTLNTIPSLGQSPGPVVVSNNSSAH\
1	1		GSOPTGGBRGGMVITGGTBUPDT ODGGBVTGDD GTT
ł	}		GSQRTSGPESSMKVTSSIPVFDLQDGGRKICPRCNAQFRVTEAL
Ì	, · · · · · · · · · · · · · · · · · · ·	•	RGHMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSPEKTAPVAS
1			/THPSSTPIPALSPPY/TKVPEPNENVGDAVQTKLIMLVDDFYY
ľ	1		GRDGGKVAQLTNFPKVATSFRCPHCTKRLKNNIRFMNHMKHHVE
			LDQQNGEVDGHTICQHCYRQFSTPFQLQCHLENVHSPYBSTTKC
	1		KICEWAFESEPLFLQHMKDTHKPGEMPYVCQVCQYRSSLYSEVD
1	1 1		VHFRMIHEDTRHLLCPYCLKVFKNGNAFQQHYMRHQKR\NVYH\
	ļ ,		CNKCRVQFLFAKDKIEHKLQHHKTFRKPKQLEGLKPGTKVTIRA
1			SRGQPRTVPVSSNDTPPSALQEAAPLTSSMDPLPVFLYPPVQRS
Ì			IQKRAVRKMSVMGRQTCLECSFEIPDFPNHFPTYVHCSLCRYST
Į.	l l		CCSRAYANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT
İ			SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGQTRDRVHDR
			NVKNMYPPPSFPTNKAATVKSAGATPAEPEELLTPLAPALPSPA
1	}		STATPPPTPTHPQALALPPLATEGAECLNVDDODEGSPVTOEPE
	l i		LASGGGGSGGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ
	[ [		RRIRRWLRRFQASQGENLEGKYLSFEAEEKLAEWVLTQREOOLP
1			VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHLTPHARRA
İ	i .		VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL
	[		DTEVLSSDDRKENALQTVGTGEPWCDVVLAILADGTVLPTLVFY
1 .	· 1		RGOMDQPANMPDSILLEAKESGYSDDEIMELWSTRVWQKHTACQ
1	}		RSKGMLVMDCHRTHLSEEVLAMLSASSTLPAVVPAGCSSKIQPL
			DVCIKRTVKNFLHKKWKEQAREMADTACDSDVLLQLVLVWLGEV
			LGVIGDCPELVQRSFLVASVLPGPDGNINSPTRNADMQEELIAS
i i	1		LEEQLKLSGEHSESSTPRPRSSPEETIEPESLHQLFEGESETES
			PYGFEEADLDLMEI
6135	2	4256	FVHGSMADTDLFMECEEEELEPWQKISDVIEDSVVEDYNSVDKT
1 1			TTVSVSQQPVSAPVPIAAHASVAGHLSTSTTVSSSGAQNSDSTK
! !		j	KTLVTLIANNNAGNPLVQQGGQPLILTQNPAPGLGTMVTQPVLR
1 1			PVQVMQNANHVTSSPVASQPIFITTQGFPVRNVRPVQNAMNQVG
			IVLNVQQGQTVRPITLVPAPGTQFVKPTVGVPQVFSQMTPVRPG
1 1	1	j	STMPVRPTTNTFTTVIPATLTIRSTVPQSQSQQTKSTPSTSTTP
	į	,	TATQPTSLGQLAVQSPGQSNQTTNPKLAPSPPSPPAVSIASPVT
	ľ		VKRPGVTGENSNEVAKLVNTLNTIPSLGQSPGPVVVSNNSSAH\
1 1			GSQRTSGPESSMKVTSSIPVFDLQDGGRKICPRCNAQFRVTEAL
]			RGHMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSPEKTAPVAS
] [			/TUDESTRIBAL SDRY /MAINSNYSSEYSYPSAKPPSPEKTAPVAS
1 1	ļ	1	/THPSSTPIPALSPPY/TKVPEPNENVGDAVQTKLIMLVDDFYY
1		ļ	GRDGGKVAQLTNFPKVATSFRCPHCTKRLKNNIRFMNHMKHHVE
1 1	1		LDQQNGEVDGHTICQHCYRQPSTPFQLQCHLENVHSPYESTTKC
<u> </u>		1	KICEWAFESEPLFLQHMKDTHKPGEMPYVCQVCQYRSSLYSEVD
j l	. 1	[	VHFRMIHEDTRHLLCPYCLKVFKNGNAFQQHYMRHQKR\NVYH\
[	. 1	ĺ	CNKCRVQFLFAKDKIEHKLQHHKTFRKPKQLEGLKPGTKVTIRA
]		ļ	SRGQPRTVPVSSNDTPPSALQEAAPLTSSMDPLPVFLYPPVQRS
1 1	1		IQKRAVRKMSVMGRQTCLECSFEIPDFPNHFPTYVHCSLCRYST
	<u></u>		CCSRAYANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Clubaria Daid R Phase D-Aspartic Acid, Es
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
ì	amino acid	1	P=Proline, Q=Glutamine, R=Arginine,
	residue of	residue of	S=Serine, T=Threonine, V=Valine,
1		amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
- [	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible rucleotide insertion)
1	1		SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGQTRDRVHDR
1			NVKNMYPPPSFPTNKAATVKSAGATPAEPEELLTPLAPALPSPA
			STATPPPTPTHPQALALPPLATEGAECLNVDDQDEGSPVTQEPE
			LASGGGGGGGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ
1			RRIRRWLRRFQASQGENLEGKYLSFEAEEKLAEWVLTQREQQLP
1			VNERTLFQKATKIGRSLEGGFKISYEWAVRFMLRHHLTPHARRA
			VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL
	}		DTEVLSSDDRKENALQTVGTGEPWCDVVLAILADGTVLPTLVFY
[	[		RGQMDQPANMPDSILLEAKESGYSDDEIMELWSTRVWQKHTACQ
1			RSKGMLVMDCHRTHLSEEVLAMLSASSTLPAVVPAGCSSKIQPL
i			DVCIKRTVKNFLHKKWKEQAREMADTACDSDVLLQLVLVWLGEV
1			LGVIGDCPELVQRSFLVASVLPGPDGNINSPTRNADMQEELIAS
ľ			LEEQLKLSGEHSESSTPRPRSSPEETIEPESLHQLFEGESETES
1			FYGFEEADLDLMEI
6136	1704	539	FGVRMALEGMSKRKRKRSVQEGENPDDGVRGSPPEDYRLGQVAS
1			SI PROFUNDE COMONIA DE COMO POR LE CONTROL DE COMONIA DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO DE COMO
			SLFRGEHHSRGGTGRLASLFSSLEPQIQPVYVPVPK\ESALASA
1			DLEEEIHQKQGQKRKNSQPGVKVADRKILDDTEDTVVSQRKKIQ
			INQEEERLKNERTVFVGNLPVTCNKKKLKSFFKEYGQIESVRFR
1			SLIPAEGTLSKKLAAIKRKIHPDQKNINAYVVFKEESAATQALK
1			RNGAQIADGFRIRVDLASETSSRDKRSVFVGNLPYKVEESAIEK
			HFLDCGSIMAVRIVRDKMTGIGKGFGYVLFENTDSVHLALKLNN
1			SELMGRKLRVMRSVNKEKFKQQNSNPRLKNVSKPKQGLNFTSKT
6137	141	2656	AEGHPKSLFIGEKAVLLKTKKKGQKKSGRPKKQRKQK
1	***	2030	RALRKRRCGPGRRGALGSGPGPQRRPGRVPEERPAPPRERKHPG
1 1			MWNMLIVAMCLA\LLGLPGKAQELQGHVS\IILAGEQLGDLAKK
			YLWQG\LFQLYLDEAGRGHSFSFHGAALTAPKQGQELMAKALES
i l			LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKD1EAQ
1 1			LQHAGLREAGGIFYFSVPPFAYEDIARNINSSCRPGPGAWLRVV
1 1	j		LEKPFGHDHFSAQQLATELGTFFQEEEMYRVDHYLGKQAVAQIL
i i	1		PFRDQNRKALDGLWNRHHVERVEIIMKETVDAEGRTSFYEEYGV
1 1			IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL
1 1	ļ		QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTFAGVLVHIDNL
1	İ		RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS
1			QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG
1 1			LRLFGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL
	1		LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS
1 1	1		QQQPEQLVPGPGPGPMPSDFQVLRAKYRESSLVSAWSEELISKL
] [	1		ANDIBATAVRAVRRFGQFHLALSGGSSPVALFQQLATAHYGFPW
, 1			AHTHLWLVDERCVPLSDPESNFQGLQAHLLQHVRIPYYNIH\AM
i i	1		PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH
]			TASLFPQSPTGLDGEQLVVLTTSPSQPHRRMSLSLPLINRAKKV
	ľ		AVLVMGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY
6138	4587		DAFLG
0230	4307	934	EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL
] [	ľ	1	TDTSHLLSAVKGQERFSLYQTRSLIHELKNKEIHFQRRRTTCAL
j !	}		TLEAGEKLLLTTDLKTKESVGRRISQLQDSWKDMEPQLAEMIKQ
}	1		FQSTVETWDQCEKKIKELKSRLQVLKAQSEDPLPELHEDLHNEK
	ļ		ELIKELEQSLASWTQNLKELQTMKADLTRHVLVEDVMVLKEQIE
!	ł		HLHRQWEDLCLRVAIRKQEIEDRLNTWVVFNEKNKELCAWLVOM
			ENKVLQTADISIEEMIEKLQKDCMEEINLFSENKLQLKOMGDOL
			IKASNKSRAAEIDDKLNKINDRWQHLFDVIGSRVKKLKETFAFI
		. 1	QQLDKNMSNLRTWLARIESELSKPVVYDVCDDQEIQKRLAEOOD
1	[	J	LQRDIEQHSAGVESVFNICDVLLHDSDACANETECDSIOOTTRS
1	1.	I	LDRRWRNICAMSMERRMKIEETWRLWQKFLDDYSRFEDWLKSAR
1		]	RTAACPNSSEVLYTSAKEELKRFEAFQRQIHERLTQLELINKOY
I		1	RRLARENRTDTASRLKQMVHEGNQRWDNLQRRVTAVLRRLRHFT

Degianing   coation   corresponding   coation   corresponding   cofirst   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino a	SEQ	Predicted	Predicted end	Amino acid coment containing cional mentida
Docation   Corresponding	1			Amino acid segment containing signal peptide
Cocresponding   co first   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   am		1 -	1	
to first amino acid residue of amino acid residue of amino acid sequence  S=Serine, T=Threonine, V=Valine, s=Serine, T=Threonine, V=Valine, s=Serine, T=Threonine, V=Valine, s=Serine, T=Threonine, V=Valine, s=Serine, T=Threonine, V=Valine, w=T-TyPtophan, Y=TyPtophan, Y=TyPtophan, Y=Stop Codon, /=possible nucleotide deletion, _\possible nucleotide deletion, _\possible nucleotide deletion, _\possible nucleotide deletion, _\possible nucleotide deletion, _\possible nucleotide deletion, _\possible nucleotide deletion, _\possible nucleotide deletion, _\possible nucleotide deletion, _\possible nucleotide deletion, _\possible nucleotide deletion, _\possible nucleotide deletion, _\possible nucleotide deletion, _\possible nucleotide deletion, _\possible nucleotide deletion, _\possible nucleotide deletion, _\possible nucleotide deletion, _\possible nucleotide deletion, _\possible nucleotide deletion, _\possible nucleotide deletion, _\possible nucleotide deletion, _\possible nucleotide deletion, _\possible nucleotide deletion, _\possible nucleotide deletion, _\possible nucleotide deletion, _\possible nucleotide deletion, _\possible nucleotide deletion, _\possible nucleotide deletion, _\possible nucleotide deletion, _\possible nucleotide deletion, _\possible nucleotide deletion, _\possible nucleotide deletion, _\possible nucleotide deletion, _\possible nucleotide deletion, _\possible nucleotide deletion, _\possible nucleotide deletion, _\possible nucleotide deletion, _\possible nucleotide deletion, _\possible nucleotide deletion, _\possible nucleotide deletion, _\possible nucleotide deletion, _\possible nucleotide deletion, _\possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide nucleotide deletion, \possible nucleotide nucleotide deletion, \p	1.5.		1 '	Halistidine Talcoleucine Kalveine
to first amino acid residue of amino acid amino acid sequence  #TYPTOPIAN, Y=TYXOSIR, X=UNANOM, *=Stop code, /=possible nucleotide deletion,	1	1		
amino acid residue of amino acid sequence	ļ			
residue of amino acid sequence    W-Tryptopham, Y-Tyxcosine, X-Unknown, *-Stop code and sequence   V-possible nucleotide deletion,   V-possible nucleotide deletion,   V-possible nucleotide deletion,   V-possible nucleotide deletion,   V-possible nucleotide insertion;   NORESPECTYESILVAMITEMDIGIPHORISESSIADEMBOLING   PODEITIATINKIPOLIVERGESIADEMBOLING   PODEITIATINKIPOLIVERGESIADEMBOLING   PODEITIATINKIPOLIVERGESIADEMBOLING   PODEITIATINKIPOLIVERGESIADEMBOLING   PODEITIATINKIPOLIVERGESIADEMBOLING   PODEITIATINKIPOLIVERGESIADEMBOLIPERIOT   DSWRKKESSERS POSICHIVANGHERGEGETYVINYS   ILLE   WIDHTORROGPSSIA   REDERAÇIY (SALGKISISGISHIMIVERGE   PSCESHIYK, (MORDORYPOPPA)SITY PLYVEKLIPER POTOGI   KEOPRINKINGHORISISTIATINE   PSTESSICH   PSCESHIYK, (MORDORYPOPPA)SITY PLYVEKLIPER PSPIDIGIS   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIKA   LRIVIK	1		1	
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SAKNRROKAHUTDEKADPRALLECREMOLEKELVEROPQUM LOGISNSLILIKGHGEDCIEREKYMUI EKKLOKEGUSODIM ALQGTONPASPLPSFDEVDSGDQPPAISVPAPRAKQFRAWITE GEBETESRYPGSTERORSFLERVVYRABPLQLILLILLACLL PSSEEDYSCTQANPY_ARSFYPMLRIVADPPLT  6139 52 1131 LGDWWSRTCGVLETFTSVLERARARGFCFTDSKWAPPLREGE TERFPHEASSKKIL/LAKGH (GGASVIVGHE)DTVKTRLOAGVV YGNTLSCIRVVYRRESMFGPFKGMSPLASILAVMSVVPGUFSN TOPFLSGHEGOEDRAS PPRITSDLLLASWNAGVVSVGLGGPVDL IKIRLQMQTPPVSGRQPRFEVQGSSCS (PRAYGGPVHCITTIV RNSGLAGHYRGASAMLREDVGVCLVFIPYVFJSENTTPEACTS PSPCAWWLAGGMAGAISWATTPMDVVKSQAVGVYLGGPVDL IKIRLGMQTPPVSGRQPRFEVQGSSCS (PRAYGGPVHCITTIV RNSGLAGHYRGASAMLREDVGVCLVFIPYVFJSENTTPEACTS PSPCAWWLAGGMAGAISWATTSTPMDVVKSQAGVYLNXKKGV LDCISGSYQKEGLKVFFRGITVRAVAGFPMSAMMFLGVELSLQA IRGGHAVTSP PSPCAWWLAGGMAGAISWATTSTPMDVANGGPMSAMMFLGVELSLQA RCGRP/OPPAPEPSSNAAVDEAIPTPRAAASAALBLPLGPAPV SVAPQAEAEARSTFGPAGGRGLGPTFRGRFQFRYQDAAGFREA FROLKEL/SPRQMLRDI\RTKEG/IVEMVQGCLLAILPEAAR RCGRP/OPPAPEPSSNAAVDEAIPTPRAAASAALBLPLGPAPV SVAPQAEAEARSTFGPAGGRGLGPTGRGGGGSLS ARABARRIVSVHAQLAHGSATGRVEGFSTGLEYAQLAGAETS PSEILVCTLNTPKIIDMELLGGQLGLEDFTFAHVKGIEKEVNVV KSEDSLGITITDMGVGYAFIKKIRKDGGVIDSVKTICVGDHIESI NGENIVGRHYDVAKKLKELKKEBLFTHKLIEPKKAFFIELRSK AGKSSGEKIGGGRATHARSKGPATVERMFSETKKI,TEKIDD VLELYMGIENDLATMTPEAGKKNVNPDEFAVALDETLGDPAPP DEFVPDVWGVIGDAKRRGL NGENIVGGRACGGDAPHVERREETTARIGFGVMSKRERRLMN LUVENVNOGENDEKDEKEQVANKGEPLALPLMVSEYCVPRGNRRR FRVQQFILQYWRDIMHRLGEPQARMERENBETIKRYDLKERL EREGUSHSLRAVSTOPPHHDHHDEYC\LMP SLCGVOIRMESTACSTSTLLYCTTTGULKSGCKSTQVPHFILDE LLLINBEASKCNIVCTOPRRISAVSLAMRVCDBLGCGREGOGGR SLCGVOIRMESRAGCSSTLUKYCVSLOFGCKSTQVPHFILDE LLLINBEASKCNIVCTOPRRISAVSLAMRVCDBLGCGREGOGGAN SLCGVOIRMESRAGCSSTLUKYCVSLYPOTGAMADLHPPYQK YSSRTQHAILYNNPIKINIDLILLELLAVLKSGFSTOVPHFILDE FFIGAHTQGLVPLKINGSRSPYVERYTEGRFCHMOKHTESS OMSSLVETTVSKASGIKKYQEXTPOTGGANTATEGAVLI FFIGAHTGGLVPLKINGSRSPYSERYVERYTEGRFCFMD YSVPEILRVPLEBLCLHHMKCMIGSPBEPLISGADDAAF TLPPFQUKKYULATNIASTGITTPOVVPUTOTARDALHPPYQK YSSRTQHAILYNNPIKINGLTLAALDRYNVKIKKHLISGTJF GCLDPVATLAAGVTKKSGPTTPIGGRGCARARLANGAMADSHL GCLDPVATLAAGVTKKSGPTTPIGGRGCARARLANGAMADSHL	}			
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REKQLSHSLRAVSTDPPHHDHDEFC\LMP  2802  270  FRMRIFLHCPWNQQMWKIWNLLETSLESCKAHLSIQKLLKER\Q \QLPVFKHRDSIVETLKRHRVVVVAGET\GSGKSTQVPHFLLED LLLNEWEASKCNIVCTQPRISAVSLANRVCDBLGCENGPGGRN SLCGYQIRMESRACESTRLLYCTTGVLLRKLQEDGLLSNVS/HM FIVDEV\HER\SVQSDFLLIILKEILQKRSDLHLILMSATVDSE KFSTYFTHCPILRISGRSYPVEVFHLEDIIEETGFVLEKDSEYC QKFLEEEEEVTINVTSKAGGIKKYQBYIPVQTGAHADLNPFYQK YSSRTQHAILYMNPHKINLDLILELLAYLDKSPQFRNIEGAVLI FLPGLAHIQQLYDLLSNDRRFYSERYKVIALHSILSTQDQAAAF TLPPPGVRKIVLATNIAETGITIPDVVFVIDTGRTKENKYHESS QMSSLVETFVSKASALQRQGRAGRVRDGFCFRWYTRERFEGFMD YSVPEILKPVLEELCLHIMKCNLGSPEDFLSKALDPPQLQVISN AMNLLRKIGACELNEPKLTPLGQHLAALPVNVKIGKMLIFGAIF GCLDPVATLAAVMTEKSPFTTPIGRKDEADLAKSALAMADSDHL				LIVENVNQENDEKDEKEQVANKGEPLALPLNVSEYCVPRGNRRR
FRMRIFLHCPWNQQMWKIWNLLETSLESCKAHLSIQKLLKER\Q\ \QLPVFKHRDSIVETLKRHRVVVVAGET\GSGKSTQVPHFLLED\ LLLNEWEASKCNIVCTQPRRISAVSLANRVCDBLGCENGPGGRN\ SLCGYQIRMESRACESTRLLYCTTGVLLRKLQEDGLLSNVS/HM\ FIVDEV\HER\SVQSDFLLIILKEILQKRSDLHLIMSATVDSE\ KFSTYFTHCPILRISGRSYPVEVFHLEDIIEETGFVLEKDSEYC\ QKFLEEEEEVTINVTSKAGGIKKYQEYIPVQTGAHADLNPFYQK\ YSSRTQHAILYMNPHKINLDLILELLAYLDKSPQFRNIEGAVLI\ FLPGLAHIQQLYDLLSNDRRFYSERYKVIALHSILSTQDQAAAF\ TLPPPGVRKIVLATNIAETGITIPDVVFVIDTGRTKENKYHESS\ QMSSLVETFVSKASALQRQGRAGRVADGFCFRMYTRERFEGFMD\ YSVPEILRVPLEELCLHIMKCNLGSPEDFLSKALDPPQLQVISN\ AMNLLRKIGACELNEPKLTPLGQHLAALPVNVKIGKMLIFGAIF\ GCLDPVATLAAVMTEKSPFTTPIGRKDEADLAKSALAMADSDHL	]	ļ <u> </u>		
\QLPVFKHRDSIVETLKRHRVVVVAGET\GSGKSTQVPHFLLED LLLNEWEASKCNIVCTQPRRISAVSLANRVCDBLGCENGPGGRN SLCGYQIRMESRACESTRLLYCTTGVLLRKLQEDGLLSNVS/HM FIVDEV\HER\SVQSDFLDIILKEILQKRSDLHLILMSATVDSE KFSTYFTHCPILRISGRSYPVEVFHLEDIIEETGFVLEKDSEYC QKFLEEEEEVTINVTSKAGGIKKYQEYIPVQTGAHADLNPFYQK YSSRTQHAILYMNPHKINLDLILELLAYLDKSPQFRNIEGAVLI FLPGLAHIQQLYDLLSNDRRFYSERYKVIALHSILSTQDQAAAF TLPPPGVRKIVLATNIAETGITIPDVVFVIDTGRTKENKYHESS QMSSLVETFVSKASALQRQGRAGRVRDGFCFRMYTREFFEGFMD YSVPEILRVPLEELCLHIMKCNLGSPEDPLSKALDPPQLQVISN AMNLLRKIGACELNEPKLTPLGQHLAALPVNVKIGKMLIFGAIF GCLDPVATLAAVMTEKSPFTTPIGRKDEADLAKSALAMADSDHL		<u> </u>		
LLLNEWEASKCNIVCTQPRRISAVSLANRVCDBLGCENGPGGRN SLCGYQIRMESRACESTRLLYCTTGVLLRKLQEDGLLSNVS/HM FIVDEV\HER\SVQSDFLJIILKEILQKRSDLHLILMSATVDSE KFSTYFTHCPILRISGRSYPVEVFHLEDIIEETGFVLEKDSEYC QKFLEEEEEUTINVTSKAGGIKKYQEYIPVQTGAHADLNPFYQK YSSRTQHAILYMNPHKINLDLILELLAYLDKSPQFRNIEGAVLI FLPGLAHIQQLYDLLSNDRRFYSERYKVIALHSILSTQDQAAAF TLPPPGVRKIVLATNIAETGITIPDVVFVIDTGRTKENKYHESS QMSSLVETFVSKASALQRQGRAGRVRDGFCFRMYTREFFEGFMD YSVPEILRVPLEELCLHIMKCNLGSPEDPLSKALDPPQLQVISN AMNLLRKIGACELNEPKLTPLGQHLAALPVNVKIGKMLIFGAIF GCLDPVATLAAVMTEKSPFTTPIGRKDEADLAKSALAMADSDHL	6143	2802	270	
SLCGYQIRMESRACESTRLLYCTTGVLLRKLQEDGLLSNVS/HM FIVDEV\HER\SVQSDFLLIILKEILQKRSDLHLILMSATVDSE KFSTYFTHCPILRISGRSYPVEVFHLEDIIEETGFVLEKDSEYC QKFLEEEEEVTINVTSKAGGIKKYQEYIPVQTGAHADLNPFYQK YSSRTQHAILYMNPHKINLDLILELLAYLDKSPQFRNIEGAVLI FLPGLAHIQQLYDLLSNDRRFYSERVAIALISTQDQAAF TLPPPGVRKIVLATNIAETGITIPDVVFVIDTGRTKENKYHESS QMSSLVETFVSKASALQRQGRAGRVRDGFCFRMYTRERFEGFMD YSVPEILRVPLEELCHHMKCNLGSPEDFLSKALDPPQLQVISN AMNLLRKIGACELNEPKLTPLGQHLAALPVNVKIGKMLIFGAIF GCLDPVATLAAVMTEKSPFTTPIGRKDEADLAKSALAMADSDHL				, , , , , , , , , , , , , , , , , , , ,
FIVDEV\HER\SVQSDFLLIILKEILQKRSDLHLILMSATVDSE KFSTYFTHCPILRISGRSYPVEVFHLEDIIEETGFVLEKDSEYC QKFLEEEEEVTINVTSKAGGIKKYQEYIPVQTGAHADLNPFYQK YSSRTQHAILYMNPHKINLDLILELLAYLDKSPQFRNIEGAVLI FLPGLAHIQQLYDLLSNDRFYSERYKVIALHSILSTQDQAAF TLPPPGVRKIVLATNIAETGITIPDVVFVIDTGRTKENKYHESS QMSSLVETFVSKASALQROGRAGRVRDGFCFRMYTRERFEGFMD YSVPEILRVPLEELCHIMKCNLGSPEDFLSKALDPPQLQVISN AMNLLRKIGACELNEPKLTPLGQHLAALPVNVKIGKMLIFGAIF GCLDPVATLAAVMTEKSPFTTPIGRKDEADLAKSALAMADSDHL				
KFSTYFTHCPILRISGRSYPVEVFHLEDIIEETGFVLEKDSEYC QKFLEEEEEVTINVTSKAGGIKKYQEYIPVQTGAHADLNPPYQK YSSRTQHAILYMNPHKINLDLILELLAYLDKSPQFRNIEGAVLI FLPGLAHIQQLYDLLSNDRRFYSERYKVIALHSILSTQDQAAAF TLPPPGVRKIVLATNIAETGITIPDVFVIDTGRTKENKYHESS QMSSLVETFVSKASALQRQGRAGRVRDGFCFRMYTRERFEGFMD YSVPEILKTVPLEELCLHIMKCNLGSPEDFLSKALDPPQLQVISN AMNLLRKIGACELNEPKLTPLGQHLAALPVNVKIGKMLIFGAIF GCLDPVATLAAVMTEKSPFTTPIGRKDEADLAKSALAMADSDHL				
QKFLEEEEEVTINVTSKAGGIKKYQEYIPVQTGAHADLNPFYQK YSSRTQHAILYMNPHKINLDLILELLAYLDKSPQFRNIEGAVLI FLPGLAHIQQLYDLLSNDRRFYSERYKVIALHSILSTQDQAAAF TLPPPGVRKIVLATNIAETGITIPDVVFVIDTGRTKENKYHESS QMSSLVETFVSKASALQRGGRAGRVROGFCFRMYTRERFEGFMD YSVPEILRVPLEELCLHIMKCNLGSPEDFLSKALDPPQLQVISN AMNLLRKIGACELNEPKLTPLGQHLAALPVNVKIGKMLIFGAIF GCLDPVATLAAVMTEKSPFTTPIGRKDEADLAKSALAMADSDHL				
YSSRTQHAILYMNPHKINLDLILELLAYLDKSPQFRNIEGAVLI FLPGLAHIQQLYDLLSNDRRFYSERYKVIALHSILSTQDQAAAF TLPPPGVRKIVLATNIAETGITIPDVVFVIDTGRTKENKYHESS QMSSLVETFVSKASALQRQGRAGRVROGFCFRWYTRERFEGFMD YSVPEILRVPLEELCLHIMKCNLGSPEDFLSKALDPPQLQVISN AMNLLRKIGACELNEPKLTPLGQHLAALPVNVKIGKMLIFGAIF GCLDPVATLAAVMTEKSPFTTPIGRKDEADLAKSALAMADSDHL				
FLPGLAHIQQLYDLLSNDRRFYSERYKVIALHSILSTQDQAAAF TLPPPGVRKIVLATNIAETGITIPDVVFVIDTGRTKENKYHESS QMSSLVETFVSKASALQRQGRAGRVRDGFCFRMYTRERFEGFMD YSVPEILRVPLEELCLHIMKCNLGSPEDFLSKALDPPQLQVISN AMNLLRKIGACELNEPKLTPLGQHLAALPVNVKIGKMLIFGAIF GCLDPVATLAAVMTEKSPFTTPIGRKDEADLAKSALAMADSDHL				
TLPPPGVRKIVLATNIAETGITIPDVVFVIDTGRTKENKYHESS QMSSLVETFVSKASALQRQGRAGRVRDGFCFRMYTRERFEGFMD YSVPEILRVPLEELCLHIMKCNLGSPEDFLSKALDPPQLQVISN AMNLLRKIGACELNEPKLTPLGQHLAALPVNVKIGKMLIFGAIF GCLDPVATLAAVMTEKSPFTTPIGRKDEADLAKSALAMADSDHL		1		
QMSSLVETFVSKASALQRQGRAGRVRDGFCFRMYTRERFEGFMD YSVPEILRVPLEELCLHIMKCNLGSPEDFLSKALDPPQLQVISN AMNLLRKIGACELNEPKLTPLGQHLAALPVNVKIGKMLIFGAIF GCLDPVATLAAVMTEKSPFTTPIGRKDEADLAKSALAMADSDHL				
YSVPEILRVPLEELCLHIMKCNLGSPEDFLSKALDPPQLQVISN AMNLLRKIGACELNEPKLTPLGQHLAALPVNVKIGKMLIFGAIF GCLDPVATLAAVMTEKSPFTTPIGRKDEADLAKSALAMADSDHL				
AMNLLRKIGACELNEPKLTPLGQHLAALPVNVKIGKMLIFGAIF GCLDPVATLAAVMTEKSPFTTPIGRKDEADLAKSALAMADSDHL		}		
GCLDPVATLAAVMTEKSPFTTPIGRKDEADLAKSALAMADSDHL				
TIYNAYLGWKKARQEGGYRSEITYCRRNFLNRTSLLTLEDVKQE				
				TIYNAYLGWKKARQEGGYRSEITYCRRNFLNRTSLLTLEDVKQE

C 676	The add the add		
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID NO:	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding to first	to first	L=Leucine, M=Methionine, N=Asparagine,
l		amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
<u></u>	sequence		\-possible nucleotide insertion)
Ì			LIKLVKAAGFSSSTTSTSWEGNRASQTLSFQEIALLKAVLVAGL
1			YDNVGKIIYTKSVDVTEKLACIVETAQGKAQVHPSSVNRDLQTH
İ			GWLLYQEKIRYARVYLRETTLITPFPVLLFGGDIEVQHRERLLS
ľ			IDGWIYFQAPVKIAVIFKQLRVLIDSVLRKKLENPKMSLENDKI
			LQIITELIKTENN
6144	1289	568	SGPGSMSGQRVDVKVVMLGKEYVGKTSLVERYVHDRFLVGPYQN
ł	ł		VSASGGARHGGRGSGGPVICTYGPDLFPLVA\TIGAAFVAKVMS
i	1		VGDRTVTLGIWDTAGSERYEAMSRIYYRGAKAAIVCYDLTDSSS
ł	•		FERAKFWVKELRSLEEGCQIYLCGTKSDLLEEDRRRRRVDFHDV
I			QDYADNIKAQLFETSSKTGQSVDELFQKVAEDYVSVAAFQVMTE
			DKGVDLGQKPNPYFYSCCHH
6145	1109	196	GGMDLSELERDNTGRCRLSSPVPAVCRKEPCVLGVDEAGRGPVL
	1		GPMVYAICYCPLPRLADLEALKVADSKTLLESERERLFAKMEDT
	1		DFVGWALDVLSPNLISTSMLGRVKYNLNSLSHDTATGLIQYALD
	1	l	QGVNVTQVFVDTVGMPETYQARLQQSFPGIEVTVKAKADALYPV
	1		\VSAASICAKVARDQAVKKWQFVEKLQDLDTDYG\SGYPNDPQD
Į			/TKAWLKEHVEPVF\GFP\QFVRF\SWRTAQTI\LEKEAEDVIR
l	i		EDSASENQEGLRKITSYFLNEGSQARPRSSHRYFLERGLESTTS
			L
6146	428	781	LKKKGKEKAEAQQVEALPGPSLDQWHRSAGEEEDGPVLTDEQKS
	1		R/YPGHEAHDQGG\WDARQSIIRKVVDPETGRTRLIKGDGEVLE
L			BIVTKERHREINKQATRGDCLAFQMRAGLLP
6147	1	2304	GTRQLPPPSPGSGPGDSPEGPEGEAPERRRKAHGMLKLYYGLSE
	1		GEAAGRPAGPDPLDPTDLNGAHFDPEVYLDKLRRECPLAQLMDS
			ETDMVRQIRALDSDMQTLVYENYNKFISATDTIRKMKNDFRKME
		•	DEMDRLATNMAVITDFSARISATLQDRHERITKLAGVHALLRKL
l	)		QFLFELPSRLTKCVELGAYGQAVRYQGRAQAVLQQYQHLPSFRA
			IQDDCQVITARLAQQLRQRFREGGSGAPEQAECVELLLALGEPA
			EELCEEFLAHARGRLEKELRNLEAELGPSPPAPDVLEFTDHG\S
			SGFVGGLCQVAAAYQELFAAQGPAGAEKLAAFARQLGSRYFALV
}	,		ERRLAQEQGGGDNSLLVRALDRFHRRLRAPGALLAAAGLADAAT
Ì			EIVERVARERLGHHLQGLRAAFLGCLTDVRQALAAPRVAGKEGP
			GLAELLANVASSILSHIKASLAAVHLFTAKEVSFSNKPYFRGEF
			CSQGVREGLIVGFVHSMCQTAQSFCDSPGEKGGATPPALLLLLS
[			RLCLDYETATISYILTLTDEQFLVQDQFPVTPVSTLCAEARETA
ļ			RRLLTHYVKVQGLVISQMLRKSVETRDWLSTLEPRNVRAVMKRV
	•		VEDTTAIDVQVLPRLAGVALTQAGGTVPSRGAGAAEDHWQSLPG
}			GGDMCIWASHGASSVARASVREPQGNKSPRMNTKRAGECLCPRS
			CSFSAQDYDIFAPILPVEKQRLRVTQEVRAGLVLVLKIRPQTNS
			CILPLPHSTGSINSDHVPTK
6148	3056	353	VPAVGGTFADGAMGEAEKFHYIYSCDLDINVQLKIGSLEGKREQ
			KSYKAVLEDPMLKFSGLYQETCSDLYVTCQVFAEGKPLALPVRT
			SYKAFSTRWNWNEWLKLPVKYPDLPRNAQVALTIWDVYGPGKAV
			PVGGTTVSLFGKYGMFRQGMHDLKVWPNCRSQMDQKPTKTPGRT
			SSTLSEDQMSRLAKLTKAHRQGHMVKVDWLDRLTFREIEMINES
			VKRSSNFMYLMGGFRCVKCDDKEYGIVYYEKDGDESSPILTSFE
			LVKVPDPQMSLENLVESKHHNLPRSLRSGPSDHDLKPYPSPRDQ
	[		LKNIVSYPPSKPPTYEEQDLVWEFRYYLTNQDKALTKILTSVIW
			DLPQGAKQALALLGKWKPMDVEDSLELLSSHYTNPTVRRYAVAR
	]		LRQADDEDLLMYLLQLVQALKYENFDDIKNGLEPTKKDSQSSVS
			ENVSNSGINSAEIDSSQIIT/SAPFPSVSSPPP\ASKTKEVPDG
	[		ENLEGDLCTFLISRASKNSTLANYLYWYVIVECEDGDTQQRDPK
			THEMYLNVMRRFSQALLKGDKSVRVMRSLLAAQQTFVDRLVHLM
			KAVQRESGNRKKKNERLQALLGDNEKMNLSDVELIPLPLEPQVK
			IRGIIPETATLFKSALMPAQLFFKTEDGGKYPVIFKHGDDLRQD
	j		QLILQIISLMDKLLRKENLDLKLTPYKVLATSTKHGFMQFIQSV
	<del></del>		

SEQ	Predicted	Predicted end	Amino agid gornant
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
l	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence		\=possible nucleotide insertion)
			PVAEVLDTEGSIONFFRKYAPSENGPNGISAEVMDTYVKSCAGY
İ			CVITYILGVGDRHLDNLLLTKTGKLPHIDFGYILGRDPKPLPPP
			MKLNKEMVEGMGGTQSEQYQEFRKQCYTAFLHLRRYSNLILNLF
[	1		SLMVDANIPDIALEPDKTVKKVQDKFRLDLSDEEAVHYMQSLID
Į		İ	ESVHALFAAVVEQIHKFAQYWRK
6149	1	1413	RVDPRVRENGTANPIKNGKTSPASKDQRTGKKTSVQGQVQKGND
ı		Į	ESESDFESDPPSPKSSEEEEQDDEEVLQGEQGDFNDDDTEPENL
		Ĭ	GHRPLLMDSEDEEEEEKHSSDSDYEQAKAKYSDMSSVYRDRSGS
1	1	ļ	GPTQDLNTILLTSAQLSSDVAVETPKQEFDVFGAVPFFAVRAQQ
j	ľ		POQEKNEKNLPQHRFPAAGLEQEEFDVFTKAPFSKKVNVQECHA
ì			VGPEAHTIPGYPKSVDVFGSTPFQPFLTSTSKSESNEDLFGLVP
1			FDEITGSQQQKVKQRSLQKLSSRQRRTKQDMSKSNGKRHHGTPT
		· ·	STKKTLKPTYRTPERARRHKKVGRRDSQSSNEFLTISDSKENIS
Í	ĺ		VALTDGKDRGNVLQPEESLLDPFGAKPFHSPD\LSWHPP\HQGL
1			s\Diradhnt\vlpgr\pronslhgsfhsadvlkmddfgavp/f
L			LTELVVQSITPHQSQQSQPV\ELDPFGAAPFPSKQ
6150	372	37	MSNIKKYIIDYDWKASIETEIDHDVMTEEKLHQINNFWSDSEYR
í	Ì		LNKHGSVLNAVLIMLAQHALLIAISSDLNAYGVVCEFDWNDGNG
Ŀ.			QEGWPPMDGSEGIRITDIDTSGIF
6151	1555	521	DSNQQSVSGTAASTLLHSFKATIYYQGTGHVQQFYGVTSPYSQT
			TPPIVQSYAQPSLQYIQGQQIFTAHPQGVVVQPAAAVTTTVAPG
	]		QPQPLQPSEMVVTNNLLDLPPPSPPKPKTIVLPPNWKTARDPEG
j	į l		KIYYYHVITROTOWDPPTWESPGDDASLEHEAEMDLGTPTYDEN
i			PMK\ASKKPKTAEADTSSELAKKSKEVFRKEMSQFIVQCLNPYR
1	<b>!</b>		KPDCKVG\RITTEDFKHLARKLTHGVMNKELKYCKNPE\DLEC
			NENVKHKTKEYIKKYMQKFGAVYKPKEDTEFRVTVGPGWEDGWS
<u></u>	<u>.                                    </u>		GKTDSRERKSCGPFCSTPVSTVLLMIHHPGEFNPADVN
6152	1366	648	NRTWSTPSTWMGVALPPLCSTGPWPVTRQITARTTCGAVPAKCP
ļ			PWC/DVHEPRCQPPDCHGHGTCVDGHCQCTGHFWRGPGCDELDC
İ	i		GPSNCSQHGLCTETGCRCDAGWTGSNCSEECPLGWHGPGCQRPC
1			KCEHHCPCDPKTGNCSVSRVKQCLOPPEATLRAGELSFFTRTAW
1			LALTLALAFLLLISTAANLSLLLSRAERNRRLHGDYAYHPLQEM
			NGEPLAAEKEQPGGAHNPFKD
6153	2	3368	GRVGARSPGRAYALLLLI CFNVGSGLHLQVLSTRNENKLLPKH
1	1		PHLVRQKRAWITAPVALLEGEDLSKKNPIAKIHSDLAEERGLKI
1 1	1		TYKYTGKGITEPPFGIFVFNKDTGELNVTSILDREETPPFLLTG
] ]	İ		YALDARGNNVEKPLELRIKVLDINDNEPVFTQDVFVGSVEELSA
			AHTLVMKINATDADEPNTLNSKISYRIVSLEPAYPPVFYLNKDT
		· i	GEIYTTSVTLDREEHSSYTLTVEARDGNGEVTDKPVKOAOVOIR
1 1	,		ILDVNDNIPVVENKVLEGMVEENQVNVEVTRIKVFDADEIGSDN
1 1	•		WLANFTFASGNEGGYFHIETDAQTNEGIVTLIKEVDYEEMKNLD
i i	ľ		FSVIVANKAAFHKSIRSKYKPTPIPIKVKVKNVKEGTHFKSSVT
1		ł	SIYVSESMDRSSKGQIIGNFQAFDEDTGLPAHARYVKLEDRDNW
			ISVDSVTSEIKLAKLPDFESRYVQNGTYTVKIVAISEDYPRKTI
1 1			TGTVLINVEDINDNCPTLIEPVQTICHDAEYVNVTAEDLDGHPN
			SGPFSFSVIDKPPGMAEKWKIARQESTSVLLOOSEKKLGRSEIO
1 1	1		FLISDNQGFSCPEKQVLTLTVCEVLHGS\GCREAOHDSYVGLGD
	1	}	AAIALMILAFLLLLLVPLLLLMCHCGKGAKGFTPIPGTIEMLHP
	l l	ł	WNNEGAPPEDKVVPSFLPVDQGGSLVGRNGVGGMAKEATMKGSS
i i	J		SASIVKGQHEMSEMDGRWEEHRSLLSGRATOFTGATGAI\MTTE
<b>!</b>	ļ.	J	TTITARATGASRDVAGAQAAAVALNEEFLKNYFTDKAASYTEED
[	1	ľ	ENHTAKDCLLVYSQEETESLNASIGCCSFIEGELDDRFLDDLGL
	İ	i	KFKTLAEVCLGQKIDINKEIEQRQKPATETSMNTASHSLCEQTM
		ļ	VNSENTYSSGSSFPVPKSLQEANAEKVTQEIVTERSVSSRQAQK
	j	Ì	VATPLPDPMASRNVIATETSYVTGSTMPPTTVILGPSQPQSLIV
LI		İ	TERVYAPASTLVDQPYANEGTVVVTERVIQPHGGGSNPLEGTQH
			The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
j	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ŀ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	{	\=possible nucleotide insertion)
			LQDVPYVMVRERESFLAPSSGVQPTLAMPNIAVGQNVTVTERVL
1			APASTLQSSYQIPTENSMTARNTTVSGAGVPGPLPDFGLEESGH
L			SNSTITTSSTRVTKHSTVQHSYS
6154	3660	2146	KKKTKMKNTLQKTVNFGAWPKPTISDKSHLLQMVSKLDLTDAKN
			SDTAHIKSIEITSILNGLQASESSAEDSEQEDERGAQDMDNNGK
1		[	EESKIDHLTNNRNDLISKEEQNSSSLLEENKVHADLVISKPVSK
1			SPERLRKDIEVLSEDTDYEEDEVTKKRKDVKKDTTDKSSKPQIK
4	į.		RGKRRYCNTEECLKTGSPGKKEEKAKNKESLCMENSSNSSSDED
i			EEETKAKMTPTKKYNGLEEKRKSLRTTGFYSGFSEVAEKRIKLL
			NNSDERLQNSRAKDRKDVWSSIQGQNPKKTLKELFSDSDTEAAA
			SPPHPAPEEGVAEESLQTVAEEESCSPSVELEKPPPVNVDSKPI
1			EEKTVEVNDRKAEFPSSGSNFSA+IPLPYLHLNRLHQSL+QKGS
1	<b>.</b>		RQQSSVTVSBPLAPNQEEVRSIKSETDSTIEVDSVAGELQDLQS
			ERE*LASRF*CQCELEQ**SARTRTS*KSLYRSEKSERCSGRRK
6:55	1		fikkaekkp*snsgkqqkegk
6155	869	121	HLLPELRGKSWITMKYVFYLGVLAGTFFFADSSVQKEDPAPYLV
			YLKSHFNPCVGVLIKPSWVLAPAHCYLPNLKVMLGNFKSRVRDG
1			TEQTINPIQIVRYWNYSHSAPQDDLMLIKLAKPAMLNPKVQALN
1	1		P\PTTNVRPGTVCLLSGLDWSQENSGRHPDLRQNLEAPVMSDRE
1	į		CQKTEQGKSHRNSLCVKFVKVFSRIFGEVAVATVICKDKLQGIE
6156	5725		VGHFMGGDVGIYTNVYKYVSWIENTAKDK
0130	5/25	3984	GTSTVTMATKKHFSIILNLLGMLLKKDNQDTRKLLMTWALEVAV
1			VMKKSETYAPLFCLPSFHKFCKGLLADTLVEDVNICLQACSSLH
1		•	ALSSSLPDDLLQRCVDVCRVQLVHRGTCIRQAFGKLLKSIPLGV
	1		FLSNNNHTEIQEISLALRSHMSKAPSNTFHPQDFSD/VISFILY
Į.			GNSHRTGKDNWLERLFYSCQRLDKRDQSTIPRNLLKTDAVLWQW
			AIWEAAQFTVLSKLRTPLGRAQDTFQTIEGIIRSLAGHTLNPDQ
			DVSQWTTADNDEGHGNNQLRLVLLLQYLENLEKLMYNAYEGCAN
			ALTSPPKVIRTFLYTNRQTCQDWLTRIRLSIMRVGLLAGQPAVT VRHGFDLLTEMKTTSLSQGNELEVSIMMVVEALCELHCPEAIQG
ł			IAVWSSSIVGKHLLWINSVAQQAEGRFEKASVEYQEHLCAMTGV
1			DCCISSFDKSVLTLASAGCKSASLKHCLNGESRKSVLSKPTDSS
l			PEVINYLGNKACECYISTADWAAVQEWQNAIHDLKKSTSSTSLN
1			LKADFNYIKSLSSFESGKFVECTEQLELLPGENINLLAGGSKEK
	}		IDMKKLLRNM
6157	946	329	MANRGPSYGLSREVQEKIEQKYDADLENKLVDWIILQCAEDIEH
1		- <del>-</del> -	PPPGRAHFQKWLMDGTVLCKLINSLYPPGQEPIPKISESKMAFK
			QMEQISQFLKAAETYGVRTTDIFQTVDLWEGKDMAAVQRTLMAL
			GSVAVTKDDGCYRGEPSWFHRKAQQNRRGFSEEQLRQGQNVIGL
L			QMGSNKGASQAGMTGYGMPRQIM*DAASCP
6158	441	1482	LGSLIVLSLHCKVIFSSQSLERAMKEKAVDLVPILAQNPGLAQN
	1		PILEGKDHNONTGVDPIIDHVQDRKTD/SRSKSPHKKRSKSRER
	1		RKSRSRSHSRDKRKDTREKIKEKERVKEKDREKEREREKEREKE
			KERGKNKORDKEREKOREKDKEKDREREREKEHEKORDKEKEKE
[			QDKEKEREKDRSKEIDEKRKKDKKSRTPPRSYNASRRSRSSSRE
}	İ		RRRRRSRSSRSPRTSKTIKRKSSRSPSPRSRNKKDKKREKERD
	Į.		HISERRERERSTSMRKSSNDRDGKEKLEKNSTSLKEKEHNKEPD
L			SSVSKEVDDKDAPRTEENKIQHNGNCQLNEENLSTKTEAV
6159	53	84	AVIAPLHISLGDRARPYLKNTEKSSTTCSRRRNQSFPPVMSLTH
			RLHLCKYWGCAVSNVCRFWEGRPLPLMIVVPYTLPVSLPVGSCV
			IITGTPILTFVKDPQLEVNFYTGMDEDSDIAFQFRLHFGHPAIM
]			NSCVFGIWRYEEKCYYLPFEDGKPFELCIYVRHKEYKVMVNGOR
•		`	IYNFAHRFPPASVKMLQVFRDISLTRVLISD*GRCVRITAVQEF
			DVSVSCDCTTAYQPG
6160	1626	1790	AGAKPFP*F*KVADAQPTESEKEIYNQVNVVLKDAEGILEDLQS
			YRGAGHEIREAIQHPADEKLQEKAWGAVVPLVGKLKKFYEFSQR

SEQ Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence Predicted end nucleotide (A=Alanine, C=Cysteine, D=Aspartic Acid Glutamic Acid, F=Phenylalanine, G=Glycidelocide, F=Phenylalanine, G=Glycidelocide, F=Phenylalanine, G=Glycidelocide, F=Phenylalanine, G=Glycidelocide, F=Phenylalanine, G=Glycidelocide, F=Phenylalanine, G=Glycidelocide, F=Phenylalanine, G=Glycidelocide, F=Phenylalanine, G=Glycidelocide, F=Phenylalanine, G=Glycidelocide, F=Phenylalanine, G=Glycidelocide, F=Phenylalanine, G=Glycidelocide, F=Phenylalanine, G=Glycidelocide, F=Phenylalanine, G=Glycidelocide, F=Proline, Q=Glutamic Acid, F=Phenylalanine, G=Glycidelocide, F=Proline, M=Methionine, N=Asparagine, P=Proline, Q=Glutamic, N=Asparagine, P=Proline, Q=Glutamic, N=Asparagine, P=Proline, Q=Glutamic, N=Asparagine, M=Tryptophan, Y=Tyrosine, Y=Unknown, *= Codon, /=possible nucleotide deletion, N=possible nucleotide deletion, N=possible nucleotide insertion)	l, E≃ .ne,
NO: nucleotide location corresponding to first amino acid residue of amino acid sequence codon, sequence location corresponding to first L=Leucine, M=Methionine, N=Asparagine, L=Leucine, M=Methionine, N=Asparagine, N=Proline, Q=Glutamine, N=Asparagine, N=Proline, Q=Glutamine, N=Asparagine, N=Proline, N=Seguence, N=Proline, N=Seguence, N=Proline, N=Seguence, N=Proline, N=Seguence, N=Proline, N=Seguence, N=Proline, N=Seguence, N=Proline, N=Seguence, N=Proline, N=Seguence, N=Proline, N=Seguence, N=Proline, N=Seguence, N=Proline, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=Seguence, N=	.ne,
location corresponding to first amino acid residue of amino acid sequence  LEAALEGLIGALTSTPYSPTQHLEREQALAKQFABILHF	
corresponding to first amino acid residue of amino acid sequence  L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *= Codon, /=possible nucleotide deletion,	Stop
to first amino acid P=Proline, Q=Glutamine, R=Arginine, amino acid residue of S=Serine, T=Threonine, V=Valine, residue of amino acid sequence Codon, /=possible nucleotide deletion, sequence \text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\t	Stop
amino acid residue of sequence S=Serine, T=Threonine, V=Valine, w=Tryptophan, Y=Tyrosine, X=Unknown, *= Codon, /=possible nucleotide deletion,	Stop
residue of amino acid w=Tryptophan, Y=Tyrosine, X=Unknown, += amino acid sequence Codon, /=possible nucleotide deletion, sequence \text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\ext{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\exititt{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\exititt{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\	Stop
amino acid sequence Codon, /=possible nucleotide deletion, sequence \text{\=possible nucleotide insertion}\text{\=possible nucleotide insertion}\text{\=LEAALRGLLGALTSTPYSPTQHLEREQALAKQFABILHF}	
sequence   \=possible nucleotide insertion)   LEAALRGLLGALTSTPYSPTQHLEREQALAKQFABILHF	осор
LEAALRGLIGALTSTPYSPTQHLEREQALAKQFAEILHF	
	TLRFD
ELKMTNPAIQNDFSYYRRTLSRMRINNVPAEGENEVNNE	
SLFYAEATPMLKTLSDATTKFVSENKNLPIENTTDCLST	
RVMLETPEYRSRFTNEETVSFCLRVMVGVIILYDHVHPV	
TSKIDMKGCIKVLKDQPPNSVEGLLNALRYTTKHLNDET	
KSMLQ*QLLTLVNKG	
6161 455 1569 PVSGSESSLRRAWASILRLMLGPRVAVSILCEDGISH*L	LEKH*
KSHVLEPLSSLALERQCLALSLDWSTGKTGRAGDQPLKI	
TGQLHLLMVNETRPRLQKVASWQAHQFEAWIAAFNYWHP	
GGDDGLLRGWDTRVPGKFLFTSKRHTMGVCSIQSSPHRE	
GSYDEHILLWDTRNMKQPLADTPVQGGVWRIKWHPFHHH	LLLAA
CMHSGFKILNCQKAMEERQEATVLTSHTLPDSLVYGADW	SWLLF
RSLQRAPSWSFPSNLGTKTADLKGASELPTPCHECREDN	DGEGH
ARPQSGMKPLTEGMRKNGTWLQATAATTRDCGVNPEEAD	SAFSL
LATCSFYDHALHLWEWEGN	
6162 1 586 RTIHATGRAGASPMHRLIVWRLAEANKQHVRCQKCLEFG	
CTGKRKYLHRPSRTAELKKALKEKENRLLLQQS IGETNV	
KKRSKSVTSSSSSSDSSASDSSSESEETSTSSSSEDSD	
SSSSSASSTTSSSSSDSDSSSSSKQ*HQHR*QL*R*	TTKEE
EKETELLHSYWTDGLKTLM 6163 1081 785 PERSTTEGGRAVELHDTONTGVARIMILLSUGLGRAVER	
TAMANADOCA KON TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOT	
TPVVFVFFFFFFHRKE*VMQKNPMKSREDEWMEKLNNLH	
MNRLIMNYLVTEGFKEAAEKFRMESGIEPSVDLETLDER	
MILKGQIQEAIALINSLHPELLDTNRYLYFHLQQQHLIE	
ETBAALEFAQTQLAEQGEESRECLTEMERTLALLAFDSP GDLLHTMQRQKVWSEVNQAVLDYENRESTPKLAKLLKIL	
ELDQKKVKYPKMTDLSKGVIEEPK	PMVÖM
6164 90 406 PCQSPGRSRMRQDKLTGSLRRGGRCLKRQGGGVGTILSN	מעע זע
SCISRTAPRLLCTLEPGVDTKLKFTLEPSLGONGFOOWY	ባይሊሊሊ በአኒያአ
VARLSTGIPKEWRRKVWLTLADHYLHSIAIDWDKTMRFT	
NPDDDSMGIQIVKDLHRTGCSSYCGQEAEQDRVVLKRVL	
WNKTVGYCQGFNILAALILEVMEGNEGDALKIMIYLIDK	
YFVNNLRALSVDMAVFRDLLRMKLPELSQHLDTLQRTAN	
GYEPPLTNVFTMQWFLTLFATCLPNQTVLKIWDSVPFEG	
RVSLAIWAKLGEQIECCETADEFYSTMGRLTQEMLENDL	
LMQTVYSMAPFPFPQLAELREKYTYNITPFPATVKPTSV	
KARDSDEENDPDDEDAVVNAVGCLGPFSGFLAPELQKYQI	
PNEEQSLRSNNIAELSPGAINSCRSEYHAAFNSMMMERM	
ALKRQYSRIKKKQQQQVHQVYIRADKGPVTSILPSQVNS	
HLLLGKKMKMTNRAAKNAVIHIPGHTGGKISPVPYEDLK	
PWRTHIRVHKKNMPRTKSHPGCGDTVGLIDEQNEASKTNO	
EAFPSGCTATAGREGSSPEGSTRRTIEGQSPEPVFGDAD	
VQAKLGALELNQRDAAAETELRVHPPCQRHCPEPPSAPEI	
SKAPQGSNSKTPIFSPFPSVKPLRKSATARNLGLYGPTE	
HFPQMSRSFSKPGGGNSGP*KMVFSSGTMLSRQLPGYPQI	YORN
GGERFG 6165 90 406 PROSPGREDMENTAGEL PROGRAM AND CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CO	
1.6501.040441.0504.014.004.014.014.014.014.014.014.014.0	
SCISRTAPRLLCTLEPGVDTKLKFTLEPSLGQNGFQQWYL	
VARLSTGIPKEWRRKVWLTLADHYLHSIAIDWDKTMRFTE	
NPDDDSMGIQIVKDLHRTGCSSYCGQEAEQDRVVLKRVLI	
WNKTVGYCQGFNILAALILEVMEGNEGDALKIMIYLIDKV	
YFVNNLRALSVDMAVFRDLLRMKLPELSQHLDTLQRTANK	
GYEPPLINVFTMQWFLTLFATCLPNQTVLKIWDSVFFEGS	
RVSLAIWAKLGEQI ECCETADEFYSTMGRLTQEMLENDLI	
LMQTVYSMAPFPFPQLAELREKYTYNITPFPATVKPTSVS	
KARDSDERNDPDDEDAVVNAVGCLGPFSGFLAPELQKYQK	.VIKB

SEO	Predicted	I Dundlered and	
ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
""	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	0040000	\=possible nucleotide insertion)
		<u></u>	PNEEQSLRSNNIAELSPGAINSCRSEYHAAFNSMMMERMTTDIN
}			ALKRQYSRIKKKQQQQVHQVYIRADKGPVTSILPSQVNSSPVIN
1			HLLLGKKMKMTNRAAKNAVIHIPGHTGGKISPVPYEDLKTKLNS
1			PWRTHIRVHKKNMPRTKSHPGCGDTVGLIDEQNEASKTNGLGAA
	j		EAFPSGCTATAGREGSSPEGSTRRTIEGQSPEPVFGDADVDVSA
ì			VQAKLGALELNQRDAAAETELRVHPPCQRHCPEPPSAPEENKAT
1			SKAPQGSNSKTPIFSPFPSVKPLRKSATARNLGLYGPTERTPTV
1	J.		HFPQMSRSFSKPGGGNSGP*KMVFSSGTMLSRQLPGYPQEYQRN
			GGERFG
6166	2	1206	HKLWRTVAMAGAEWKSLEECLEKHLPLPDLQEVKRVLYGKELRK
			LDLPREAFEAASREDFELQGYAFEAAEEQLRRPRIVHVGLVONR
	1		IPLPANAPVAEQVSALHRRIKAIVEVAAMCGVNIICFOEAWTMP
			PAFCTREKLPWTEFAESAEDGPTTRFCQKLAKNHDMVVVSPILE
	]		RDSEHGDVLWNTAVVISNSGAVLGKTRKNHIPRVGDFNESTYYM
	<u> </u>		EGNLGHPVFQTQFGRIAVNICYGRHHPLNWLMYSINGAEIIFNP
1	[		SATIGALSESLWPIEARNAAIANHCFTCAINRVGTEHFPNEFTS
į.			GDGKKAHQDFGYFYGSSYVAAPDSSRTPGLSRSRDGLLVAKLDL
ŀ			NLCQQVNDVWNFKMTGRYEMYARELAEAVKSNYSPTIVKE*PAS
			VPALG
6167	1220	1844	YGIVTGPSLCAGDKQPKKQEKNPVLVSPEFVDEALCACEEYLSN
1	İ		LAHMDIDKDLEAPLYLTPEGWSLFLQRYYQVVHEGAELRHLDTO
1 .			VQRCEDILQQLQAVVPQIDMEGDRNIWIVKPGAKSRGRGIMCMD
Į.		1	HLEEMLKLVNGNPVVMKDGKWVVQKYIERPLLIFGTKFDLRQWF
1			LVTDWNPLTVWFYRDSYIRFSTQPFSLKNLDK+APLYLTPEGWS
1	[		LFLQRYYQVVHEGAELRHLDTQVQRCEDILQQLQAVVPQIDMEG
_			DRNIWIVKPGAKSRGRGIMCMDHLBEMLKLVNGNPVVMKDGKWV
			VQKYIERPLLIFGTKFDLRQWFLVTDWNPLTVWFYRDSYIRFST
6168	84		QPFSLKNLDK
0100	04	1392	VWPVPSVSAMPPKKQAQAGGSKKAEQKKKEKIIEDKTFGLKNKK
			GAKQQKFIKAVTHQVKFGQQNPRQVAQSEAEKKLKKDDKKKELQ
			ELNBLFKPVVAAQKISKGADPKSVVCAFFKQGQCTKGDKCKFSH
1			DLTLERKCEKRSVYIDARDEELEKDTMDNWDEKKLEEVVNKKHG
i l			EAEKKKPKTQIVCKHFLEAIENNKYGWFWVCPGGGDICMYRHAL
			PPGFVLKKKKKKKKEDEISL*DLIERERSALGPNVTKITLESF LAWKKRKRQEKIDKLEQDMERRKADFKAGKALVISGREVFEFRP
1	<u> </u>		ELVNDDDEEADDTRYTQGTGGDEVDDSVSVNDIDLSLYIPRDVD
] ]	]		ETGITVASLERFSTYTSDKDENKLSEASGGRAENGERSDLEEDN
	ļ		EREGTENGAIDAVPVDENLFTGEDLDELEEELNTLDLEE
6169	112	662	APAAAMAERPEDLNLPNAVITRIIKEALPDGVNISKEARSAISR
			AASVFVLYATSCANNFAMKGKRKTLNASDVLSAMEEMEFQRFVT
}			PLKEALEAYRREQKGKKEASEQKKKDKDKKTDSEEQDKSRDBDN
			DEDEBRLEEEEQNEEEEVDN*KGRETVAPWKVPLEMRRATCFCE
			AFPCWAE
6170	62	667	STKVMLPNTGRLAGCTVFITGASRGIGKAIALKAAKDGANIVIA
	Į		AKTAQPHPKLLGTIYTAAEEIEAVGGKALPCIVDVRDEQQISAA
	1		VEKAIKKFGGIDILVNNASAISLTNTLDTPTKRLDLMMNVNTRG
	<u> </u>	i	TYLASKACIPYLKKSKVAHIPNISPPLNLNPVWFKQHCGRW*VV
		İ	G*GDGLCLICFELNLCMSDVITICT
6171	382	941	HFMQSDVELDCDIEPCGHTKFPPTLPLSTTVIVCSCHPVATAST
			MAEAFSKTTSEEDQSIQEPKEANSMTAQKQKK*GLRGSRRRHAN
			SGGDIFGDSFAAYFPRVLKQVHQALSLSQEAVSVMDSMVRDILD
		;	RIATEAGHLAHYSKCVTITSRDIRMAVCLLLPGKMGKLAESQGT
			NATLRYTKSK
6172	651	54	GLCRAGGAHRFSRTHVEAALKMLRREARLRREYLYRKAREEAQR
	1		SAQERKERLRRALEENRLIPTELRREALALQGSLEFDDAGGEGV
			TSHVDDEYRWAGVEDPKVMITTSRDPSSRLKMFAKELKLVFPGA

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
i	corresponding	to first	A-mistraine, laisoleucine, kalysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid	1	P=Proline, Q=Glutamine, R=Arginine,
	residue of	residue of	S=Serine, T=Threonine, V=Valine,
		amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence '		\=possible nucleotide insertion)
j	1		QRMNRGRHEVGALVRACKANGVTDLLVVHEHRGTPVGLIVSHLP
	1	l	FGPTAYFTLCNVVMRHDIPDLGTMSEAKPHLITHGFSSRLGKRV
1	1		SDILRYLFPVPKDDSHRVITFANQDDYISFRHHVYKKTDHRNVE
1	1		LTEVGPRFELKLYMIRLGTLEQEATADVEWRWHPYTNTARKRVF
		ŀ	LSTE*AAPRPLGOLL
6173	3	288	SVDHREVQVLSQSMPLTPHQAVLRGERPYMCVECGKCFGRSSHL
1			LQHQRIHTGEKPYVCSVCGKAFSQSSVLSKHRTIHTGEKPYECN
į.	1		ECGKAFRVSSDLAQHHKIHTGEKPHECLECRKAFTQLSHLIQHQ
	1		RIHTGERPYVCPLCGKAFNHSTVLRSHQRVHTGEKPHRCNECGK
			TECHNETI I CHORTHWOENDYMOGROUND BOND TO THE TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTA
	1		TFSVKRTLLQHQRIHTGEKPYTCSECGKAPSDRSVLIQHHNVHT
J .			GEKPYECSECGKTFSHRSTLMNHERIHTEEKPYACYECGKAFVQ
1	1		HSHLIQHQKVHRKL*PTCVLSVGSALAGVPTSFSISVSTLERSP
6174	1050	<u>_</u> _	MCAVYVGRPSARAQSLVNTGQFTQVRSPMSVMSVEKPLE
01/4	1060	959	PRPPGKRWMVAGLGNPGLPGTRHSVGMAVLGQLARRLGVAESWT
			RDRHCAADLALAPLGDAQLVLLRPRRLMNANGRSVARAAELFGL
			TAEEVYLVHDELDKPLGRLALKLGGSARGHNGVRSCISCLNSNA
1		,	MPRLRVGIGRPAHPEAVQAHVLGCFSPAEQELLPLLLDRATDLI
	·		LDHIRERSQGPSLGP*H*WFSKKA
6175	2204	334	RYFRADPRSRSGQPRAEGLGAFAEGPLRAMAAPVKGNRKQSTEG
1 1			DALDPPASPKPAGKQNGIQNPISLEDSPEAGGEREEEQEREEEQ
1			AFLVSLYKFMKERHTPIERVPHLGFKQINLWKIYKAVEKLGAYE
			LVTGRRLWKNVYNELGGSPGSTSGATCTRRHY*RLVLPYVRHLK
			GEDDKPLPTSKPRKQYKMAKENRGDDGATERPKKAKEERRMDQM
			MPGKTKADAADPAPLPSQEPPRNSTEQQGLASGSSVSFVGASGC
1 1			PEAYKRLLSSFYCKGTHGIMSPLAKKKLLAQVSKVEALQCQEEG
1 1			CBUCARDOS CRAIRIU PROPOSDEIGI MENGANGAN SKVEALQCQEEG
1	1		CRHGAEPQASPAVHLPESPQSPKGLTENSRHRLTPQEGLQAPGG
1 1			SLREEAQAGPCPAAPIFKGCFYTHPTEVLKPVSQHPRDFFSRLK
1 1			DGVLLGPPGKEGLSVKEPQLVWGGDANRPSAFHKGGSRKGILYP
			KPKACWVSPMAKVPAESPTLPPTFPSSPGLGSKRSLEEEGAAHS
1 1			GKRLRAVSPFLKEADAKKCGAKPAGSGLVSCLLGPALGPVPPEA
1 1			YRGTMLHCPLNFTGTPGPLKGQAALPFSPLVIPAFPAHFLATAG
l i			PSPMAAGLMHFPPTSFDSALRHRLCPASSAWHAPPVTTYAAPHF
<u> </u>			FHLNTKL
6176	1040	402	PLSALRAMAEVHVIGQIIGASGFSESSLFCKWGIHTGAAWKLLS
			GVREGQTQVDTPQIGDMAYWSHPIDLHFATKGLQGWPRLHFOVW
	1		SQDSFGRCQLAGYGFCHVPSSPGTHQLACPTWRPLGSWRBOLAR
] [			AFVGGGPQLLHGDTIYSGADRYRLHTAAGGTVHLEIGLLLRNFD
			RYGVEC*GTLPPTSPPSTPRTPSDGGGWHSGQEHRL
6177	1400	992	VPIESLVGKVHNFPLIAFYCCEKGKRQPHKSLHDRCFGEALDPN
1		-	CSHCYLDQIKRSDFLGFSGYSPHFVAISTNSEHKMQPSSMQQAL
, I	1		PSQ*PYWTDPRPALVPCCSHRPDVHRSRPGPGLPGTSGCSDRPP
[ ]	1	1	VCPI
6178	1027	254	
	~~~′	454	STORGGI KGVARAASLVGRRRAGTGMALLLCLVCLTAALAHGCL
1 1		i	HCHSNFSKKFSFYRHHVNFKSWWVGDIPVSGALLTDWSDDTMKE
1 1	ł		LHLAIPAKITREKLDQVATAVYQMMDQLYQGKMYFPGYFPNELR
1	İ		NIFREQVHLIQNAIIESRIDCQHRCGIFQYETISCNNCTDSHVA
1	-		CFGYNCESSAQWKSAVQGLLNYINNWHKQDTSMRPRSSAFSWPG
			THRAAPAFLVLPALRCLEPPHLANLSLEDAA+CLKQH
6179	806	276	RGETREMAGNLLSGAGRRLWDWVPLACRSFSLGVPRLIGIRLTL
]]	ļ	j	PPPKVVDRWNEKRAMFGVYDNIGILGNFEKHPKELIRGPIWLRG
] [WKGNELQRCIRKRKMVGSRMFADDLHNLNKRIRYLYKHFNRHGK
<u> </u>			FR+KRKLRTSEKAHLSPWRRETVLFPVRKRLCIFSVIKWGFFGI
6180	156	1833	DHHILKAASTTHVCARGNIFAIPNTRCLEC*ATATPSSLECQN*
Į [1		SHLSLCPLPATTSGLTPNSMIPEKERQNIAERLLRVMCADLGAL
j	į	Ì	CHROCKER WE ASSET FROM THE RENDER VMCADLGAL
1	1	i	SVVSGKEFLKLAGTLVDSGARYGAFSVTEILGNFNTLALKHLPR MYNOVKVKVTCALGSNACLGIGVTCHSQSVGPDSCYILTAYQAE

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ĺ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ļ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ł	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			GNHIKSYVLGVKGADIRDSGDLVHHWVQNVLSEFVMSEIRTVYV
į .			TDCRVSTSAFSKAGMCLRCSACALNSVVQSVLSKRTLQARSMHE
\$			VIELLNVCEDLAGSTGLAKETFGSLEETSPPPCWNSVTDSLLLV
i			HERYEQICEFYSRAKKMNLIQSLNKHLLSNLAAILTPVKQAVIE
i			LSNESQPTLQLVLPTYVRLEKLFTAKANDAGTVSKLCHLFLEAL
}	J		KENFKVHPAHKVAMILDPQQKLRPVPPYQHEEIIGKVCELINEV
			KESWABBADFEPAAKKPRSAAVENPAAQEDDRLGKNEVYDYLQE
i			PLFQATPDLFQYWSCVTQKHTKLAKLAFWLLAVPAVGARSGCVN
			MCEQALLIKRRRLLSPEDMNKLMFLKSNML
6181	169	1032	TRTLLSPVLLPGPRWKPWRRRPMGPLALPAWLQPRYRKNAYLFI
1	1	2032	YYLIQFCGHSWIFTNMTVRFFSFGKDSMVDTFYAIGLVMRLCQS
}	1		VSLLELLHIYVGIBSNHLLPRFLQLTERIIILFVVITSQEEVQE
j	1		KYVVCVLFVFWNLLDMVRYTYSMLSVIGISYAVLTWLSQTLWMP
1	}		IYPLCVLAEAFAIYQSLPYFESFGTYSTKLPFDLSIYFPYVLKI
		,	YLMMLFIGMYFTYSHLYSERRDILGIFPIKKKKM*STAFQCDTR
		i.	KDRLWIQCSK*NTGSILVEKFLVF
6182	1769	1224	AS*IDYQLNTLLKEFQLTEENTKLRYLTCSLIEDMAAAYFPDCI
			VRPFGSSVNTFGKLGCDLDMFLDLDETRNLSAHKISGNFLMEFQ
			VKNVPSERIATQKILSVLGECLDHFGPGCVGVQKILNARCPLVR
1			FSHQASGFQCDLTTNNRIALTSSELLYIYGALDSRVRALVFSVR
1]		CWARAHSLTSSIPGAWITNFSLTMMVIFFLORRSPPILPTLDSL
i			KTLADAEDKCVIEGNNCTFVRDLSRIKPSQNTETLELLLKEFFE
			YFGNFAFDKNSINIRQGREQNKPDSSPLYIQNPFETSLNISKNV
ı	í		SQSQLQKFVDLARESAWILQQEDTDRPSISSNRPWGLVSLLLPS
1			APNRKSFTKKKSNKFAIETVKNLLESLKGNRTENFTKTSGKRTI
İ			STQT
6183	1118	452	HLDRYIKSPGSGSSTPAPPSHLLLYLLHPQSTRTMGCCGCSRGC
			GSGCGGCGSSCGGCGSGCGGCGSSCGGCGS
			RCYVPVCCCKPVCSWVPACSCTSCGSCGGSKGGCGSCGGSKGGC
i I			GSCGCSQSSCCKPCCCSSGCGSSCCQSSCCKPCCCQSSCCVPVC
			CQSSCCKPCCCQSNCCVPVCCQCKI*GSGPRPSGFSCLVKAFLM
1 .			VP
6184	1	2191	IVTVREEDGAPAVAPPGVVVSRANKRSGAGPGGSGGGGARGAEE
			EPPPPLQAVLVADSFDRRFFPISKDQPRVLLPLANVALIDYTLE
Į i			FLTATGVQETFVFCCWKAAQIKEHLLKSKWCRPTSLNVVRIITS
			ELYRSLGDVLRDVDAKALVRSDFLLVYGDVISNINITRALEEHR
			LRRKL+KNVSVMTMIFKESSPSHPTRCHEDNVVVAVDSTTNRVL
			HFQKTQGLRRFAFPLSLFQGSSDGVEVRYDLLDCHISICSPQVA
j i			QLFTDNFDYQTRDDFVRGLLVNEEILGNQIHMHVTAKEYGARVS
[NLHMYSAVCADVIRRWVYPLTPEANFTDSTTQSCTHSRHNIYRG
	1		PEVSLGHGSILEENVLLGSGTVIGSNCFITNSVIGPGCHIEPGD
	İ		NVVLDQTYLWQGVRVAAGAQIHQSLLCDNAEVKERVTLKPRSVL
1	Į.		TSQVVVGPNITLPEGSVISLHPPDAEEDEDDGEFSDDSGADQEK
i i	!		DKVKMKGYNPAEVGAAGKGYLWKAAGMNMEEEEELQQNLWGLKI
	İ		NMEEESESESEQSMDSEEPDSRGGSPQMDDIKVFQNEVLGTLQR
	İ		GKEENISCDNLVLEINSLKYAYNISLKEVMQVLSHVVLEFPLQQ
]			MDSPLDSSRYCALLLPLLKAWSPVFRNYIKRAADHLEALAAIED
	ļ		FFLEHEALGISMAKVLMAFYQLEILAEETILSWFSQRDTTDKGQ
I	1	ĺ	QLRKNQQLQRFIQWLKEAEEESSEDD
6185	791	44	PCTSCVLWATLHLPASTRKAPQAECGMISITEWQKIGVGITGFG
		- -	IFFILFGTLLYFDSVLLAFGNLLFLTGLSLIIGLRKTFWFFFQR
	1		HKLKGTSFLLGGVVIVLLRWPLLGMFLETYGFFSLFKGFFPVAF
			GFLGNVCNIPFLGALFRRLQGTSSMV*KTEMSSLNLDHWLKGAK
			REEWEPPPQSPALTHSPTYPGPPQVQKERNGAEQLTSNPQVDSR
l i			GCQEAEMQTPRRIGWGWYHTLTLYLWEEK
6186	569	238	VYGIDSSNTNTHGAEERNRKLKKHWKLCHAQSRLDVNGLALKMA
	<u>-</u>		

SEQ	Predicted	Predicted end	Desire and comments
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A-Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	W-Wichiding T-T-clausian me, G=Glycine,
1 .	corresponding	to first	H-Histidine, I=Isoleucine, K=Lysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of	1	S=Serine, T=Threonine, V=Valine,
j	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
		sequence	Codon, /=possible nucleotide deletion,
ļ	sequence		\⇒possible nucleotide insertion)
			KERKVKNKVKNKADTEEVFNNSPTNQEKMPTSAILPDFSGSVIS
			NIRNQMETLHSQPHQEENLCFENSFSLINLLPINAVEPTSSOOI
ł	{	ļ	PNRETSEANKERRKMTSKSSESNIYSPLTSFITADSELHDIIKD
i			LEDCLMVGLHTCGDLAPNTLRIFTSNSEIKGVCSVGCCYHLLSR
			EFENQHKERTQEKWGFPMCHYLKEERWCCGRNARMSACLALERV
	•		AAGQGLPTESLFYRAVLQDIIKDCYGITKCDRHVGKIYSKCSSP
	1		LDYVRRSLKKLGLDESKLPBKI IMNYYEKYKPRMNELEAFNMLK
1	}		VVLAPCIETLILLDRLCYLKEQEDIAWSALVKLFDPVKSPRCYA
ľ			VIALKKQQ*FPLKQIIRCISL*DSAGCAEEVSVGDGGPALRDAP
			PSGSRVGSRYD
6187	1701	771	DAWGPETRLARILNPDSFIEPRPGRLPELEATRPHMEPKASCPA
1	J !	· · · •	AAPLMERKFHVLVGVTGSVAALKLPLLVSKLLDIPGLEVAVVTT
[.		FDAKHEVGDODTDUTLVCDADENTANIADADADA
1			ERAKHFYSPQDIPVTLYSDADEWEMWKSRSDPVLHIDLRRWADL
1 .]		LLVAPLDANTLGKVASGICDNLLTCVMRAWDRSKPLLFCPAMNT
1			AMWEHPITAQQVDQLKAFGYVEIPCVAKKLVCGDEGLGAMAEVG
1 1			TIVDKVKEVLFQHSGFQQS*PGISVMGVPLYSEWVQAKSVKMDV
			GKIGGYPHLLNGGPALSLPRGQACSRLNWTEGPGLSFFQPGEAA
6188			A
9700	238	1534	KGFVNAGPLMAELQVSPQWKAPEMSQICLSCGHPSA*GPRWASW
			NIGVFICIRCAGIHRNLGVHISRVKSVNLDQWTQEQIQCMQEMG
1 1	ł		NGKANRLYEAYLPETFRRPQIDPAVEGFIRDKYEKKKYMDRSLD
			INAFRKEKDDKWKRGSEPVPEKKLEPVVFEKVKMPOKKEDPOLP
	1		RKSSPKSTAPVMDLLGLDAPVACSIANSKTSNTLEKDLDLLASV
1	'		PSPSSSGSRKVVGSMPTAGSAGSVPENLNLFPEPGSKSEEIGKK
1			QLSKDSILSLYGSQTPQMPTQAMFMAPAQMAYPTAYPSFPGVTP
1 1	i i		PNSIMGSMMPPPVGMVAQPGASGMVAPMAMPAGYMGGMQASMMG
			VPNGMMTTQQAGYMAGMAAMPQTVYGVQPAQQLQWNLTQMTQQM
Li			AGMNFYGANGMMNYGQSMSGGNEQAANQTLSPQMWK
6189	1297	793	LGEPLGDLCELIPGDVQQLQMGEVHPGTGAQGSAAQSVAG3VQL
1 1	1		TQLSHARQRPSCQGSQLIALDLQHMDISRQPRWQHVQPVARQVQ
1			RAQQAQLAEGVAVHLWAGDAVVAEVELLQEVGGGKVFAANACDL
1			VVQDHEGAHAARQATGHALQRVIVQVRRVQPLEAL*RVPSGLPR
1	·		RVRAPMILHNQITGIGREDFATTYFLEELNLSYNRITSPOVHRD
1 1		`.i	AFRKLRLLRSLDLSGNRLHMLPPGLPRNVHVLKVKRNBLAALAR
1 1	ł		GALAGMAQLRELYLTSNRLRSRALGPRAWVDLAHLQLLDIAGNQ
1 1	ļ		LTEIPEGLPESLEYLYLQNNKISAVPANAFDSTPNLKGIFLRFN
, , J	.	,	KLAVGSVVDSAFRRLKHLQVLDIEGNLEFGDISKDRGRLGKEKE
1	Į.		EEEEDEVEEEETR EEEEDEVEEEETR
6190	66	1309	
[]		1303	ILVGNVSFLLSFAEYVCNCSVVGSLNVNRCNQTTGQCECRPGYQ
	Ì	l	GLHCETCKEGFYLNYTSGLCQPCDCSPHGALSIPCNSSGKCQCK
			VGVIGSICDRCQDGYYGFSKNGCLPCQCNNRSASCDALTGACLN
	Ī		CQENSKGNHCEECKEGFYQSPDATKECLRCPCSAVTSTGSCSIK
1	J	j	SSELEPECDQCKDGYIGPNCNKCENGYYNFDSICRKCQCHGHVY
	1	}	PVKTPKICKPESGECINCLHNTTGFWCENCL*GYVHDLEGNCIK
į I	1		KVILPTPEGSTILVSNASLTTSVPTPVINSTFTPTTLQTIFSVS
] [TSENSTSALADVSWTQFNIIILTVIIIVVVLLMGFVGAVYMYRE
[1	YONRKLNAPFWTIELKEDNISFSSYHDSIPNADVSGLLEDDGNE
1-7-			VAPNGQLTLTTPIHNYKA
6191	1212	1511	VNLCHGGLLHLSTHHLGIKPSMH*LFPLMLSFPHLTPQQPKCPS
1		ļ	MIDWIKKIWYIYTMEYYATIKRNEIMFFAGTWMEMEAIILSKLM
			QDYMFSLISGS
6192	3	950	TRGCGNKMAGKKNVLSSLAVYAEDSEPESDGEAGIEAVGSAAEE
1 1			KGGLVSDAYGEDDFSRLGGDEDGYEBEEDENSRQSEDDDSETEK
] 1		į	PEADDPKDNTEAEKRDPQELVASFSERVRNMSPDEIKIPPEPPG
		1	RCSNHLQDKIQKLYERKIKEGMDMNYIIQRKKEFRNPSIYEKLI
			QFCAIDELGTNYPKDMFDPHGWSEDSYYEALAKAQKIEMDKLEK

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H-Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ļ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
l l	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
}	sequence	·	\=possible nucleotide insertion)
			AKKERTKIEFVTGTKKGTTTNATSTTTTTASTAVADAQKRKSKW
			DSAIPVTTIAQPTILTTTATLPAVVTVTTSASGSKTTVISAVGT
			IVKKAKQ
6193	3	950	TRGCGNKMAGKKNVLSSLAVYAEDSEPESDGEAGIEAVGSAAEE
	j		KGGLVSDAYGEDDFSRLGGDEDGYEEEEDENSROSEDDDSETEK
			PEADDPKDNTEAEKRDPQELVASFSERVRNMSPDEIKIPPEPPG
ł	}		RCSNHLQDKIQKLYBRKIKEGMDMNYIIQRKKEFRNPSIYEKLI
1			QFCAIDELGTNYPKDMFDPHGWSEDSYYEALAKAOKIEMDKLEK
}			AKKERTKIEFVTGTKKGTTTNATSTTTTTTASTAVADAOKRKSKW
ľ			DSAIPVTTIAQPTILTTTATLPAVVTVTTSASGSKTTVISAVGT
63.04			IVKKAKQ
6194	3	950	TRGCGNKMAGKKNVLSSLAVYAEDSEPESDGEAGIEAVGSAAEE
			KGGLVSDAYGEDDFSRLGGDEDGYEEEEDENSRQSEDDDSETEK
i i			PEADDPKDNTBAEKRDPQELVASFSERVRNMSPDEIKIPPEPPG
			RCSNHLQDKIQKLYERKIKEGMDMNYIIQRKKEFRNPSIYEKLI
		1	QPCAIDELGTNYPKDMFDPHGWSEDSYYEALAKAQKIEMDKLEK
j !			AKKERTKIEFVTGTKKGTTTNATSTTTTTASTAVADAQKRKSKW
1 1			DSAIPVTTIAQPTILTTTATLPAVVTVTTSASGSKTTVISAVGT
6195	736	235	IVKKAKQ
	/30	235	VANGLQSNMPKFYCDYCDTYLTHDSPSVRKTHCSGRKHKENVKD
1	i i		YYQKWMEEQAQSLIDKTTAAFQQGKIPPTPFSAPPPAGAMIPPP
i i			PSLPGPPRPGMMPAPHMGGPPMMPMMGPPPPGMMPVGPAPGMRP
6196	1512	623	PMGGHMPMMPGPPMMRPPARPMMVPTRPGMTRPDR
		023	KTGKRRSAAYVRNILDNAEQVISNLEARNLGPRLTPLLQEEDSH
			QRLLMGLMVSBLKDHFLRHLQGVEKKKIEQMVLDYISKLLDLIC
			HIVETNWRKHNLHSWYLHFNSRGSAAEFAVFHIMTRILEATNSL FLPLPPGFHTLHTILGVQCLPLHNLLHCIDSGYLLLTETAVIRL
í í			MKDLDNTEKNEKLKFSIIVRLPPLIGQKICRLWDHPMSSNIISR
1			NHVTRLLQNYKKQPRNSMINKSSFSVEFLPLNYFIEILTDIESS
1 1			NQALYPFEGHDNVDAEFVEEAALKHTAMLLGL
6197	3	819	ADPEGTE BAVMSRYTRPPNTSLFIRNVADATRPEDLRREFGRYG
1 1			PIVDVYIPLDFYTRRPRGFAYVQFEDVRDAEDALYNLNRKWVCG
1			RQTEIQFAQGDRKTPGQMKSKERHPCSPSDHRRSRSPSQRRTRS
1 1			RSSSWGRNRRRSDSLKESRHRRFSYSQSKSRSKSLPRRSTSARQ
i I			SRTPRRNFGSRGRSRSKSLQKRSKSIGKSQSSSPQKQTSSGTKS
1			RSHGRHSDSIARSPCKSPKGYTNFETKVQTAKHSHFRSHSRSRS
			YRHKNSW
6198	111	1912	SEAALSPSFISPACFLLRKLPALEDGTLPHPDTLGMNYEGARSE
	ľ		RENHAADDSEGGALDMCCSERI.PGLPQPIVMEALDBAEGLODSO
,		Í	REMPPPPPPPPPPDPAQKPPPRGAGSHSLTVRSSLCLFAASOFL
[]			LACGVLWFSGYGHIWSQNATNLVSSLLTLLKOLEPTAWLDSGTW
1 1	J	I	GVPSLLLVFLSGGLVLVTTLVWHLLRTPPEPPTPLPPEDRROSV
1 1			SROPSFTYSEWMBEKIEDDPLDLDPVPETPVFDCVMDIKPEADP
[[ł	TSLTVKSMGLQERRGSNVSLTLDMCTPGCNEEGFGYLMSPREES
1 1		1	AREYLLSASRVLQAEELHEKALDPFLLQAEFFEIPMNFVDPKEY
]		-1	DIPGLVRKNRYKTILPNPHSRVCLTSPDPDDPLSSYINANYIRG
1 1	ļ		YGGEEKVYIATQGPIVSTVADFWRMVWQEHTPIIVMITNIEEMN
l l		ļ	EKCTEYWPEEQVAYDGVEITVQKVIHTEDYRLRLISLKSGTEER
	1	1	GLKHYWFTSWPDQKTPDRAPPLLHLVREVEEAAQQEGPHCAPII
		İ	VHCSAGIGRTGCFIATSICCQQLRQEGVVDILKTTCQLRQDRGG
6199	144	1217	MIQHCEQYQFVHHVMSLYEKQLSHQSPE
	-33	1211	MARENGESSSSWKKQAEDIKKIFEFKETLGTGAFSEVVLAEEKA
I			TGKLFAVKCIPKKALKGKESSIENEIAVLRKIKHENIVALEDIY
1			ESPNHLYLVMQLVSGGELFDRIVEKGFYTEKDASTLIRQVLDAV
1			YYLHRMGIVHRDLKPENLLYYSQDEESKIMISDFGLSKMEGKGD
			VMSTACGTPGYVAPRVLAQKPYSKAVDCWSIGVIAYILLCGYPP

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ĺ	location	corresponding	Walistiding Tatalanaha, Gagiycine,
1	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
i	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
I	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	seductice	Codon, /=possible nucleotide deletion,
	ocquence	<u> </u>	\=possible nucleotide insertion)
1			FYDENDSKLFEQILKAEYEFDSPYWDDISDSAKDFIRNLMEKDP
		1	NKRYTCEQAARHPWIAGDTALNKNIHESVSAQIRKNFAKSKWRQ
Ì	1		AFNATAVVRHMRKLHLGSSLDSSNASVSSSLSLASQKDCASGTF HAL*
6200	702	96	1
1200	1 702	36	LPEVPHSLRPRVKPHLCCAQPAVRVMARLPKLAVFDLDYTLWPF
ł			WVDTHVDPPFHKSSDGTVRDRRGQDVRLYPEVPEVLKRLQSLGV
			PGAAASRTSEIEGANQLLELFDLFRYFVHREIYPGSKITHFERL
			QQKTGIPFSQMIFFDDERRNIVDVSKLGVTCIHIQNGMNLQTLS
6201	2809	2383	OGLETFAKAOTGPLRSSLERSPFEA
1212	2003	2303	GQTPRVRWKMRRSLRAGKRRQTAGRKSKSPPKVPIVIQDDSLPA
			GPPPQIRILKRPTSNGVVSSPNSTSRPTLPVKSLAQREAEYAEA
1			RKRILGSASPBEEQEKPILDRPTRISQPEDSRQPNNVIRQPLGP
6202	2	426	DGSQGFKQRR
	_	440	INADRAAVASSLLSRPTRKMAPQKDRKPKRSTWRFNLDLTHPVE
Į.			DGIFDSGNFEQFLREKVKVNGKTGNLGNVVHIERFKNKITVVSE
ł			KQFSKRYLKYLTKKYLKKNNLRDWLRVVASDKETYBLRYFQISQ DEDESESED
6203	419	2550	
1		2350	RCPRPPATAGAAASRPDRSPPSGISGSEAAAGAGAAAAPASQHPA
			TGTGAVQTEAMKQILGVIDKKLRNLEKKKGKLDDYQERMNKGER
			LNQDQLDAVSKYQEVTNNLEFAKELQRSFMALSQDIQKTIKKTA
1			RREQLMREBAEQKRLKTVLELQYVLDKLGDDEVRTDLKQGLNGV
			PILSEEELSLLDEFYKLVDPERDMSLRLNBQYEHASIHLWDLLE
1			GKEKPVCGTTYKVLKEIVERVFQSNYFDSTHNHQNGLCEEEEAA SAPAVEDQVPEAEPEPAEEYTEQSEVESTBYVNRQFMAETQFTS
			GEVEOUDENE UPTURE TRUE COORDAY CROSS CONTROL C
			GEKEQVDEWTVETVEVVNSLQQQPQAASPSVPEPHSLTPVAQAD PLVRRQRVQDLMAQMQGPYNFIQDSMLDFENQTLDPAIVSAQPM
1			NPTQNMDMPQLVCPPVHSESRLAQPNQVPVQPEATQVPLVSSTS
1			EGYTASQPLYQPSHATEQRPQKEPIDQIQATISLNTDQTTASSS
			LPAASQPQVFQAGTSKPLHSSGINVNAAPFQSMQTVFNMNAPVP
] }	j		PVNEPETLKQQNQYQASYNQSFSSQPHQVEQTELQQEQLQTVVG
] . [ì		TYHGSPDQSHQVTGNHQQPPQQNTGFPRSNQPYYNSRGVSRGGS
			RGARGLMNGYRGPANGFRGGYDGYRPSFSNTPNSGYTQSQFSAP
1 1		i	RDYSGYQRDGYQQNFKRGSGQSGPRGAPRGRGGPPRPNRGMPQM
1 1	ĺ		NTQQVN
6204	2933	787	CTHNLISLLGGRALIHFNRFLNLKIQEGEAHNIFCPAYDCFQLV
1	· i	= * <u>.</u>	PGDIIKSVVSKENDKRYLQFDIKAFVENNPAIKWCPTPGCDRAV
1	j		RLTKQGSNTSGSDTLSFPLLRAPAVDCGKGHLFCWECLGEAHEP
1 1			CDCQTWKNWLQKITEMKPEELVGVSEAYEDAANCLWLLTNSKPC
1 1	ļ	į	ANCKSPIQKNEGCNHMQCAKCKYDFCWICLEEWKKHSFVHWEVI
1	1	j	YRCTRYEVIQHVEEQSKEMTVEAEKKHKRFQELDRFMHYYTRFK
1 1			NHEHSYQLEQRLLKTAKEKMEQLSRALKETEGGCPDTTFIEDAV
}			HVLLKTRRILKCSYPYGFFLEPKSTKKEIFELMQTDLEMVTEDL
1			AQKVNRPYLRTPRHKIIKAACLVQQKRQEFLASVARGVAPADSP
1 1	1	- 1	EAPRRS FAGGTWDWEYLGFASPEEYAEFQYRRHRQRRRGDVHS
1			LLSNPPDPDEPSESTLDIPEGGSSSRRPGTSVVSSASMSVLHSS
į f	-	ļ	SLRDYTPASRSENQDSLQALSSLDEDDPNILLAIQLSLQESGLA
1 1		1	LDEETRDFLSNEASLGAIGTSLPSRLDSVPRNTDSPRAALSSSE
1 1	Į	ļ	LLELGDSLMRLGAENDPFSTDTLSSHPLSEARSDFCPSSSDPDS
į į	[1	AGQDPNINDNLLGNIMAWPHDMNPQSIALIPPATTEISADSQLP
į l	ĺ	•	CIKDGSEGVKDVELVLPEDSMFEDASVSEGRGTQIEENPLEENI
Li		}	PGGGKQHPOAW
6205	ī	1200	RAHRGKMALEVGDMEDGQLSDSDSDMTVAPSDRPLQLPKVLGGD
]		-	SAMRAFQNTATACAPVSHYRAVESVDSSEESFSDSDDDSCLWKR
[İ		KRQKCFNPPPKPBPFQFGQSSQKPPVAGGKKINNIWGAVLQEQN
			QDAVATELGILGMEGTIDRSRQSETYNYLLAKKLRKESQEHTKD
			LDKELDEYMHGGKKMGSKBEBNGQGHLKRKRPVKDRLGNRPEMN

SEQ	Predicted	Predicted end	I Amiro and I
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
į.	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1 .	sequence	Jogac	\=pcssible nucleotide insertion)
			YKGRYBITAEDSQEKVADEISFRLQEPKKDLIARVVRIIGNKKA
1			IELLMETAEVEQNGGLFIMNGSRRRTPGGVFLNLLKNTPSISEE
			QIKDIFYIENQKEYENKKAARKRRTQVLGKKMKQAIKSLNFQED
			DDTSRETFASDTNEALASLDESQEGHAEAKLEAEEAIEVDHSHD
i		•	LDIF
6206	10	1442	IISERRERSCLHLVCIRCSCDVVEMGSVLGLCSMASWIPCLCGS
I	i .		APCLLCRCCPSGNNSTVTRLIYALFLLVGVCVACVMLIPGMEEQ
			LNKIPGFCENEKGVVPCNILVGYKAVYRLCFGLAMFYLLLSLLM
1	1		IKVKSSSDPRAAVHNGFWFFKFAAAIAIIIGAFFIPEGTFTTVW
			FYVGMAGAFCFILIQLVLLIDFAHSWNESWVEKMEEGNSRCWYA
			ALLSATALNYLLSLVAIVLFFVYYTHPASCSENKAFISVNMLLC
1			VGASVMSILPKIQESQPRSGLLQSSVITVYTMYLTWSAMTNEPE
			TNCNPSLLSIIGYNTTSTVPKEGQSVQWWHAQGIIGLILFLLCV
			FYSSIRTSNNSQVNKLTLTSDESTLIEDGGARSDGSLEDGDDVH
	į		RAVDNERDGVTYSYSFFHFMLFLASLYIMMTLTNWYRYEPSREM
J			KSQWTAVWVKISSSWIGIVLYVWTLVAPLVLTNRDPD
6207	2924	1471	TVMAEAATPGTTATTSGAGAAAATAAAASPTPIPTVTAPSLGAG
			GGGGGSDGSGGGWTKQVTCRYFMHGVCKEGDNCRYSHDLSDSPY
1 1			SVVCKYFQRGYCIYGDRCRYEHSKPLKQEEATATELTTKSSLAA
1 1			SSSLSSIVGPLVEMNTGEAESRNSNFATVGAGSEDWVNAIEPVP
1 1			GQPYCGRTAPSCTEAPLQGSVTKEESEKEQTAVETKKQLCPYAA
1 .			VGECRYGENCVYLHGDSCDMCGLQVLHPMDAAQRSQHIKSCIEA
1 1			HEKDMELSFAVQRSKDMVCGICMEVVYEKANPSERRFGILSNCN
1 1			HTYCLKCIRKWRSAKQFESKIIKSCPECRITSNFVIPSEYWURE
] [-		KEEKQKLILKYKEAMSNKACRYFDEGRGSCPFGGNCFYKHAVDD
1 1	1		GRREEPQRQKVGTSSRYRAQRRNHFWELIEERENSNPFDNDEER
7300			VVTFELGEMLLMLLAAGGDDELTDSEDEWDLFHDELEDFYDLDI.
6208	2924	1471	TVMAEAATPGTTATTSGAGAAAATAAAASPTPIPTVTAPSIGAG
1 F	İ		GGGGGSDGSGGGWTKQVTCRYFMHGVCKEGDNCRYSHDLSDSDV
1	}		SVVCKYFORGYCIYGDRCRYEHSKPLKOBEATATELTTKSSLAA
1	i		SSSLSSIVGPLVEMNTGEAESRNSNFATVGAGSEDWVNAIEFVP
]]			GOPYCGRTAPSCTEAPLOGSVTKEESEKKQTAVETKKQLCPYAA
, ,			VGECRYGENCVYLHGDSCDMCGLQVLHPMDAAQRSQHIKSCIEA
1 1			HEKDMELSFAVQRSKDMVCGICMEVVYEKANPSERREGTISMON
1			HTYCLKCIRKWRSAKQFESKIIKSCPECRITSNFVIPSEYWVEE
	}		KEEKQKLILKYKEAMSNKACRYFDEGRGSCPFGGNCFYKHAYPD
] [GRREEPOROKVGTSSRYRAQRRNHFWELIBERENSNPFDNDEEB
6209	1758	829	VVTFELGEMLLMLLAAGGDDELTDSEDEWDLFHDELEDFYDLDL
"			ERLCFPCMQSKIYSYMSPNKCSGMRFPLQEENSVTHHEVKCQGK
		İ	PLAGIYRKREEKRNAGNAVRSAMKSEEQKIKDARKGPLVPFPNQ
	1		KSEAAEPPKTPPSSCDSTNAAIAKQALKKPIKGKQAPRKKAQGK
1	İ		TQQNRKLTDFYPVRRSSRKSKAELQSEERKRIDELIESGKEEGM
	[KIDLIDGKGRGVIATKQFSRGDFVVEYHGDLIEITDAKKREALY
i			AQDPSTGCYMYYFQYLSKTYCVDATRETNRLGRLINHSKCGNCQ
	1		TKLHDIDGVPHLILIASRDIAAGEELLYDYGDRSKASIEAHPWL KH
6210	3761	387	· · ·
1			IFGMSKLRMVLLEDSGSADFRRHFVNLSPFTITVVLLLSACFVT
·			SSLGGTDKELRLVDGENKCSGRVEVKVQEEWGTVCNNGWSMEAV
l		. 1	SVICNOLGCPTAIKAPGWANSSAGSGRIWMDHVSCRGNESALWD
]			CKHDGWGKHSNCTHQQDAGVTCSDGSNLEMRLTRGGNMCSGRIE
j	ļ		IKFOGRWGTVCDDNFNIDHASVICRQLECGSAVSFSGSSNFGEG
1	j	l	SGPIWFDDLICNGNESALWNCKHQGWGKHNCDHAEDAGVICSKG
		ĺ	ADLSLRLVDGVTECSGRLEVRFQGEWGTICDDGWDSYDAAVACK
1	ĺ		QLGCPTAVTAIGRVNASKGFGHIWLDSVSCQCHEPAVWQCKHHE WGKHYCNHNEDAGVTCSDGSDLELRLRGGGSRCAGTVEVEIQRL
	[}	LGKVCDRGWGLKEADVVCRQLGCGSALKTSYQVYSKIQATNTWL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine.
J	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ŀ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion.
·	Sequence		\=possible nucleotide insertion)
			FLSSCNGNETSLWDCKNWQWGGLTCDHYEEAKITCSAHREPRLV
			GGDIPCSGRVEVKHGDTWGSICDSDFSLEAASVLCRELQCGTVV
	,	i	SILGGAHFGEGNGQIWAEEPQCEGHESHLSLCPVAPRPEGTCSH
1		ŀ	SRDVGVVCSRYTBIRLVNGKTPCEGRVELKTLGAWGSLCNSHWD
1			IEDAHVLCQQLKCGVALSTPGGARFGKGNGQIWRHMFHCTGTEQ
			HMGDCPVTALGASLCPSEQVASVICSGNQSQTLSSCNSSSLGPT
	Ì		RPTIPEESAVACIESGQLRLVNGGGRCAGRVEIYHEGSWGTICD
			DSWDLSDAHVVCRQLGCGEAINATGSAHFGEGTGPIWLDEMKCN
1			GKESRIWQCHSHGWGQQNCRHKEDAGVICSEFMSLRLTSEASRE
1	}	j	ACAGRLEVFYNGAWGTVGKSSMSETTVGVVCRQLGCADKGKINP
İ			ASLDKAMSIPMWVDNVQCPKGPDTLWQCPSSPWEKRLASPSEET WITCDNKIRLQEGPTSCSGRVEIWHGGSWGTVCDDSWDLDDAQV
i			VCQQLGCGPALKAPKEAEFGQGTGPIWLNEVKCKGNESSLWDCP
	1		ARRWGHSECGHKEDAAVNCTDISVQKTPQKATTGRSSRQSSFIA
1	1		VGILGVVLLAIFVALPFLTKKRRQRQRLAVSSRGENLVHQIQYR
			EMNSCLNADDLDLMNSSGGHSEPH
6211	3761	387	1FGMSKLRMVLLEDSGSADFRRHFVNLSPFTITVVLLLSACFVT
]			SSLGGTDKELRLVDGENKCSGRVEVKVQEEWGTVCNNGWSMEAV
			SVICNQLGCPTAIKAPGWANSSAGSGRIWMDHVSCRGNESALWD
1	Į į		CKHDGWGKHSNCTHQQDAGVTCSDGSNLEMRLTRGGNMCSGRIE
			IKFQGRWGTVCDDNFNIDHASVICRQLECGSAVSFSGSSNFGEG
			SGPIWFDDLICNGNESALWNCKHQGWGKHNCDHAEDAGVICSKG
			ADLSLRLVDGVTECSGRLEVRFQGEWGTICDDGWDSYDAAVACK
1			QLGCPTAVTAIGRVNASKGFGHIWLDSVSCQGHEPAVWQCKHHE
1			WGKHYCNHNEDAGVTCSDGSDLELRLRGGGSRCAGTVEVEIQRL
		•	LGKVCDRGWGLKEADVVCRQLGCGSALKTSYQVYSKIQATNTWL FLSSCNGNETSLWDCKNWQWGGLTCDHYBEAKITCSAHREPRLV
	•		GGDIPCSGRVEVKHGDTWGSICDSDFSLEAASVLCRELQCGTVV
1		•	SILGGAHFGEGNGQIWAEEFQCEGHESHLSLCPVAPRPEGTCSH
			SRDVGVVCSRYTEIRLVNGKTPCEGRVELKTLGAWGSLCNSHWD
ľ		•	IEDAHVLCQQLKCGVALSTPGGARFGKGNGQIWRHMFHCTGTEQ
			HMGDCPVTALGASLCPSEQVASVICSGNQSQTLSSCNSSSLGPT
<u> </u>			RPTIPEESAVACIESGQLRLVNGGGRCAGRVEIYHEGSWGTICD
1			DSWDLSDAHVVCRQLGCGEAINATGSAHFGEGTGPIWLDEMKCN
1			GKESRIWQCHSHGWGQQNCRHKEDAGVICSEFMSLRLTSEASRE
	1		ACAGRLEVFYNGAWGTVGKSSMSETTVGVVCRQLGCADKGKINP
'			ASLDKAMSIPMWVDNVQCPKGPDTLWQCPSSPWEKRLASPSEET
	1		WITCDNKIRLQEGPTSCSGRVEIWHGGSWGTVCDDSWDLDDAQV
!	i		VCQQLGCGPALKAFKEAEFGQGTGPIWLNEVKCKGNESSLWDCP
1 1	ľ		ARRWGHSECGHKEDAAVNCTDISVQKTPQKATTGRSSRQSSFIA
			VGILGVVLLAIFVALFFLTKKRRQRQRLAVSSRGENLVHQIQYR
6212	1	1134	EMNSCLNADDLDLMNSSGGHSEPH
	-	7773	LKWELRPGGAVWGTGRGAGTGAPRSCCCQTNPGPPSSLRRAFRR RELPFPACHEIGLGAEAGSGPPPAPAARESRSRAMEEEASSPGL
		l	GCSKPHLEKLTLGITRILESSPGVTEVTIIEKPPAERHMISSWE
	İ	ł	QKNNCVMPEDVKNFYLMINGFHMTWSVKLDEHIIPLGSMAINSI
		ļ	SKLTQLTQSSMYSLPNAPTLADLEDDTHEASDDQPEKPHFDSRS
	.	Į	VIFELDSCNGSGKVCLVYKSGKPALAEDTEIWFLDRALYWHFLT
			DTFTAYYRLLITHLGLPQWQYAFTSYGISPQAKQRVSMYKPITY
			NTNLLTEETDSFVNKLDPSKVFKSKNKIVIPKKKGPVQPAGGQK
L			GPSGPSGPSTSSTSKSSSGSGNPTRK
6213	1	1134	LKWELRPGGAVWGTGRGAGTGAPRSCCCQTNPGPPSSLRRAFRR
		}	RELPFPACHEIGLGAEAGSGPPPAPAARESRSRAMEEEASSPGL
	}	[-	GCSKPHLEKLTLGITRILESSPGVTEVTIIEKPPAERHMISSWE
		1	QKNNCVMPEDVKNFYLMTNGFHMTWSVKLDEHIIPLGSMAINSI
			SKLTQLTQSSMYSLPNAPTLADLEDDTHEASDDQPEKPHFDSRS

Deginning nucleotide location corresponding control control control control control control control corresponding control contro	SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
Indication Corresponding to first smino acid residue of amino acid residue of amino acid residue of amino acid sequence Paperoline, October Papero				Amino acid segment containing signal peptide
location corresponding to first amino acid residue of amino acid amin				Clutamic Acid Palbonial
corresponding to first smino acid residue of residue of amino acid residue of amino acid residue of amino acid sequence solvent servine, collutanine, valainine, sequence solvent sequence solven				Unitability Acid, Fernenylatanine, GeGlycine,
amino acid residue of amino acid residue of servine, T-firencine, V-valine, amino acid amino acid sequence of Servine, T-firencine, V-valine, amino acid sequence of Servine, T-firencine, V-valine, S-Stop Code, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide, V-possible,		E .		Assisting, Islandine, Kabysine,
amino acid residue of amino acid sequence S-Serine, T-Threonine, V-Valine, amino acid sequence Sequence	Ì			Debeucine, memethionine, NeAsparagine,
residue of amino acid aequence		1		Performe, Q=Grucamine, R=Arginine,
sequence Codon, /-possible nucleotide deletion, -possible nucleotide insertion VIFELDSCHISGERVCLVYKSGKFALASDEFIFEDDRALYMEFT TPTFAYFRLITHLEJEPMOVAFTYSVESPGAKOKSMYKPTY TPTFAYFRLITHLEJEPMOVAFTYSVESPGAKOKSMYKPTY NTNLITEETDSFUNKLDSSVEKSKINKUVPKKKGPVQPAGGCK GSGSGSGTSTSSTSSSSSGSGTAFTYFT G214 2	1		l .	S=Serine, T=Threonine, V=Valine,
Appossible nucleotide insertion	1			w=Tryptopnan, Y=Tyrosine, X=Unknown, *=Stop
VIFELDSCRIGSCHVILVYRSGKPALABDETETFFLDSALTYHIFTT DTPTAYTRILITHGLGNQWAPTEVATSGROADGAWKKPTTY DTPTAYTRILITHGLGNQWAPTEVATSGROADGAWKKPTTY NTNLITEETDSFVNKLDSSKYEKSKNSKUIPPKKKGPVQPAGGQK GPSGPSGPSTSKSSSGSGNFTKSKSSGSGNFTKK GPSGPSGPSGPSTSKSSSGSGNFTKSKPAFTYVGGFRGMSFRGWV VLCTSAKPRILIPPLSKMANSGRAQVLALYRAMLRESKRFRGWV VLCTSAKPRILIPPLSKMANSGRAQVLALYRAMLRESKRFRGWV VLCTSAKPRILIPPLSKMANSGRAQVLALYRAMLRESKRFRGWV VLCTSAKPRILIPPLSKMANSGRAQVLALYRAMLRESKRFRGWV VLCTSAKPRILIPPLSKMANSGRAQVLALYRAMLGESKRFRGWOWN VLCTSAKPRILIPPLSKMANSGRAQVLALYRAMLGESKRFRGWAV VLCTSAKPRILIPPLSKMANSGRAQVLALYRAMLGESKRFRGWAV VLCTSAKPRILIPPLSKMANSGRAQVLALYRAMLFUSTST VLCTSAKPRILIPPLSKMANSGRAQVLALYRAMLFUSTST VLCTSTAKPRILIPPLSKMANSGRAVILTYPALGRAQGLOCK ANPETSGMIKDCKKKVAVAVHLRQTVQVDDGLEIKAYVAGRUKKKO ANPETSGMIKDCKKKVAVAVHLRQTVQVDDGLEIKAYVAGRUKKKO ANPETSGMIKDCKKKVAVAVHLRQTVQVDDGLEIKAYVAGRUKKKO ANPETSGMIKDCKKKVAVAVHLRQTVQVDDGLEIKAYVAGRUKKKO ANPETSGMIKDCKKKVAVAVHLRQTVQVDDGLEIKAYVAGRUKKKO ANPETSGMIKDCKKKVAVAVHLRQTVQVDDGLEIKAYVAGRUKKKO ANPETSGMIKDCKKKVAVAVHLRQTVQVDDGLEIKAYVAGRUKKKO ANPETSGMIKDCKKKVAVAVHLRQTVQVDDGLEIKASPARQCL LLETPHRENALYRAMGEVTULTYSKANSKYLKISGKKKLEMEGRGVLKKK MUVEYMSFSAKADAKGINUNGGAPEPSGVLAKKKORQCHLKKK ANVEYMSFSAKADAKGINUNGGAPEPSGVLAKKRAQCL LPBAKKPRILIFGTLIMKONSFELVSSEQALKEGIGABROKRTYG KREDERAVSKYNANGERSKRAVCYSSEVSKLIGKSREPQGGFFMSS GANCEBGSARWKTLTFPVALDGVAVSMANVYLKSHHGBRERE FLAYPHLARITR KSPRGAGNAHTLHHPRIVNDLIPDGSVTTESVL GANCEBGSARWKTLTFPVALDGVAVSMANVYLKSHHGBRERE FLAYPHLARITR KSPRGAGNAHTLHHPRIVNDLIPDGSVTTESVL GANCEBGSARWKTLTFPVALDGVAVSMANVYLKSHHGBRERE FLAYPHLARITR KSPRGAGNAHTLHHPRIVNDLIPDGSVTTESVL GANCEBGSARWKTLTFPVALDGVAVSERGARGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	1	1	sequence	Codon, /=possible nucleotide deletion,
DTPTAYYRLITHIGLEPMOYAFTSYGISPAKORGYMYKTY NINLITETETSYRNLDPSKYRKSKNIVIPKKGYOPPAGGYK GPSGPSGPSTSTKSSSSGSMPTRK	<u> </u>	sequence	<u> </u>	\=possible nucleotide insertion)
6214 2 460 HBLAPSAIRPARILIGIPSKYPKSKNIKTYPKKKGPVQPAGGQK GPSGPSGPSTSKSSSGSGRAPTER VHTAVARIRDAFRENKRYKDPVBIQTLVNKAKRDLGVIRRQVH LGQLYSTDKLII LERNDMPRT 6215 2 1849 FVAGGPRGGSSAETMPSILRVTPLJAGGDVGRSCILVSIAGKNV MLDCGMMCPTBOMDRTPDPSYITVNGRITDPLDCVIISHPLUG CARLPYFSEMWGYDGPIYMTHPTQAICPILLSKAYNGKKGE ANPPTSGMIKDCKKKVVAVHLKQTVQVDELEIKAYYAGHUSA ANPPTSGMIKDCKKKVVAVHLKQTVQVDDELEIKAYYAGHUSA ANPPTSGMIKDCKKKVVAVHLKQTVQVDDELEIKAYYAGHUSA ANPPTSGMIKDCKKKVVAVHLKQTVQDDELEIKAYYAGHUSA ANPPTSGMIKDCKKKVVAVHLKQTVQVDDELEIKAYYAGHUSA ANPPTSGMIKDCKKKVVAVHLKQTVQDDELEIKAYYAGHUSA ANPPTSGMIKDCKKKVVAVHLKQTVQDDELEIKAYYAGHUSA ANPPTSGMIKDCKKKVVAVHLKQTVQDDELEIKAYYAGHUSA ANPPTSGMIKDCKKKVVAVHLKQTVQDDELEIKAYYAGHUSA ANPPTSGMIKDCKKKVVAVHLKQTVQDDELEIKAYYAGHUSA ANPPTSGMIKDCKKKVVAVHLKQTVQDDELEIKAYYAGHUSA ANPPTSGMIKDCKKKVVAVHLKQTVQDDELEIKAYYAGHUSA ANPPTSGMIKDCKKKVVAVHLKQTVQDDELEIKAYYAGHUSA ANPPTSGMIKDCKKKVVAVHLKQTVQDDELEIKANYYKLKUSEKKHEPIKA CHLLEFTERMENDHPOTVQCGTTGMSKANYYKLKSERAKKHEPIKA KURSTANTARASHTVLTFVALDGVAVSKMIKLSGKKLKGUPQAB ANGEGERANVANTARTARVSHIKKSUKLKOVQCHPDGSVTVESVL LQANAPSEDPOTVLLIVSMTYQDEELGSFILTSLIKKGUPQAB CARLFORDERSTARAVSHIKKSUKJAGHUSAYAGH	1			VIFELDSCNGSGKVCLVYKSGKPALAEDTEIWFLDRALYWHFLT
6214 2 460 HELAPSAIRUSARISIANGUSANAPYFVEGFRIGNSFUGNV VUGTSAKRTELFFLEKMANSSRAQUALVRAMLESKRFSAYN YRTYAVRIR INAPERIKNYKOPVEI (JUNKAKREDLGVIRRQVH IOGUYSTOKLI LERROMPRI TISMIK KOKKKUVAVHHUTOVUDDELGHILEDYRKIAVDKKGE AMPTISMIK KOKKKUVAVHHUTOVUDDELGHILEDYRKIAVDKKGE AMPTISMIK KOKKKUVAVHHUTOVUDDELGHILEDYRKIAVDKKGE LILLETYRERMILKVPI YSTOLIFEKANIYKKEJ PHTUKKRE LILLETYRERMILKVPI YSTOLIFEKANIYKKEJ PHTUKKRE LILLETYRERMILKVPI YSTOLIFEKANIYKKEJ PHTUKKRE KANFUKKRE LILLETYRERMILKVPI YSTOLIFEKANIYKKEJ PHTUKKRE KANFUKKRE LIKAPDRAPANDEGMVUPTARJEGNOLILLE LILLETYRERMILKVPI YSTOLIFEKANIYKEJ PHTUKKRE KANFUKKRE LIKAPDRAPA (KIEGELRUNCUMPANDETVILLES PUDISLIGLIKRENAGOL LIPEKAKRELIKGHI KAPDRAPANDEGMVUPTAVISJEK (LIKAPRAPA) KANFUKTINI KANFUKANIYKEJ PHTUKRIK KANFUKANIYKE LIREDOK KANFUK KANFUKANIYKE LIREDOK KANFUK KANFUKANIYKE LIREDOK KANFUK KANFUKANIYKE LIREDOK KANFUK KANFUKANIYKE KANFUKALIPADA KANFUKANIYKE KANFUKALIPADA KANFUKANIYKE KANFUKALIPADA KANFUKANIYKE KANFUKALIPADA KANFUKANIYKE KANFUKALIPADA KANFUKANIYKE KANFUKALIPADA KANFUKANIYKE KANFUKALIPADA KANFUKANIYKE KANFUKALIPADA KANFUKANIYKE KANFUKALIPADA KANFUKANIYKE KANFUKALIPADA KANFUKANIYKE KANFUKALIPADA KANFUKANIYKE KANFUKALIPADA KANFUKANIYKE KANFUKALIPADA KANFUKANIYKE KANFUKALIPADA KANFUKANIYKE KANFUKALIPADA KANFUKANIYKE KANFUKALIPADA KANFUKANIYKE KANFUK	•			DTFTAYYRLLITHLGLPQWQYAFTSYGISPQAKQRVSMYKPITY
6214 2 460 HELAPSAIREARIGIPARROGENAAPFFREGERIUGEVUM VUCTSAKTELEPTEIKMANSRAQVLAIYRAMIREKREPSYGN VUCTSAKTELEPTEIKMANSRAQVLAIYRAMIREKREPSYAN VETYAVRRIRDAFRENKIVKDPVEIQTIVMKAKRDLGVIRROVH 10QLVSTDKLI IERRIMPRT 6215 2 1849 FVÄGGFREGSERAETHPEIRVTPLOAGGODVGRSCILVSIAGKNV MLDCGHMMGFRDDRRFPDFSYTYONGRITDFLLOVIISHALDHKOL CALPYSERMOVENGDIVMTPPQAICFILLEFYKLAUPKKGE AMFETSGMIKOCMKKVVAVHLHOTVQVDBLEIEKAYVAGHVIGA AMFOIKVGSESVYTODYMMFDRHIGARNIVEPIRLOTHEVALLAUPKKGE AMFETSGMIKOCMKKVVAVHLHOTVQVDBLEIEKAYVAGHVIGA AMFOIKVGSESVYTODYMMFDRHIGARNIVEPIRLOTHEVALLAUPKKGE LILLETFREENHIKVPIPSTERITHERAMIVYKFIPSTRAULTSTEN VATTIRDSKRCRERDELKKVVETVERGGKVLIPVEAGAGGLC ILLETFREENHIKVPIPSTERITHERAMIVYKFIPSTRAULTSTEN VATTIRDSKRCRERDELKKVVETVERGGKVLIPVEAGAGGLC ILLETFREENHIKVPIPSTERITHERAMIVYKFIPSTRAULTSTEN VATTIRDSKRCRERDELKKVVETVERGGKVLIPVEAGAGGLC ILLETFREENHIKVPIPSTRAULTSTEN VATTIRDSKRCRERDELKKVVETVERGGKVLIPVEAGAGGLC ILLETFREENHIKVPIPSTRAULTSTEN VATTIRDSKRCRERDELKKVVETVERGKVLIVERSKAKKOLLOGARDEL ILLETFREENHIKVPIPSTRAULTSTEN VATTIRDSKRCHENER VERVER MOVESMESFSALADAKGINTINKVENTVORSCHALERSERPOLGEPINS GRACEGESTALTGUNGSTAULTSTEN VATTIRDSKRCHENER VATTISTEN VATTIRDSKRCHENER VATTISTEN VAT				NTNLLTEETDSFVNKLDPSKVFKSKNKIVIPKKKGPVQPAGGQK
VIGTSARGTLEFFELSKAAASSRAQVLALVERAIRLESKRFSANT YRTYAVBRIRDFFELSKAVKDPVBIQTLVIKKAKRDLGVIERQVH 16215 2 1849 FVAGGPRGSGSAAETHPEIRVTPLGAGGDVGRSCILVSIAGKRV MIDCOMMENGTHDERFPDFSITVINGRICHPIDLCVIISHPHLDH CGALPYSEMVGVGGIYATTHPTQAICPILLEDYRKIAVDKKGE ANFFISCMIKOMKKVVAVHLHOTTVUVDBLELAVYAGKULAG ANFOLKWIGSESVYTTGDYMMTPDRHLGAGANIDKCRPNLLITEST VATTIRDSKRCRERDFIKKVHETVERGGKVLITVPBALGARGLC ILLETFWERMBILKVPIYSTGLIFERGANTYKHFIPTNAGKIRKT FVQRNMTERKHIKAFDRAFADNGDMVVPATPGMLHAGGSLOIP RRWAGNEKRMVHMEGVCVGGTVCHKLLISGGRUERGRVLEKFIKK MOVEYNSFSAHADAKGIMGLWGGARPESVLLVMGEAKKMEFIKK MOVEYNSFSAHADAKGIMGLWGGARPESVLLVMGEAKKMEFIKK KEGELRUNCVMANAGEVTUHTSTSSIPVOLGIKREMAGGIL LEPAKKRRLLHGTLINKDSMFRLVSSEGALKHGLABHOLRFTC RVHLHDTRREGGTALEVYSHKASVLKOMCONDESVTESVL LQMAAPSEDPGTXVLLVSSTYODERLGSFITSLLKKGLPQABS 6216 11 393 QTTREFERSALRGSSKRAMVAVGVSSVSFLLGRSFROLGFFTX GRÜGEBGSARMKKTLTFFVALPGVAVMMLAVVLKSHGGHERPE FIAVPHLRIKTRFFPALPGVAVMMLAVVLKSHGGHERPE FIAVPHLRIKTRFFPALPGVAVMMLAVVLKSHGGHERPE FIAVPHLRIKTRFFPALPGVAVMMLAVVLKSHGGHERPE FIAVPHLRIKTRFFPALPGOSGKKKRGEGGBPGKEBGE REFEVTSCUSEVADAMCARPHEVGGRVGFREGEGGBPKEBGE LERKLF1GGLSFETTUDSLREHFEKMGTLTDCVVMMDPGVTKRSRG REFEVTSCUSEVADAMCARPHEVGGRVGFREGEGGBPKEBGE LERKLF1GGLSFETTUDSLREHFEKMGTLTDCVVMMDPGVTKRSRG REGSTYGGGGGVTOMTSMGGGGGNTGGGGGGGGGGGGGGG GGSRGSYGGGGGVTOMTSMGGGGGGNTGGGGGGGGGGGGGGGGGGGGGGGGGGGG				
VIGITSARRTRIPFFLSKMANSSRAQULALYRAMLRESKRFSAYN YNTYAVRIR INDAFERSKWIN VDVB LOTUNNAKARDLGVIRRQVH 1GQLYSTDKLI IERRIMPRT FVAGGPEGSGSSASETMPE IRVTPLGAGGDVGRSCILVSIAGKUN MLDCGMHMGFRIDDRRPPDSYITQNGRITDPLDCVITSHPHLDH CGALPYSEMVGYDGITMTHPTQAICPILLEDYRKIADVKKE ANFFISKMI KORKKVAVAHLHGTQVUDDELEVALAVYAGHUGA ANFOIK WGSESVYTTGDYMTPDRHLGAGNIDKCRPNLLITEST YATTIRDSKGRERDLKKVEHTVENGKKLI LYYAGRUGAG ANFOIK WGSESVYTTGDYMTPDRHLGAGNIDKCRPNLLITEST YATTIRDSKGRERDLKKVEHTVENGKKLI LYYAGRUGAG ANFOIK WGSESVYTTGDYMTPDRHLGAGNIDKCRPNLLITEST YATTIRDSKGRERDLKKVEHTVENGKKLI LYYAGRUGAG ANFOIK WGSESVYTTGDYMTPDRHLGAGNIDKCRPNLLITEST YATTIRDSKGRERDLKKVEHTVENGKRUT PENGLAGNGGL LILLETFMERMILKVPI YSTGLIFEKAMIYYKLP I PWITNGKRT FVORMPEFERI IKAPDRAPANDGPMVYPAT POMLHAGGSLOLF RWAGNEKMMINIMGVCVQGTVGHK.LSGORKLEMEGRQVLEVK MQVEYMSFSAHADAKSINGLUGAGPESVILLVHGRAKKMEHKKR KIEQELRVNCYMPANGETVTLPTSPS I PWEISIGLIKRENGREPIKG KIEQELRVNCYMPANGETVTLPTSPS I PWEISIGLIKRENGREPIKG KIEQELRVNCYMPANGETVTLPTSPS I PWEISIGLIKRENGREPIKG KIEQELRVNCYMPANGETVTLPTSPS I PWEISIGLIKRENGREPIKG RWHADTRIKESPLAGRATIKKSVLKDNCVQHLIPBGYVTESVL LLQNAMSBEDPOTKYLLVSWTYQDEBLGSFJLKSLGLARENGERPGGREPGGREPGGREPGGGGGAGAGGGGGAGAGGGGGAGAGGGGAAGEGGAAGAGGAAGAGGAAGAGAGAGAGAGAGAGAGAGAGAGA	6214	2	460	HBLAPSAIRRAARLGLGPARWQSRAAAFYFVRGFRTGWSFVGWV
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G215 1849 FVAGGPRGSSAREMPETRYTPLGAGODVGRSCILVSTAGKNV	1			YRTYAVRRIRDAFRENKNVKDPVEIQTLVNKAKRDLGVIRROVH
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MEDCOMEMORPDDRPSYTTONGRITDFLOCUTISHHLDM CGALPYPSEWVYDGGT YMFROTALCHEUPYRKIDVEKGE ANFFTSOMI KDCMKKVVAVHLHGTVQVDDELBIKAYVAGHULGA ANFFTSOMI KDCMKKVVAVHLHGTVQVDDELBIKAYVAGHULGA ANFFTSOMI KDCMKKVVAVHLHGTVQVDDELBIKAYVAGHULGA ANFFTSOMI KDCMKKVVAVHLHGTVQVDDELBIKAYVAGHULGA ANFOI KVGSESVVYTGDYMTDDRHLGAMIDKCRPMLLITEST YATTI RDSKRCRERDFLKKVHETVERGGKULFVFALGRAGELC FVQRNMPEFEHI KAFDRAFADNGPMVYTGCHLANGASKLIF FVQRNMPEFEHI KAFDRAFADNGPMVYTGCHLANGASKLIF RKWARGNEKMMVIMPGYCVQGTVGHKILSGGRKLEMERGQVLEVK MOVEYMFSESHADAKGINGLVGAGPEFVLUGGAKKMEFILKQ KIEQELEVNCYMPANGETVTLPTSPSIPVGISLGLIKREMAGGL LEPAKKPRILHGTLIMKDDNFFLVSSEDAKLGARBOLGTE KVHLHDTRKROSTALRVYSHLKSUKDHCVQHLPDGSVTVESVL LQDAAPSEDDGTKVLLUSWTYQDEELGSPLITSLIKKKHLPQAFS GNOEBGSARMKKTLTFVPALPGVAVSMLNVYLKSHRGHERPE FLATPHLRITTSTPPMGDOINTLEHNEHVPLPTGVEBE 6217 9 1178 TRVGRGESGLKMEVKPPFGRPPDSSGRRRRRGEEGGDVESEG GNEGEGSAGMKKLTTFVPALPGVAVSMLNVYLKSHRGHERPE FLATPHLRITTSTPPMGDOINTLEHNEHVPLPTGVEBE RKKFIGGSISFTTIDSLEHFEKWGTLOVKRDPGYKRGRG FGFVTYSCUEBVDAAMCARPHKVDGRVVEPKDAYSREGVKGGRG GRGRGGGGGGGGGGGGGGGGGGGGGGGGGGGG	6215	2	1849	FVAGGPRGSGSAAETMPEIRVTPLGAGODVGRSC11.VSTAGKNV
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ANFFTSOMINDCMKKVVAVHLHOTUQVDDELEIKAYYAGHULGA ANFOIKVGSESVYTOVINMTDRHAMADIKORRNILITEST VATTIRDSKECRERDFLKKVHETVERGGKVLIPVFALGRAGELC ILLETFMERNNLKVPIYSTGLIEKANNYYKLIPFTNTNOKIRKT FVQRNMEFFHIKAPDRAFADNSGFWVVPATPGMLHAGGSLGIF RKWAGNEKNNYTHPGYCVQGTVCHKKLSGQKKLEMEGRQVLEVK MOVETWRSFSAHADAKGIMQLUGGADE PULLVUKGHEKKKEPIKQ KIEGELRVNCYMPANGETVTLPTSPSIPVGISLGLIKREMAGGL LEPAKKPRLHGTLIMKOSNFRLVSSEQALKEGLAEHQLRFTC RVHLHDTRKEQETALRVYSHLKSUKDICVQHLPDGSVTVESVL LQANAPSEDPGTKVLLVSHTYQDEELGSFLITSLLKKGLPQAPS GAHGEGSARMWKTLTFFVALLPGVAVSHLMVYLKSHTGGHERPE FIAPHLRITRIFPFPENSALRGSSRMAVVGVSSKLJGRSRPGLGFFNSS GAHGEGSARMWKTLTFFVALLPGVAVSHLMVYLKSHTGGHERPE FIAPHLRITRIFPFPENGARGASSKAMVVGVSKLJGSRPFTCLGFFNSS GAHGEGSARMWKTLTFFVALLPGVAVSHLMVYLKSHTGGHERPE FIAPHLRITRIFPFPENGARGASKAMVGVSVSKLJGSRPFTCLGFFNSS GAHGEGSARMKTLTFFVALLPGVAVSHLMVYLKSHTGGHERPE FIAPHLRITRITRIFPENGGAHTLFINNVPLPTGYCEDG LEKKLFIGGLSFETTDDSLERHFEKMGTLTDCVMRDPGTKSRGG FGFVTYSCVEBVDAMACARPHKVDGRVDFVAVRDPGTVKSRG RGFTVTSCVEBVDAMACARPHKVDGRVDFVVBPKRAVSEDSVKFGA HLTVKKIFVGGIKEDTEYNLHDYFEKGKKIETIEVMEDROSGK KRGJAFFTFEDDHDTVDKIVVGXYHTINNCEVKALLSKGEMGS AGSGRGSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	1			CGALPYFSEMVGYDGPIYMTHPTOAICPILLEDYRKIAVDYKCE
ANFQIKVGSESVYTGDYNNTPDRHLGAAMIDKCRPNLLITEST VATTIRDSKRCRERBFLKKHPETVERKVHETVERGKUL PYPALGRAQELC ILLETFWERNNIKVPIYFSTGLTEKANHYYKLFIPHTNOKIRKT FVQRNMFEFKHIKAFDRAFADNGGMVVFATPGONLHAGGSLOIF RRWAGNEKNNYTMPGYVQGTVCHKLSGQRKLEMEERGVLEVK MQVEYMSFSAHADARGIMQLUGGABPESVLLUNGGAKKMEFIKG KIEGELRUNCYMPANGETVVILTPSSTUDTSLGLLKREMAQGL LPBAKKPRLLHGTLIMKDSNFRLVSSEQALKBEGLAEHGLRFTC RVHHHDTRKRQETALRYYSHLKSVLKDHCVQHLPDGSVYVESVL LQDAAPSEDPGTYKLLVSWTYQDEBLFJTSLLKKGLPQAPS GAHGEBGSAMMKTLTVSWSTYDEBLFJTSLLKKGLPQAPS GAHGEBGSAMMKTLTVSWTYDDEBLFJTSLLKKGLPQAPS FIAYPHLRIRTKPFPWGDGNHTLFNNPHVNPLDTGYEDR 6217 9 1178 TRVGRGESGLKWFVPFPGRFQDSGRRRRRGEGEHDPKEPE FIAYPHLRIRTKPFPWGDGNHTLFNNPHVNPLDTGYEDR 6217 9 1178 TRVGRGESGLKWFVPFPGRFQDSGRRRRRGEGHDPKEPE FIAYPHLRIRTKPFPWGDGNHTLFNNPHVNPLDTGYEDR 6217 9 1178 TRVGRGESGLKWFVPFGRFQDSGRRRRRGEGHDPKEPE FIAYPHLRIRTKPFPWGDGNHTLFNNPHVNPLDTGYEDR 6217 9 1178 TRVGRGESGLKWFVPFGRFQDSGRRRRRGEGHDPKEPE FIAYPHLRIRTKPFPWGDGNHTLFNNPHVNPLDTGYEDR 6218 TRVGRGESGLKWFYPFGRFQDSGRRRRRGGGGGYKGRG GGSRGSYGGGGGGYGGRGGGGGGGGGGGGGGGGGGG	1	[ANFFTSQMIKDCMKKVVAVHLHOTVOVDDELEIKAYVACHWICA
VATTIRDSKRCERDFLKKVHETVERGGKVLIPYFALGRAQELC				AMFQIKVGSESVVYTGDYNMTPDRHLGAAWIDKCRPNY.I.TTPGT
ILLETTMERNILKUPTYFSTEITEKANNTYKLPITPHTNOKIRKT FVORMPEFRHIR KAPRAPANDROPMUVPATDEMLHAGQSLOIF RKWAGNEKNIMVIMPGYCVQGTVGHKILSGQRKLEMEGRQVLEVK MUVEYMSFSHADANGIMQLUQGAPESUULUWGEAKKMEPIKQ KEEQELRANCYMPANAGETVTLTPETPSIPUUSIGGLKKEMBAGGL LPEAKKPRLHGTLINKOSNREUTVLTPETPSIPUUSIGGLKKEMBAGGL LPEAKKPRLHGTLINKOSNREUTVLTPSIPIPUUSIGGLKKEMBAGGL LPEAKKPRLHGTLINKOSNREUVSSCOALKBIGLAEHOLBFTC RVHLHDTURKGETJARLWYSHLKSUCHCVQHIPDGSVTVESVL LQAJAPSEDPGTKVLLVSWTYQDEELGSFLTISLLKKGDPQAPS GAHGEEGSARMWITTFVALPGVAVSMLNVYLKSHHGEHRPPE FIAYPHLRIKTRFPPMGDONHTLEHNPHVAPLDTGYEDS GAHGEEGSARMWITTFVALPGVAVSMLNVYLKSHHGEHRPPE FIAYPHLRIKTRFPPMGDONHTLEHNPHVAPLDTGYEDS REFYTYSCVERVDAAMCARPHKVDGRVVEPKRAGEEGHDPKEPEQ LRKLFIGGLSFFTTDDSLREHFEKWGTLTDCVVMRDPGTKSRG FGFVTYSCVERVDAAMCARPHKVDGRVVEPKRAGEGSEGVSKPGA HITVKKIFVGGIKEDTERVINLEDVFEKYGKTETISWEDROGGK KRGFAFTFEDHDHTVDKIVVQKYHTINGHNCSVKKALSKQEMQS AGSQRGGGSGINFMGRGGNFGGGGGFGRGGNFGRGGGFGKGG GGSRGS'GGGGDGGYNGGGGDNYGGGGNYGGGGFGKGGGGGGGGG GGSRGS'GGGGGTNGTWEGGNYGGGGNYGGGGFGRGGGGGGGGGG GGSRGS'GGGGGTNGTWEGGNYGGGGNYGGGGGFGNGGGGGGGGGGGGGGGGGGGGG				
FVQRIMPEFKHIKAFDRAFADNEGPMVVPATEGMLAGGSLQIF RRMAGNEKMNY IMPGCVQGTYGHKILSGQRKLEMEGRQVLEVK MQVEYMSFSAHADAKGIMQLVGQAEPESVLLVWGENKKMEFLKQ KIEQELRVMCYMPANGETVTLPTSPSTPUGISLGLLKREMAGGL LPEAKKPRLHGFILMKONSTRUVSSQALKBEGLAGHGURFUG RVHHHDTRKRGETALRVSHLKSVLKDHCVQHLPDGSVTVESVL LQAAAPSEDPGTKVLLVSWTYQDELGFFLUSSLKGKLDQAPS 6216 11 393 QTTRPEPRNSALRQSRSKHAVVGVSSVSRLLGRSRPQUGFPMSS GANGEEGSARMWKTLTFVALPGVAVSMLNVVLKSHHGEHERPE FIAVPHHLRIKTREPPMGGNATUHNVMPLDTGVEDR 6217 9 1178 TRVGRGESGLKMEVKPPPGRQNVGLVCVMRDPGTKSRG GFGVTVSCVEVBAAMCARPHKVDCVTCVMRDPGTKSRG FGFVTVSCVEVBAAMCARPHKVDCVTSPKRAVSREDSVKPGA HLTVKKIFVGGIKEDTEFFUNGRVFVFKRAVSREDSVKPGA HLTVKKIFVGGIKEDTEFFUNGRVFVFKRAVSREDSVKPGA AGSQRGRGGGSGNFVGRGGNFGRGGVGGGGGGGG GGSRGSVGGGGGGVNFGGGGGGGGGGGGGGGGGGGGGGGGGGGG	Ī	į		ILLETFWERNNLKVPIYFSTGLTEKANHYYKI,FI DWTNOKTDKT
RKWAGNEKNWIMPGYCVOGGTVGIKLINGGRKLEMBGRQVLEVK MOYETWAFSAHADAKIMQILVOGADEVALLWGEAKKMEPIKQ KIEQELRVNCYMPANGETVTLPTSPSIPVGISLGLLKREMAGGIL LPBAKKPRLHGTLIMKDSNFRLVSSEQALKELGLAEHGLEPTC RVHLHDTHRKGGETALRVYSHLKSVHCVGVHIPDOSVTVESVI LQNANPSEDDGTKVLLUSHTVQDEELGSFLTISLLKKGLPQAPS 6216 11 393 QTTRPEPRISALRQSKSKMAVVGVSSVSVSLIGGRSPGOSVTVESVI LQNANPSEDDGTKVLLVSHTVQDEELGSFLTISLLKKGLPQAPS 6217 9 1178 TRVGRGESGLKMBVKPPPDRPDDFSVSRLIGGRSPROGGES FIAVPHLRIKTKFPFWGDONHTLEHNPHVNPLDTGYEDS FIAVPHLRIKTKFPFWGDONHTLEHNPHVNPLDTGYEDS RKGRSGSKGMERGSGSKGMAVGVSSVSVVDYKRKAVSKEBDFVKPGA PGFVTYSCVEEVDAAMCARPHKVDGRVVDFKRAVSREDSVKPGA HLTVKKIFVGGILGEDTEEYNLRDYFEKYGKIETISVMEDROSGK KRGRAFVTFDDHDTVDKIVVQKYHTIMGHNCSVKKALSKQEMQS AGSQRGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	1	1		FVQRNMFEFKHIKAFDRAFADNPGPMVVFATPGMI.HAGGGI.OTP
MOVEYMSTSAHADAKGIMULUGADAPESULLUNGEANKMEPILKO KIEGELRUNCYM PANGETYTLTSPS I PVGISLGLIKREMAQGI LPEAKKPRLHGTLIMKDSNFRIVSSEQALKKIGLABHQILBTC RVHLHDTRKEGETALRVYSHLKSVLKDHCVQHLPDGSYTVESVI. LQAXAPSEDDGTKVLLVSWTYQBELGSFITSLIKKGUPQAPS 6216 11 393 QTTRPEPENSALRQSRSKMAVVGVSSVSRLLGRSRPQIGRPMSS GANGEBGSAKMMKTLITFYALPGVAVVKMINVYLKSHHGHERRPE FIAYPHLRIRTKPPPMGDGMTHLFHNPHVNPLPTGYEDS 6217 9 1178 TRVGRGESGLKMEVKPPPGRPQDSGRRRRRGEGHDPKEPEQ LRKLP IGGLSFETTDOSLREHFSKWGTLTDCVVMRDPQTKRSRG FGFVTYSCVEEVDAAMCARPHKVDGRVVEPKRAVSREDSVKPGA HLTVKKIFVGGIKEDTEEVNLENYFSKYKKIETIEVMEDQGSK KRGFAFVTFDDHDTVOKIVVQKYHTINGHNCGVKKALSKQEMQS AGSQRGRGGGGSGNFMGRGNFGGGGNYGGGGPGYGGG GGSRGSYGGGGGYDGYBEGONFGGGNYGGGGRYGGGGGPGYG NQGGYGGGGYDGYBEGONFGGGNYGGGGRYSFGRGGGGGPGYG GGSRGSYGGGGGYDGYBEGONFGGGNYGGGGRYDFGWSGGGPGYG NGPMKGGSFGGRSGGSFGGGGGGGGGGGGGGGGGGGGGGGGGGG		ĺ		RKWAGNEKNMVIMPGYCVOGTVGHKILSGORKTEMEGROVIEWK
KIEGELRVNCYMPANGETVILPTSPSIPVGISIGLILKREMAGGI LPERKYPRLIHGTLIMKDSNFRLVSSEQALKELGLAEHQLRFTC RVHLHDTRKRGETALRVYSHLKSVLKDHCVQHLPDGSVTVESVL LQAAAPSEDPGTKVILVSWTYQDEBLGSFITSLLKKGLPQAPS GARGEGSARMWKTLTFFVALPGVAVSMLNYVLKSHHGEHBRYPE FIAPPHRAIRTKFPPWGDGNHTLFHNPHVNPLPTGYEDB 6217 9 1178 TRVGKGEGSGLWBVKPPPGRFDGSGRRRRRGESGHDPKRPGE LRKLFIGGLSFETDDSLREHFEKWGTLTDCVVMRDPQTKRSRG FGFVTYSCVEEVDAAMCARPHKVDCRVVEPYRAVSREDSVKPGA HLTVKKIFVGGI KEDTEVYNLEVPKYKKETETSVMEDRQSG KRGAFYPTDDHDTVDKIVVQKYHTINGHNCEVKKALSKQEMQS AGSQRGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	1.			MOVEYMSFSAHADAKGIMOLVGOARPESVLIJVHGRAKKMERI,KO
LPEAKKPRLINGTLIMKOSNFRLVSSEQALKBLGLAERJCLRFTC RVHLHDTRKBQETALRVYSHLKSVKDHCVQHLPDGSVTVESVL LQNANPSEDPGTKVLLVSWTYQDEBLGSFLTSLLKKGLPQAPS 6216 11 393 GTTRPEPRNSALRQSRSKMAVVGVSSVSRLGGRSRPGLGRFMSS GAHGEEGSARMWKTLTFFVALPGVAVSMLNVYLKSHIGHERPPE FIAYPHLRIKTKFPPMGDGMHTLFHNPHVNDLPTGYEDB 6217 9 1178 TRVGRGESGLKMEVKPPPGRPQDSGRRRRRGEGGHDPKEPEQ LRKLFIGGLSFETTDDSLREHFEKWGTLTDCVVMRDPQTKRSRG FGFVTYSCVEEVDAAMCARPHKVDGRVVPPKRAVSREDSVKPGA HLTVKKIFVGGIKEDTTEVNLRDYFFKYGKTETIEVMEDRQSGK KRGPAFVPFDDHDTVDKIVVQKYHTINGHNCEVKKALSKQEMQS AGSQRGRGGSGFMFGGGGNYGGGGNYNDFGNYSGGGG GGSRGSYGGGGGYGGFGGGGNYGGGGNYNDFGNYSGQGG NYGPMKGGSFGGRSSGSPYGGGGGSGGGGGGGGGGGGGGGGGGGGGGGGG	1			KIEOELRVNCYMPANGETVTLPTSPSIPVGISLGLLKPRMAOGI.
RYHLHDTRKEGETALRVSHLKSULKDHCVQHLPDGGSVTUSJUL LQANAPSEDPGTKVLLUSHTVQDEBLGSFLTSLLKKGLPQAPS 6216 11 393 QTTRPEPRNSALRQSRSKMAVVGVSSVSRLIGRSRFQLGRPMSS GAHGEEGSARMWKTLTFVALPGVAVSMLNVYLKSHGGEHSRPQ GAHGEEGSARMWKTLTFVALPGVAVSMLNVYLKSHGGEHSRPQ FIATYPHLRIRTRFPPMGGDRTHVPNPLPTGYEDR 6217 9 1178 TRVGRGESGLKMEVKPPPGRPQFDSGRRRRRGEGGIDPKEPPG LRKLPIGGLSFETTDDSLREHFEKMGTLTDCVVMRDPCTKRSRG FGFVYSCUSEWDAMACARPHKVDGRVVEPKRAVSREDSVKPGA HLTVKKIFVGGIKEDTEEYNLRDYFEKYGKIETIEVMEDRQSGK KRGFAFVYFDDHDTVDKIVVQKYTINGHNCEVKKALSKGEMQS AGSQRGRGGSGSSMPMRGGROFGGGONFGGGROFGGGYGGG GGSRGSYGGGGGSMFMGGGNYGGGGNFGGGROFGRGGYGGG GGSRGSYGGGGGSSGSMPMGGGGNYGGGGNFGRGGRGYGGG GGSRGSYGGGGGSGSSGSMPMGGGGNYGGGGNFGRGGRGYGGG GGSRGSYGGGGGSGSGSMPMGGGGNYGGGNFGNFGNSGQQOS NYGPMKGGSFGGRSSGSPYGGGGSGSGFGRGRGGRGGGOS AGSQRGGGGGSGSGSMPGGGGNYGGGNYDDFGNYSQQQOS NYGPMKGGSFGGRSSGSPYGGGGSGGSGFGRGFGRGYGGG GGSRGSYGGGGGSGGSGSGSRFFGNADDLKRFLYKKLPSVEGLHAIVVSDRDGVFVIKVA NDNAPBHALRRGFLSTFALATDQSSKLGJSKNKSIICYXTTYQV VQYRRLPLIVVSFIASSANTGLIVSLEKELAPLPFELIRQVVEVS 6219 2 890 AGFGGGGAGGTRCAGAEAEMASAGGEDCESPAPBADRPHQRPFL IGVSGGTASGKSTVCEKIMELLGONEDCHMETLKNIVGGKTVEVP TYDFVTHSRLPETTVVYPADVVLFEGILVFYSQEIRDMFHLRLF VDTDSDVRLSRRVLRDVRRGRDEDDLMMETLKNIVGGKTVEVP TYDFVTHSRLPETTVVYPADVVLFEGILVFYSQEIRDMFHLRLF VDTDSDVRLSRRVLRDVRRGRDEDGILVFYSQEIRDMFHLRLF VDTDSDVRLSRRVLRDVRRGRDLEQUTYTTTVKAFEEFCLP TKXYADVIIFRGUDNAVAINLIVQHTQDTLMGDICKMRRGGSNG RSYKRTTSEFGDHFGMLTSGKRSHLESSRPH 6220 227 764 EQNISLEMGCTIEKALADAKALVERLDDHAAESLIEQTTALN KRVEAMKQYGETQELMEVARHRPRSTLVMGIQQGMRQIRELQO ENKELRTSLEEHQSALELIMSKYREGMFRLLANGKKDDPGIIMK LKEQHSKIDMVRRNKSEGFFLDASRTHLEAPQHGLERRHLEANQ NVH 6221 98 916 RWINDLDTVKTRLMQYDAVVNSPHRQVKGMPDTLVKTYK YEGVRGLYKGFVVGLFSTHGALQFMAYELLKLKKYNGHINRLDE AMTLCTINPLWYTKTRLMQYDAVVNSPHRQVKGMPDTLVKTYK YEGVRGLYKGFVVGLFSTHGALQFMAYELLKLKKYNGHINRLDE AQLSTVEYISVAALSKIFAVAATYPYQVVRARLQDOHMFYSGVI DVITKTWRKEGVGGFYKGIAPMLIRVTPACCTTFVVYENVSHFL	1			LPEAKKPRLLHGTLIMKDSNFRLVSSEOALKELGLAEHOLDETC
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CTTR PPRNSALRQSRSKMANVGVSSVSRLIGRSRPQLGRPMSS GAMGEGGSARMKXTLTFFVALPGVAVSMLVVLKSHHGBHERPE FIAYHLKIKTKPFPWGDONHTLFHNPHVNPLPTGYEDB 1178 TRVGRGESGLKMEVKPPPGRPQPDSGRRRRRGEEGHDPKEPEQ LRKLF IGGLSFETTDDSLREHFEKMGTLTDCVVMRDPQTKRSRG FGFVTYSCVEEVDAAMCARPHKVDGRVVEPKRAVSREDSVKPGA AGSQRGRGGGSGSINFMGGGNFGGGGNFGGRGNFGGRGGFGGGG GGSRGSYGGGGSGNFMGGGNYGGGGGNYGGGGGGGGGGGGGGGGGGGGGGGG	1			LONANPSEDPGTKVLLVSWTYODERLGSFLTSLLKKGLDONDG
GAHGEGGSARMMKTLTFFVALEGVAVSMLNVYLKSHHGEHERPE FIAYPHLRIRTKFFFWGDGMHTLFHNPHVMPLFTGYEDB TRVGRGESGLKMEVKPPFGRFQPDGSGRRRRRGEEGGHDFKEPEG LRKLF1GGLSFETTDDSLREHFEKWGTLTDCVVMRDPQTKRSRG PGFVTYSCVEBVDAAMCARPHKVDGRVYBEKRAVSEEDSVKPGA HLITVKK1FVGG1KEDTEEVNLEDVFEKKGKETF1EVMEDRQSGK KRGPAFVFFDDHDTVDK1VVQKYHTINGHNCEVKKALSKQEMQS AGSQRGGGGGGMFGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	6216	11	393	OTTRPEPRNSALROSESKMAVVCVSSVSDLLGBSDDOLCDDMSS
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STATES	1			
LRKLFIGGLSFETTDDSLREHFEKWGTLTDCVVMRDPQTKRSRG PGFVTYSCVERVDAMACRPHKVDGRVVERKAVSREDSVKPGA HLTVKKIFVGGI KEDTEYNIRDYFEKYGKIETIEVMEDRQSGK KRGPAFVTFDDHDTVDKIVVQKYHTINGHNCEVKKALSKQEMQS AGSQRGRGGGSGNFMGRGGNFGGGGGNFGRGGNFGGRGGYGGGG GGSRGS-YGGDGGYNGFGGDGNYGGGGNYNDFGNYSGQQQS NYGPMKGGSFGGSSGSPYGGGGNYGGGGNYNDFGNYSGQQQS NYGPMKGGSFGGRSGSGSGYGGRFF 6218 1305 906 SCERRGFIMADDLKRFLYKKLPSVEGLHAIVVSDDGVPVIKVA NDNAPEHALRFGFLSTFALATOQGSKLGLSKNKSIICVYNTYQV VQFNRLPLVVSFIASSSANTGLIVSLEKELAPLFEELRQVVEVS 6219 2 890 AGFGGAGAGTRCAGAEAMASAGGEDCESPAPBADREHQRPFL IGVSGGTASGKSTVCEKIMELLGQNEVEQRQRKVVILSQDRFYK VLTABQKAKALKGQYNFDHPDAFDNDLMRTLKNIVEGKTVEVP TYDFVTHSRLPETTVVYPADVVLFEGILVFYSQEIRDMFHLRLF VDTDSDVRLSRRVLRDVRRGRDLEGLITGYTTFVKPAFEERCLP TKKYADVIIPRGVDNMVAINLIVQHIQDILNGDICKWHRGGSNG RSYKRTFSEPGDHPGMLTSGKRSKLESSSRPH 6220 227 764 EQNISLENSCYTEKALADAKALVERLRDHDDAAESLIEQTTALN KRVEAMKQYQEEIQELNEVVARHPRRSTLVWGIQOEMRQIRELQQ ENKELRTSLEENGCALELINSKYREQMFRLLMASKKDDPGIIMK LKEQHSKIDMVHRNKSEGFFLDASRHILEAPQHGLERRHLEANQ NVH 6221 98 916 RWIWDLNPVSDGLELRPKYNGILHCLTTIWKLDGLRGLYQGVTP NINGAGLSWGLYFVFYNAIKSYKTEGRAERLEATEYLVSAAEAG AMTLCITNPLWVTKTRLMLQYDAVVNSPHRQYKGMPDTLVKIYK YEGURGLYKGFVPGLFGTSBALQFMAYELLKLKYNCHINRLPE AQUSTUSYISVAALSKIFAVAATYPYQVVRARLQDQHMFYSGVI DVITKTWRKECVGGFYKGIAPNLIRVTFACCITFVVYENVSHFL	6217	9	1178	
FGFVTYSCVEBVDAAMCARPHKVDGRVVEPKRAVSREDSVKPGA HLTVKKIFVGGIKEDTEEYNLRDYFEKYGKIETIEVMEDRQSGK KRGPAFVTFDHDHTVDKIVVQKYHTINGHNCEVKKALSKQEMQS AGSQRGRGGGSGNFMGRGNFGGGGNFGRGGYGGGG GGSRGSYGGGDGGYNGFGGGNFGRGGNFGGGGGGGGGGGGGGGGGGGGGGG	i i			LRKLFIGGLSFETTDDSLREHFEKWGTLTDCVVMRDDCTVDCDC
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GGSRGSYGGDGYNGFGGDGGNYGGGGNYNDFGNYGQQQS NQGGGYGGGGYDRDGNFGGNYGGGGNYNDFGNYSGQQQS NYGPMKGSFGGRSSGSPYGGGYGGGGSGGYGRFF SCERRGFIMADDLKRFLYKKLFSVEGLHAIVVSDRDGVPVIKVA NDNAPEHALRPGFLSTFALATDQGSKLGLSKNKSIICYYNTYQV VQFNRLPLVVSFIASSSANTGLIVSLEKELAPLFEELRQVVEVS 6219 2 890 AGPGEGAGAGTRCAGAEAEMASAGGEDCESPAPRADRFHCRPFL IGVSGGTASGKSTVCEKIMELLGQNEVEQRQRKVVLLSQDRFYK VLTAEQKAKALKGQYMFDHPDAFDNDLMHRTLKNIVEGKTVEVP TYDFVTHSRLPETTVVYPADVVLFEGILVFYSQEIRDMFHLRLF VDTDSDVRLSRRVLRDVRRGRDLEQILTQYTTFVKPAFEBFCLP TKKYADVIIPRGVDNWAINLIVQHIQDILNGDICKWHRGGSNG RSYKRTFSEPGDHPGMLTSGKRSHLESSSRPH KRVEAMKQYQESIQELNEVARHRPRSTLVMGIQQENRQIRELQQ ENKELRTSLEEHQSALELIMSKYREQMFRLLMASKKDDPGIIMK KRVEAMKQYQESIQELNEVARHRPRSTLVMGIQQENRQIRELQQ ENKELRTSLEEHQSALELIMSKYREQMFRLLMASKKDDPGIIMK LKEQHSKIDMVHRNKSEGFFLDASRHILEAPQHGLBRRHLEANQ NVH 6221 98 916 RWIWDLNPVSDGLELRPKYNGILHCLTTIWKLDGLRGLYQGVTP NIWGAGLSWGLYFVFYNAIKSYKTEGRAERLEATEYLVSAAEAG AMTLCITNPLWVTKTRLMLQYDAVVNSPHRQYKGMPDTLVKIYK YEGVRGLYKGFVPGLFGTSHGALQFMAYELLKLKYNQHINRLPE AQLSTVEYISVAALSKIFAVAATYPYQVVRARLQDQHMPYSGVI DVITKTWRKEGVGGFYKGIAPNLIRVTPACCITFVVYENVSHFL	1 :			AGSORGRGGGSGNFMGRGGNFGGGGGGNFGGRGGNFGGRGGVCGGG
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6224 1 133 LRTISSMAWGPLLTTLAHCTGSWAQSVLTQPFSVSGARIPHEK 6225 3259 938 LLSCHRLAICKLPFSVESRKTVMGPGGARRQAFLAFGDVTUDPT QKEWRLLSPAQRALVREVTLENYSHLVSLGILHSKYEBLIRRLEQ GEVPWGERRRRPGPCAGIYAEHVLRPKNLGLAHQRQQQLQFSD QSPOSDTAKGQEKKSTKPMAFSSPLKHAVSSRRRNSVVEIES SQQQRENPTEIDKVLKGIENSRWGAFKCAERGQDPSRKMMVIH KKAHSRQKLPTCRECHQQFRDESALLLHQNTHTGEKSYVCSVCG RGFSLKANLLRHQRTHSGEKFFLCKVCGRGYTSKSYLTVHRERTH TGEKPYECQECGRFFNDKSSYNKHLKAHSGEKPFVCKBCGRGYT NKSYFVVHKRIHSGEKPYCQECGRGFSNKSHLITHQRTHSGEK PFACRQCKQSFSVKGSLLRHQRTHSGEKPFVCKDCERSFSQKST LVVHQRTHSGEKPFVCCRGGGFIQKSTLVKHQITHGBEKPFVC KDCGRGFIQKSTFTLHQRTHSGEKPFVCKDCERGFSKSYNKH LRAHLGEKRFFCAGCGFILKSTLITHQRTHSGEKPFVCKDCERGFSKSYNKH LRAHLGEKRFFCAGCGGFILKSTLITHQRTHSGEKPFVCKDCERGFN KGGNLLTHQRTHSGEKPFVCNVCGQFSWKRSLTRHWRIHSKE KSFSLKANLLRHQWTHSGEFFNCKDCGRGFILKSTLIFHQKTH SGEKPFICSECQOGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN WKGNLLTHQRTHSGEKPFVCNVCGQFSWKRSLTRHWRIHSKE KSFVCQECKRGYTSKSDLTVHERIHTGERFYECQECGRKFSNKS YYSKHLKKRHLREKRFCTGSVGEASS 6226 29 266 TKVSELLGGSQRLFFLPWRRCCRCGLGFRVSPMAGPRVEVDGS IMEGGGGSLRVSTGLSWLLSLPWRAQRIRAGRSYA MSASSLLEGRPKGGGRKVQNGSVHQKDGLNDDDFEPYLSPQARF NNAYTAMSDSYLPSYYSPSIGFSYSLGEAMSTGGDTAMPYLTS YQQLSNGEPFLPDDAMFGQPGALGSTPFLOQHGNFYPSGIDFS AGGNNSSQGGSTQSSGYSSNYAYAPSSLGGAMIDGQSAFANETL NKAPGMNTJDGGMAALKLGSTEVASNVPKVVGSAVGGSSTSNI VASNSLPPATIAPPKPASNADIASKPAKQDYRLKTKNGLAGSSL PPPPIKHNMDIGTWDNKGPVAKAPSQALVONIGQPTQGSPQPVG QQANNSPPVAQASVGQGTQPLPPPPPPQPAQLSVQQQAAQPTRWV APRNRGSGFGHNGVDCNGVQGSQAGSGSTSSPBPHPVLEKLRISIN NYNPRDFDWNLKHRGVPIILSSVNSCHFCOVABRKSAVDTNTCAG WNSQDKWKGRFGPUVRIFYVDVSDOLRHUTENNENKSAVDTNTCAG WNSQDKWKGRFGVPVLIFYVDVSDOLRHUTENNENKSAVDTNTCAG WNSQDKWKGRFGVPVLIFYNDVSDOLRHUTENNENKSAVDTNTCAG	1]		OOVEKEOOKGVODITEC
LLSCHRLATCKLEPFSVESRKTVMGPGGARRQAFLAFGDUTUDFT OKKEWRLLSPAQRALYREVTLENYSHLVSLGILHSKFBLIRRLEQ GEVPWGERRRRPGPCAGIYABEVLLPKNIGLAHQRQQQLQFSD QSPGSDTABGQBKEKSTKRMAPSSPPLRHAVSSRRRNSVVEIES SQGRENPTEIDKVLKGIENSRWGAFKCAERGQDFSRMMVIIH KKAHSRQKLPTCRECHQGFRDESALLHONTHTGEKSYVCSVCG RGFSLKANLLRHQRTHSGEKPFLCKVCGRGYTSKSYLTVHERTH TGEKPYECQECGRFFNDKSSYNKHLXAHSGEKKFVCXECGRGYT NKSYFVVHKRIHSGEKPYRCQECGRGFSNKSHLITHGRTHSGEK PFACRQCKQSFSVKGSLLRHQRTHSGEKPFVCKDCCERSFSQKST LVYHQRTHSGEKPFVCRCQCGGFJGKSTLVKHQITHSEEKSFVC KDCGRGFJGKSFTTLHQRTHSGEKPFNCKDCGRGFTLKSSYNKH LRAHLGEKRFFCRDCGRGFTLKFNLTIHGRTHSGEKFFMCKQCE KSFSLKANLLRHQWTHSGERFPNCKDCGRGFTLKSTLFHGKTH SGGKPFICSECGQGFIWSFNLVHQLAHSGKQFFVCKECGRGFN WKGNLLTHQRTHSGEKFPVCNVCGGFSKRSLTRHWRIHSKE KSFVCQECKRGYTSKSDLTVHERIHTGERPYECQECGRKFSNKS YYSKHLKRHLREKRFCTGSVGEASS FYSCLEGGSQRLFFLDFWRRLCRCGLGFRVSPMAGPRVEVDGS INEGGGGSLRVSTGLSWLLSLPWRAQRIRAGRSYA MSASSLLEGGRPKGGGNKVQNGSVIQKDGLNDDFFSYLSFQARF NNAYTAMSDSYLPSYYSPSIGFSYSLGRAMSTGGDTAMPYLTS YCQLSNGEPHFLPDAMFQQPGALGSTPFLGGHGFFFYFSGIDFS AWGNNSSQGGSTDSSGYSSNYAYAPSSLGGMIDGGSAFANETL NKAPGMNTIDQGMAALKLGSTEVASNVPKVVGSAVGSGSITSNI VASNSLPPATIAPPKRASWADIASKPAKQOPKLKTKNGIAGSSL PPPPIKHNMDIGTWDNKGPVAKAPSQALVQNIGQPTOGSPQPVG QQANNSPPVAQASVGQOTQPLPPPPPPQLACVQQAAQPTRAV APRNRSSGFGHNGVDGNGVGQSQAGSGSTFSEPHPVLEKLRSIN NYNPKDFDMNLKHRGRVFIIKSSHFENDRINGVPTNERD WKSQDKWKGRFDVWILFSVNGSGHFCGVAEMKSAVDYNTCAG WWSQDKWKGRFDVWILFSVNGSGHFCGVAEMKSAVDVNTCAG WWSQDKWKGRFDVWNSGSHPVNSGSHFCGWAEMKSAVDVNTCAG	6224	1	133	
OKEMRLLSPAGRALYREVTLENYSHLUSLAILHSKPELIRRLEQ GEVPWGEERRRPGPCAGIYAEHVLRPKNIGLAHQROQOLOFSD QSPOSDTABGGEKEKSTKPMAPSSPPLRHAVSSRRRNSVVELES SQGQREMPTEIDKVLKGIENSRWGAFKCAERGQDFSRKMMVIIH KKAHISRQKLFTCRECHQOFRDESALLHQNTHITGEKSYVCSVCG RGFSLKANLHAHQRTHSGEKPFLCKVCGRGYTSKSYLTVHERTH TGEKFYECQECGRRFNDKSSYNKHLXAHSGEKPFVCKECGRGYT NKSYFVVHKRIHISGEKPFVCKDCCGRGFSNKSHLITHQRTHSGEKF PFACRQCKQSFSVKGSLLRHQRTHSGEKPFVCKDCERSFSQKST LVYHQRITHSGEKPFVCRCGQGFJOKSTLVKHQITHSGEKSFVCK KDCGRGFJQRSTFTLHQRTHSGEKPFVCKCCEGRFTDKSSYNKH LRAHLGEKRFFCRDCGRGFTLKFNLTHGRTHSGEKSFNCKQCE KSFSLKANLLHAHOWTHSGERPFNCKDCGRGFILKSTLLFHQKTH SGEKPFICSECGQGFIWKSNLVKHQLAHSGKQFFVCKECGRGFN WKGNLLTHQRTHSGEKPFVCNVCGGGFSWKSLTRHHWRIHSKE KFFVCQECKRGYTSKSDLTVHERIHTGERFYECQECGRKFSNKS YYSKHLKRHLREKRFCTGSVGEASS 6226 29 266 TKVSELLGGSQRLFFLPDWRRLCRCGLGPRVSPMAGPRVEVDGS IMEGGGGSLRVSTGLSHLLSLPWRAQRIRAGRSYA MSASSLLEGRFKGGGNKVQNGSVHQKDGLNDDDFEFYLSPQARP NNAYTAMSDSYLFSYYSPSIGFSYSLGERAWSTGGDTAMPYLTS YGQLSNGEPFFLPDAMFGQPGALGSTPFLGQHGFNFPFSGIDFS AMGNNSSQGSTQSSGYSSYNYAYAPSSLGGRAWSTGGDTAMPYLTS YGQLSNGEPFFLPDAMFGQPGALGSTPFLGQHGFNFPFSGIDFS AMGNNSSQGSTQSSGYSSYNYAYAPSSLGGRAWSTGGDTAMPYLTS YGQLSNGEPFFLPDAMFGQPGALGSTPFLGQHGFNFPFSGIDFS AMGNNSSQGSTQSSGYSSYNYAYAPSSLGGRAWSTGGDTAMPYLTS YGQLSNGEPFFLPDAMFGQPGALGSTPFLGQHGFNFPFSGIDFS AMGNNSSQGSTQSSGYSSYNYAYAPSSLGGAMUTGQSFARNETL NKAPGMNTIDQGMAALKLGSTEVASNVPKVVGSAVGSGSITSNI VASNSLPPATIAPPKPASWADIASKPAKQQPKLKTKNGIAGSSL PPPPIKHNMDIGTWDNKGPVAKAPSQALVQNIQQPTOGSPQPVG QQANNSPPVAQASVGQGTQSQSGSSTFSEPHPVLEKLRSIN NYNPKDFDMNLKHGRVFIIKSYSEDDIHRSIKYNIWCSTEHGNK RLDAAYRSMNGKGPVYLLFSVNGSGHFCGVABMKSAVDYNTCAG WWSQDKWKGRFDVWLIFVKNDYNSGBHFCGLABMKSAVDYNTCAG WWSQDKWKGRFDVWLIFVKNDYNSGBHFCGLABMKSAVDYNTCAG WWSQDKWKGRFDVWLIFVKNDYNSGBHFCGLABMKSAVDYNTCAG	6225	3259		LISCHRIATORIDESUESPUMUMODOCAPROARI ARCOURTER
GEVPWGEERRRPGPCAGIYABHVLRPKNIGLAHQRQQQLQFSD QSFQSDTABGQEKEKSTKPMAPSSPPLRHAVSSRRRNSVYELES SQGQREMPTEIDKVLKGIENSRWGAFKCAERGQDFSRKMWIIH KKAHSRQKLPTCRECHQGFRDESALLLHQNTHTGEKSYVCSVCG RGFSLKANLLRHQRTHSGEKFFLCKVCGRGYTSKSYLTVHERTH TGEKPYECQECGRRFADKSSYNKHLKAHSGEKPFVCKECGRGYT NKSYFVVHKRIHSGEKPYRCQECGRGFSNKSHLITHQRTHSGEK PFACRCCKQSFSVKGSLLRHQRTHSGEKPFVCKDCERSFSQKST LVYHQRTHSGEKPFVCECGCGFTQKSTLVKHQITHSEEKPFVC KDCGRGFIQKSTFTLHQRTHSEEKPYGCRECGRFFDKSSYNKH LRAHLGEKRFFCRDCGRGFTLKSNLTHQRTHSGEKPFMCKQCE KSFSLKANLLRHQWTHSGERPFNCKDCGRGFILKSTLLFHQKTH SGEKPFICSECGQGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN WKGNLLTHQRTHSGEKPFVCNVCGQGFSWKRSLTRHHWRIHSKE KPFVCQECKRGYTSKSDLTVHERIHTCERPYECQECGRFFNKS YSKHLKRHLREKRFCTGSVGEASS 6226 29 266 TKVSELLGGSQRLFFLPLWRRLCRCGLGPRVSPMAGPRVEVDGS IMEGGGSLRVSTGLSWLLSLPWRAQRIRAGRSYA MSASSLLEQRPKGQGNKVQNGSVHQKDGLNDDFFFYLSPQARP NNAYTAMSDSYLPSYYSPSIGFSYSLGEAMSTGGDTAMPYLTS YGQLSNGEPFFLPDAMFGQPGALGSTPFLGQHGFNFFPGGIDFS AWGNNTSQGGSTGSSGYSSNYAPSSLGGAMIDGQSAFANETL NKAPGMNTIDQGMAALKLGSTEVASNYKWVGSAVGSGITSNI VASNSLPPATIAPPKPASWADIASKPAKQQPKLKTKNGLAGSSL PPPPIKHNNDIGTWDNKGPVARAPSQALVQNIGQPTQGSPQPVG QQANNSPPVAQASVGQQTQPLPPPPPPPAQALSVQQQAAQPTRWV APRNRGSGFGHNGVDGNVGQSQAGSGSTSSEPHPVLEKLRSIN NYNPKDFDWNLKHGRVFIIKSYSEDDIHRSIKYNIWCSTEHGNK RLDAAYRSMNGKGPVYLLFSVWGSGHFCGVAEMKSAVDYNTCAG WSQDKWKGRFDVWIFFYKDVSWGSGHFCGVAEMKSAVDYNTCAG	1]		OKEWRII.SDAODAT.VDFUMI DAVGUI UGI ATI MOVARI TARE
QSPQSDTABGQBKEKSTKPMAPSSPPLRHAVSSRRRNSVEIES SQGQRENPTEIDKVLKGIENSRWGAFKCABRGQDFSRKMMVIIH KKAHSRQKLPTCRECHQGFRDESALLLHQNTHTGEKSYVCSVCG RGPSLKANLLRHQRTHSGEKPFLCKVCGRGYTSKSYLTVHERTH TGEK.PYECQECGRFRDKSSYNKHLKAHSGEKPFVCKECGRGYT NKSYFVVHKRIHSGEKPFVCRCCGCGFSNKSHLITHQRTHSGEK PFACRQCKQSFSVKGSLLRHQRTHSGEKPFVCKDCERSFSQKST LVYHQRTHSGEKPFVCRECGQFIQKSTLVKHQITHSEEK.PVC KDCGRGFIQKSTFTLHQRTHSGEKPFVCCKDCERSFSQKST LVYHQRTHSGEKPFVCCBCGGFILKSTLVKHQITHSEEK.PVC KDCGRGFIQKSTFTLHQRTHSGEKPFMCKQCE KSFSLKANLLRHQWTHSGERPFNCKDCGRGFILKSTLLFHQKTH SGEKPFICSECGQGFIWKSNLVXHQLAHSGKQPFVCKECGRGFN WKGNLLTHQRTHSGEKPFVCNVCGQGFSWKRSLTRHHWRIHSKE KSFSLCANLLRHQWTHSGERPFNCKDCGRGFILKSTLLFHQKTH SGEKPFICSECGQGFIWKSNLVXHQLAHSGKQPFVCKECGRGFN WKGNLLTHQRTHSGEKPFVCNVCGQGFSWKRSLTRHHWRIHSKE KSFSLCANLLRHQWTHSGERPFVCNVCGQGFSWKRSLTRHHWRIHSKE KSFSLCANLLRHQWTHSGERPFVCNVCGQGFSWKRSLTRHHWRIHSKE KSFSLCANLLRHQWTHSGERPFVCNVCGQGFSWKRSLTRHHWRIHSKE KSFSLCANLLRHQWTHSGERPFVCNCGCGFSWKSLTRHWRIHSKE KSFSLCANLLRHQWTHSGERPFVCNCGCGGRFNKS YYSKHLKRHLREKRFCTGSVGEASS 6226 29 266 TKVSELLGGSQRLFFLPDAWRQRIRAGRSYA MSASSLLEGRPKGGONKVQNGSVHQKDGLNDDDFEPYLSPQARP NNAYTAMSDSYLPSYYSPSIGFSYSLGEAWSTGGDTAMPYLTS YGQLSNGEPHFLPDAMFCQPGALGSTFFLGQHGFNFFPSGIDFS AAGNNSSQCQSTOSSGYSSNYAYAPSSLGGAMIDGQSAFANETL NKAPGMNTIDQGMAALKLGSTEVASNVPKVVGSAVGSGSITSSI VASNSLPPATIAPPKPASWADIASKAQPKLKTKNGIAGSSL PPPPIKHNMDIGTWDNKGPVALAPSQALVQNIGQPTQSPQPVG QQANNSPPVAQASVGQQTQPLPPPPPPPAQLSVQQAAQPTRNV APRNRGSGFGHNGVDGNGVGQSQAGSGSTFSEPHPVLEKLRSIN NYNPRDFDMNLKHGRVFIIKSYSEDDIHRSIKYNIWCSTEHGNK RLDAAYRSMNGKGPVYLLFSVNGSGHFTCGVAEMKSAVDYNTCAG WSQDKWKGRFDVWIFFVKDVPNSOLRHIBLENNENVENTSPD	1 1		,	GEVPWGEERRRRPGPCAGTVARUULDRYNTGLAUODOOG OFOR
SQGQRENPTEIDKULKGIENSRWGAFKCAERGQDFSRKMMVIIH KKAHSRQKLPTCRECHQGFRDESALLLHQNTHTGEKSYVCSVCG RGFSLKANLLRHQRTHSGEKPFLCKVCGRGYTSKSYLTVHERTH TGEKPYECQECGRRFNDKSSYNKHLXAHSGEKPFVCKECGRGYT NKSYFVVHKRIHSGEKPFLCEGGGFSNKSHLITHQRTHSGEK PFACRQCKGSFSVKGSLLRHQRTHSGEKPFVCKDCERSFSQKST LVYHQRTHSGEKPFVCRECGGGFIQKSTLVKHQITHSGEKPFVCK KDCGRGFIQKSTFTLHQRTHSGEKPFVCKDCGRGFRFRDKSSYNKH LRAHLGEKRFFCRDCGRGFTLKPNLTTHQRTHSGEKPFMCKQCE KSFSLKANLLRHQWTHSGERPFNCKDCGRGFILKSTLLFHQKTH SGEKPFICSECGQGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN WKGNLLTHQRTHSGEKPFVCNVCGGGFSWKRSLTRHHWRIHSKE KSFVCQECKRGYTSKSDLTVHERIHTGERPYECQECGRKFSNKS YYSKHLKRHLREKRFCTGSVGEASS FYSKHLKRHLREKRFCTGSVGEASS 1MEGGGQSLRVSTGLSWLLSLPWRAQRIRAGRSYA 6226 29 266 TKVSELLGGSQRLFFLPLWRRAQRIRAGRSYA MSASSLLEQRFKGQGNKVQNGSVHQXDGLNDDDFEPYLSPQARF NNAYTAMSDSYLPSYYSPSIGFSYSLGBAWSTGGDTAMPYLTS YCQLSNGEPHFLPDAMFGQPGALGSTPFLGQHGFNFYPSGIDFS AWGNNSSQGGSTQSSGYSSNYAYAPSSLGGAMIDGQSAFANETL NKAPGMNTIDQGMAALKLGSTEVASNVPKVVGSAVGSGSITSNI WASNSLPPATIAPPKPASWADIASKPAKQOPKLKTKNGIAGSSL PPPPIKHNMDIGTWDNKGPVAKAPSQALVQNIGQPTQGSPQPVG QQANNSPPVAQASVCQQTQPLPPPPPPQPALSVCQQAAQPTRWV APRNRGSGFGHNGVDGNGVGQSQAGSGSTPSEPHPVLEKLRSIN NYNPKDFDMNLKHGRVFIIKSYSEDDIHRSIKYNIWCSTEHGNK RLDAAYRSMNGKGPVYLLFSVNGSGHFCGVAEMKSAVDYNTCAG WWSQDKWKGRFDVWWIFVKDVPNSOLRHIRLENNENKPVTNSRD	1			OSFOSDTARGOEKEKSTKPMARGSDDI.PHAVCGPDDMCINETEC
KKAHSROKLPTCRECHQOFFDESALLHONTHTEEKSYVCSVCG RGFSLKANLLRHQRTHSGEKPFLCKVCGRGYTSKSYLTVHERTH TGEKPYEQQECGREFNDKSSYNKHLKAHSGEKPFVCKECGRGYT NKSYFVVHKRIHSGEKPFRCQECGRGFSNKSHLITHQRTHSGEK PFRACRQCKQSFSVKGSLLRHQRTHSGEKPFVCKDCGRSFSQKST LVYHQRTHSGEKPFVCRECGQGFIQKSTLVKHQITHSEEKPFVC KDCGRGFIQKSTFTLHQRTHSGEKPFVCKDCGRGFRRDKSSYNKH LRAHLGEKRFFCRDCGRGFTLKPNLTIHQRTHSGEKPFMCKQCE KSFSLKANLLHHQWTHSGERPFNCKDCGRGFILKSTLLFHQKTH SGEKPFICSECQGGFIQKSTLVKHQLAHSGKQPFVCKECGRGFN WKGNLLTHQRTHSGEKPFVCNVCGGGFSWRRSLTRHHWRIHSKE KPFVCQECKRGYTSKSDLTVHERIHTGERPYECQECGRKFSNKS YYSKHLKRHLREKRFCTGSVGEASS 6226 29 266 TKVSELLGGSQRLFFILPWRRLCRCGLGFRVSPMAGPRVEVDGS IMEGGGSLRVSTGLSWLLSLPWRAQRIRAGRSYA MSASSLLEQRPKGQGNKVQNGSVHQXDGLNDDDFEPYLSPQARP NNAYTAMSDSYLPSYYSPSIGFSYSLGEAMSTGGDTAMPYLTS YGQLSNGEPHFLPDAMFGQPGALGSTPFLQQHGFNFYPSGIDFS AWGNNSSQGGSTOSSGYSSNYAYAPSSLGGAMIDGQSAPANETL NKAPGMNTIDQGMAALKLGSTEVASNVPKVVGSAVGSGSITSNI WASNSLPPATIAPPKPASWADIASKPAKQQPKLKTKNGIAGSSL PPPPIKHNMDIGTWDNKGPVAKAPSQALVQNIGQPTGGSPQPVG QQANNSPPVAQASVCQQTQPLPPPPPPQPAQLSVQQQAAQPTRNV APRNRGSGFGHNGVDGNGVGQSQAGSGSTPSEPHPVLEKLRSIN NYNPKDFDMNLKHGRVFIIKSYSEDDIHRSIKYNIWCSTEHGNK RLDAAYRSMNGKGPVYLLFSVNGSGHFCGVAEMKSAVDYNTCAG WWSQDKWKGRFDVWWIFVKDVPNSOLRHIRLENNENDVYNTNSPD				SOGORENPTEIDKVI.KGIENSPWGAEKCAPPGODECPWMWITTU
RGFSLKANLLRHQRTHSGEKPFLCKVCGRGYTSKSYLTVHERTH TGEKPYECQECGRFFNDKSSYNKHLKAHSGEKPFVCKECGRGYT NKSYFVVHKRIHSGEKPYRCQECGRGFSNKSHLITHQRTHSGEK PFACRQCKQSFSVKGSLRHQRTHSGEKPFVCKDCERSFSQKST LVYHQRTHSGEKPFVCRECGQGFIQKSTLVKHQITHSBEKPFVC KDCGRGFIQKSTFTLHQRTHSGEKPFVCRCCERFRDKSSYNKH LRAHLGEKRFFCRDCGRGFTLKPNLTIHQRTHSGEKPFMCKQCE KSFSLKANLLRHQWTHSGERPFNCKDCCRGFILKSTLLFHQKTH SGEKPFICSECGQGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN WKGNLLTHQRTHSGEKPFVCNVCGQGFSWKRSLTRHHWRIHSKE KFFVCQECKRGYTSKSDLTVHERIHTGERPFECQECGRKFSNKS YYSKHLKRHLREKRFCTGSVGEASS 6226 29 266 TKVSELLGGSQRLFFLPLWRRLCRCGLGPRVSPMAGPRVEVDGS IMEGGGQSLRVSTGLSWLLSLPWRAQRIRAGRSYA NASSELLEGRFKGQGNKVQNGSVHQKDGLNDDDFEPYLSPQARP NNAYTAMSDSYLPSYYSPSIGFSYSLGEAMSTGGDTAMPYLTS YGQLSNGEPHFLPDAMFQQPGALGSTFFLGOHGFN*PPSGIDFS AWGNNSSQGQSTQSSGYSSNYAYAPSSLGGAMIDGQSAFANSTL NKAPGMNTIDQCMAALKLGSTEVASNVPKVVGSAVGSGSITSNI VASNSLPPATIAPPKPASWADIASKPAKQOPKLKTKNGIAGSSL PPPPIKHNMDIGTWDNKGPVAKAPSQALVQNIGQPTQGSPQPVG QQANNSPPVAQASVGQQTQPLPPPPPPPPAQALVQNIGQPTGGSPQPVG QQANNSPPVAQASVGQQTQPLPPPPPPPAQALVQNIGQPTGGSPQPVG QQANNSPPVAQASVGQQTQPLPPPPPPPAQASVQQAAQPTTRNV APRNRGSGFGHNGVDGNUGGSGGSTPSEPHPVLEKLRSIN NYNPKDFDMNLKHGRVFIIKSVNGSGHFCGVAEMKSAVDYNTCAG WSQDKWKGRFDVRNIFVKDVYNSOLRHIRLENNENKPVTNSRD				KKAHSROKLFTCRECHOGFRDESALLTHONTHTGPKSVVCSVCC
TGEKPYECGEGGRENDKSSYNKHLXAHSGEKPFVCKECGRGYT NKSYFVVHKRIHSGEKPYRCQEGGGFSNKSHLITHORTHSGEK PFACRQCKQSFSVKGSLLRHQRTHSGEKPFVCKDCERSFSQKST LVYHQRTHSGEKPFVCRECGGFJQKSTLVKHQITHSEEKPFVC KDCGRGFIQKSTFTLHQRTHSEEKPYGCRECGRFRDKSSYNKH LRAHLGERFFFCRDCGRGFTLKFNLTIHQRTHSGEKPFMCKQCE KSFSLKANLLRHQWTHSGERPFNCKDCGRGFILKSTLLFHQKTH SGEKPFICSECGOGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN WKGNLLTHQRTHSGEKPFVCNVCGQGFSWKRSLTRHWRIHSKE KFFVCQBCKRGYTSKSDLTVHERIHTGERPYECQECGRKFSNKS YYSKHLKRHLREKRFCTGSVGEASS 6226 29 266 TKVSELLGGSQRLFFLPLWRRLCRCGLGPRVSPMAGGRVEVDGS IMEGGGQSLRVSTGLSWLLSLPWRAQRIRAGRSYA MSASSLLEQRPKGGNKVQNGSVHQKDGLNDDDFEPYLSPQARP NNAYTAMSDSYLPSYYSPSIGFSVSLGEAMSTGGDTAMPYLTS YGQLSNGEPHFLPDAMFGQPGALGSTPFLGQHFNFPFSGIDFS AWGNNSSQGSTOSSGYSSNYAYAPSSLGGAMIDGGSAFANETL NKAPGHNTIDQGMAALKLGSTEVASNVPKVVGSAVGSSITSNI VASNSLPPATIAPPKPASWADIASKPAKQOPKLKTKNGIAGSSL PPPPIKHNMDIGTWDNKGPVAKAPSQALVQNIGQPTQGSPQPVG QQANNSPPVAQASVGQQTQPLPPPPPPQPAQLSVQQQAAQPTRWV APRNRGSGFGHNGVDGNGVGQSQAGSGSTPSEPHPVLEKLRSIN NYNPKDFDWNLKHGRVPIIKSYSEDDIHRSIKYNIWCSTBHGNK RLDAAYRSMNGKGPVYLLFSVNGSGHFCGVAEMKSAVDYNTCAG WSQDKWKGRFDVRWIFYKDVPNSOLRHIRLENNENKPYNNSPD				RGFSLKANLLRHORTHSGEKPFLCKVCGRGYTSKSYLTVHEDTU
NKSYFVUHKRIHSGEKPYRCQECGRGFSNKSHLITHQRTHSGEK PFACRQCKQSFSVKGSLLRHQRTHSGEKPFVCKDCERSFSQKST LVYHQRTHSGEKPFVCRECGQGFIQKSTLVKHQITHSEEKPFVC KDCGRGFIQKSTFTTLHQRTHSGEKPFVCKDCERSFSQKST LVYHQRTHSGEKPFVCRECGGFIQKSTLVKHQITHSEEKPFVC KDCGRGFIQKSTFTTLHQRTHSGEKPFVCRCQCE KSPSLKANLLRHQWTHSGERPFNCKDCGRGFILKSTLLFHQKTH SGEKPFICSECGQGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN WKGNLLTHQRTHSGEKPFVCNVCGQGFSWKRSLTRHHWRIHSKE KFFVCQBCKRGYTSKSDLTVHERIHTGERPYECQECGRKFSNKS YYSKHLKRHLREKRFCTGSVGEASS 6226 29 266 TKVSELLGGSQRLFFLPLWRRLCRCGLGPRVSPMAGPRVEVDGS IMEGGGQSLRVSTGLSWLLSLPWRAQRIRAGRSYA NNAYTAMSDSYLPSYSPSIGFSYSLGEAAWSTGGDTAMPYLTS YGQLSNGEPHFLPDAMFQQPGALGSTPFLQHGFNFFPSGIDFS AWGNNSSQGQSTQSSGYSSNYAYAPSSLGGAMIDGQSAFANETL NKAPGMNTIDQGMAALKLGSTEVASNVPKVVGSAVGSGSITSNI VASNSLPPATIAPPKPASWADIASKPAKQQPKLKTKNGIAGSSL PPPPIKHNMDIGTWDNKGPVAKAPSQALVQNIGQPTQGSPQPVG QQANNSPPVAQASVGQQTQPLPPPPPPPAPALSVQQQAAQPTRWV APRNRGSGFGINGVDGNGVGQSQAGSGSTPSEPHPVLEKLRSIN NYNPKDFDWNLKHGRVIIKSYSEDDIHRSIKYNIWCSTBHGNK RLDAAYRSMNGKGPVYLLFSVNGSGHFCGVAEMKSAVDYNTCAG WWSQDKWKGRPDVRWIFYKDVPNSOLRHIRLENNENKPYTNSPD	1			TGEKPYECOECGRRFNDKSSYNKHLKAHSGRKDEVCKECGPGVT
PFACROCKOS FSVKGSLLRHQRTHSGEKPFVCKDCERS FSQKST LVYHQRTHSGEKPFVCRECGOGFIQKSTLVKHQITHSEEK?FVC KDCGRGFIQKSTFTLHQRTHSEEKPYGCRECGRFRDKSSYNKH LRAHLGEKRFFCRDCGRGFTLKPNLTIHQRTHSGEKPFMCKQCE KSFSLKANLLRHQWTHSGERPFNCKDCGRGFILKSTLLFHQKTH SGEKPFICSECGQGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN WKGNLLTHQRTHSGEKPFVCNVCGQGFSWKRSLTRHHWRIHSKE KPFVCQECKRGYTSKSDLTVHERIHTGERPYECQECGRKFSNKS YYSKHLKRHLREKRFCTGSVGEASS 6226 29 266 TKVSELLGGSQRLFFLPLWRRLCRCGLGPRVSPMAGPRVEVDGS IMEGGGQSLRVSTGLSWLLSLPWRAQRIRAGRSYA MSASSLLEQRPKGQGNKVQNGSVHQKDGLNDDDFEPYLSPQARP NNAYTAMSDSYLPSYYSPSIGFSYSLGEAAWSTGGDTAMPYLTS YGQLSNGEPHFLPDAMFGQPGALGSTFFLGQHGFN*FPSGIDFS AWGNNSSQGSTGSSGYSSNYAYAPSSLGGAMIDGQSAFANETL NKAPGMNTIDQGMAALKLGSTEVASNVPKVVGSAVGSGSITSNI VASNSLPPATIAPPKPASWADIASKPAKQOPKLKTKNGIAGSSL PPPPIKHNMDIGTWDNKGPVAKAPSQALVQNIGQPTQGSPQPVG QQANNSPPVAQASVGQQTQPLPPPPPPQPAQLSVQQAAQPTRWV APRNRGSGFGHNGVDGNGVGQSQAGSGSTPSEPHPVLEKLRSIN NYNPKDFDWNLKHGRVFIIKSYSEDDIHRSIKYNIWCSTEHGNK RLDAAYRSMNGKGPVYLLFSVNGSGHFCGVAEMKSAVDYNTCAG WWSQDKWKGRFDVRWIFVKDVPNSOLRHIRLENNENKPYTNSRD		ļ		NKSYFVVHKRIHSGEKPYRCOECGRGFSNKSHIJTHORTHSGEK
LVYHQRTHSGEKPFVCRECGQGFIQKSTLVKHQITHSEEK?PVC KDCGRGFIQKSTFTLHQRTHSEEKPYGCRECGRRFRDKSSYNKH LRAHLGEKRFFCRDCGRGFTLKFNLTIHQRTHSGEKPFMCKQCE KSPSLKANLLRHQWTHSGERPFNCKDCGRGFILKSTLLFHQKTH SGEKPFICSECGQGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN WKGNLLTHQRTHSGEKPFVCNVCGQGFSWKRSLTRHHWRIHSKE KPFVCQECKRGYTSKSDLTVHERIHTGERPYECQECGRKFSNKS YYSKHLKRHLREKRFCTGSVGEASS 6226 29 266 TKVŠELLGGSQRLFFLPLWRRLCRCGLGPRVSPMAGPRVEVDGS IMEGGGQSLRVSTGLSWLLSLDWRAQRIRAGRSYA 6227 2581 890 MSASSLLEQRPKGQGNKVQNGSVHQKDGLNDDDFEPYLSPQARP NNAYTAMSDSYLPSYYSPSIGFSYSLGEAAWSTGGDTAMPYLTS YGQLSNGEPHFLPDAMFQQPGALGSTPFLQHGFN*PPSGIDFS AWGNNSSQGSTQSSGYSSNYAPAPSSLGGAMIDGQSAFANETL NKAPGMNTIDQGMAALKLGSTEVASNVPKVVGSAVGSGSITSNI VASNSLPPATIAPPKPASWADIASKPAKQOPKLKTKNGIAGSSL PPPPIKHNMDIGTWDNKGPVAKAPSQALVQNIGQPTQGSPQPVG QQANNSPPVAQASVGQQTQPLPPPPPPQPAQLSVQQAAQPTRWV APRNRGSGFGHNGVDGNGVGQSQAGSGSTPSEPHPVLEKLRSIN NYNPKDFDWNLKHGRVFIIKSYSEDDIHRSIKYNIWCSTEHGNK RLDAAYRSMNGKGPVYLLFSVNGSGHFGGVAEMKSAVDYNTCAG WWSQDKWKGRFPVRWIFVKDVPNSCDRHIRLENNENKPVTNSRD	1 1			PFACRQCKQSFSVKGSLLRHORTHSGEKPFVCKDCERSFSOKST
KDCGRGFIQKSTFTLHQRTHSEEKPYGCRECGRRFRDKSSYNKH LRAHLGEKRFFCRDCGRGFTLKPNLTTHQRTHSGEKPFMCKQCE KSFSLKANLLRHQWTHSGERPFNCKDCGRGFILKSTLLFHQKTH SGEKPFICSECGQGFTMKSNLVKHQLAHSGKQPFVCKECGRGFN WKGNLLTHQRTHSGEKPFVCNVCGQGFSWKRSLTRHHWRIHSKE KPFVCQECKRGYTSKSDLTVHERIHTGERPYECQECGRKFSNKS YYSKHLKRHLREKRFCTGSVGEASS 6226 29 266 TKVŠELLGGSQRLFFLPLWRLCRCGLGPRVSPMAGPRVEVDGS IMEGGGQSLRVSTGLSWLLSLPWRAQRIRAGRSYA 6227 2581 890 MSASSLLEQRPKGQCNKVQNGSVHQKDGLNDDDFEPYLSPQARP NNAYTAMSDSYLPSYYSPSIGFSYSLGEAAWSTGGDTAMPYLTS YGQLSNGEPHFLPDAMFQQPGALGSTPFLQQHGFNFFPSGIDFS AWGNNSSQGQSTGSSGYSSNYAYAPSSLGGAMIDGQSAFANETL NKAPGMNTIDQGMAALKLGSTEVASNVPKVVGSAVGSGSITSNI VASNSLPPATIAPPKPASWADIASKPAKQQPKLKTKNGIAGSSL PPPPIKHNMDIGTWDNKGPVAKAPSQALVQNIGQPTQGSPQPVG QQANNSPPVAQASVGQQTQPLPPPPPPQPAQLSVQQAAQPTRWV APRNRGSGFGHNGVDGNGVGQSQAGGSGTPSEPHPVLEKLRSIN NYNPKDFDWNLKHGRVFIIKSYSEDDIHRSIKYNIWCSTEHGNK RLDAAYRSMNGKGPVYLLFSVNGSGHFGGVAEMKSAVDYNTCAG VWSQDKWKGRFFDVRWIFVKDVPNSCDRHIRLENNENKPVTNSRD				LVYHQRTHSGEKPFVCRECGQGFIQKSTLVKHOITHSEEKPFVC
LRAHLGEKRFFCROCGRGFTLKPNLTIHQRTHSGEKPFMCKQCE KSFSLKANLLRHQWTHSGERPFNCKDCGRGFILKSTILFHQKTH SGBKPFICSECGQGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN WKGNLLTHQRTHSGEKPFVCNVCGQGFSWKRSLTRHHWRIHSKE KPFVCQECKRGYTSKSDLTVHERIHTGERPYECOECGRKFSNKS YYSKHLKRHLREKRFCTGSVGEASS 6226 29 266 TKVSELLGGSQRLFFLPLWRRLCRCGLGFRVSPMAGPRVEVDGS IMEGGGQSLRVSTGLSWLLSLPWRAQRIRAGRSYA NASSSLLEGRPKGGONKVQNGSVHQKDGLNDDDFEPYLSPQARF NNAYTAMSDSYLPSYYSPSIGFSYSLGEAWSTGGDTAMPYLTS YGQLSNGEPHFLPDAMFQQPGALGSTPFLQQHGFNFFPSGIDFS AWGNNSSQGQSTQSSGYSSNYAYAPSSLGGAMIDGQSAFANETL NKAPGMNTIDQGMAALKLGSTEVASNVPKVVGSAVGSGSITSNI VASNSLPPATIAPPKPASWADIASKPAKQQPKLKTKNGIAGSSL PPPPIKHNMDIGTWDNKGPVAKAPSQALVQNIGQPTQGSPQPVG QQANNSPPVAQASVGQQTQPLPPPPPQPAQLSVQQAAQPTRWV APRNRGSGFGHNGVDGNGVGQSQAGSGSTPSEPHPVLEKLRSIN NYNPKDTDWNLKHGRVFIIKSYSEDDIHRSIKYNIWCSTEHGNK RLDAAYRSMNGKGPVYLLFSVNGSGHFGVAEMKSAVDYNTCAG WWSQDKWKGRFFDVRWIFVKDVPNSCDLRHIRLENNENKPVTTNSRD				KDCGRGFIQKSTFTLHQRTHSEEKPYGCRECGRRFRDKSSYNKH
KSFSLKANLLRHQWTHSGERPFNCKDCGRGFILKSTLLFHQKTH SGEKPFICSECGQGFIWKSNLVWHQLAHSGKQPFVCKECGRGFN WKGNLLTHQRTHSGEKPFVCNVCGQGFSWKRSLTRHHWRIHSKE KPFVCQECKRGYTSKSDLTVHERIHTGERPYECQECGRKFSNKS YYSKHLKRHLREKRFCTGSVGEASS 6226 29 266 TKVSELLGGSQRLFFLPLWRRLCRCGLGPRVSPMAGPRVEVDGS IMEGGGQSLRVSTGLSWLLSLPWRAQRIRAGRSYA 6227 2581 890 MSASSLLEQRPKGQGNKVQNGSVHQKDGLNDDDFEPYLSPQARP NNAYTAMSDSYLPSYYSPSIGFSYSLGEAWSTGGDTAMPYLTS YGQLSNGEPHFLPDAMFGQPGALGSTPFLQHGFNFPFSGTDFS AWGNNSSQGSTQSSGYSSNYAYAPSSLGGAMIDGQSAFANETL NKAPGMNTIDQGMAALKLGSTEVASNVPKVVGSAVGSGSITSNI VASNSLPPATIAPPKPASWADIASKPAKQOPKLKTKNGIAGSSL PPPPIKHNMDIGTWDNKGPVAKAPSQALVQNIGQPTQGSPQPVG QQANNSPPVAQASVGQQTQPLPPPPPPPPAQLSVQQAAQPTRWV APRNRGSGFGHRGVDGNGVQGSQAGSGSTPSEPHPVLEKLRSIN NYNPKDFDWNLKHGRVFIIKSYSEDDIHRSIKYNIWCSTEHGNK RLDAAYRSMNGKGPVYLLFSVNGSGHFCGVAEMKSAVDYNTCAG VWSQDKWKGRFDVRWIFVKDVPNSCDRHIRLENNENKPVTNSRD				LRAHLGEKRFFCRDCGRGFTLKPNLTIHORTHSGEKPFMCKOCE
SGEKPICSECGQGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN WKGNLLTHQRTHSGEKPFVCNVCGQGFSWKRSLTRHHWRIHSKE KPFVCQECKRGYTSKSDLTVHERIHTGERPYECQECGRKFSNKS YYSKHLRRHLREKRFCTGSVGEASS 6226 29 266 TKVSELLGGSQRLFFLPLWRRLCRCGLGPRVSPMAGPRVEVDGS IMEGGGQSLRVSTGLSWLLSLPWRAQRIRAGRSYA MSASSLLEQRPKGQGNKVQNGSVHQKDGLNDDDFEPYLSPQARP NNAYTAMSDSYLPSYYSPSIGFSYSLGEAAWSTGGDTAMPYLTS YGQLSNGEPHFLPDAMFQQPGALGSTFFLQQHGFNFPSGIDFS AWGNNSSQGSTQSSGYSSNYAYAPSSLGGAMIDGQSAFANETL NKAPGMNTIDQGMAALKLGSTEVASNVPKVVGSAVGSGSITSNI VASNSLPPATIAPPKPASWADIASKPAKQOPKLKTKNGIAGSSL PPPPIKHNMDIGTWDNKGPVAKAPSQALVQNIGQPTQGSPQPVG QQANNSPPVAQASVGQQTQPLPPPPPPQPAQLSVQQAAQPTRWV APRNRGSGFGHNGVDGNGVGQSQAGSGSTFSEPHPVLEKLRSIN NYNPKDFDWNLKHGRVFIIKSYSEDDIHRSIKYNIWCSTEHGNK RLDAAYRSMNGKGPVYLLFSVNGSGHFGGVAEMKSAVDYNTCAG VWSQDKWKGRFDVRWIFVKDVPNSCDLRHIRLENNENKPVTNSRD	j j	·		KSFSLKANLLRHQWTHSGERPFNCKDCGRGFILKSTLLFHOKTH
WKGNLTHQRTHSGEKPFVCNVCGQGFSWKRSLTRHHWRIHSKE KPFVCQECKRGYTSKSDLTVHERIHTGERPYECQECGRKFSNKS YYSKHLKRHLREKRFCTGSVGEASS 6226 29 266 TKVŠELLGGSQRLFFLPLWRRLCRCGLGPRVSPMAGPRVEVDGS IMEGGGQSLRVSTGLSWLLSLPWRAQRIRAGRSYA MSASSLLEQRPKGQGNKVQNGSVHQKDGLNDDDFEPYLSPQARP NNAYTAMSDSYLPSYYSPSIGFSYSLGEAAWSTGGDTAMPYLTS YCQLSNGEPHFLPDAMFGQPGALGSTFFLGQHGFN*FPSGIDFS AWGNNSSQGSTGSSGYSSNYAPAPSSLGGAMIDGQSAFANETL NKAPGMNTIDGGMAALKLGSTEVASNVPKVVGSAVGSGSITSNI VASNSLPPATIAPPKPASWADIASKPAKQOPKLKTKNGIAGSSL PPPPIKHNMDIGTWDNKGPVAKAPSQALVQNIGQPTQGSPQPVG QQANNSPPVAQASVGQQTQPLPPPPPPQPAQLSVQQAAQPTRWV APRNRGSGFGHNGVDGNGVGQSQAGSGSTPSEPHPVLEKLRSIN NYNPKDFDWNLKHGRVFIIKSYSEDDIHRSIKYNIWCSTEHGNK RLDAAYRSMNGKGPVYLLFSVNGSGHFCGVAEMKSAVDYNTCAG VWSQDKWKGRFDVRWIFVKDVPNSCDRHIRLENNENKPVTNSRD	j			SGEKPFICSECGQGFIWKSNLVKHQLAHSGKOPFVCKECGRGFN
KPFVCQECKRGYTSKSDLTVHERIHTGERPYECQECGRKPSNKS YYSKHLKRHLREKRFCTGSVGEASS 6226 29 266 TKVSELLGGSQRLFFLPLWRRLCRCGLGPRVSPMAGPRVEVDGS IMEGGGQSLRVSTGLSWLLSLPWRAQRIRAGRSYA 6227 2581 890 MSASSLLEQRPKGQGNKVQNGSVHQKDGLNDDDFEPYLSPQARP NNAYTAMSDSYLPSYYSPSIGFSYSLGEAAWSTGGDTAMPYLTS YGQLSNGEPHFLPDAMFQQPGALGSTPFLGQHGFN**PPSGIDFS AWGNNSSQGQSTQSSGYSSNYAYAPSSLGGAMIDGQSAFANETL NKAPGMNTIDQGMAALKLGSTEVASNVPKVVGSAVGSGSITSNI VASNSLPPATIAPPKPASWADIASKPAKQQPKLKTKNGIAGSSL PPPPIKHNMDIGTWDNKGPVAKAPSQALVQNIGQPTQGSPQPVG QQANNSPPVAQASVGQQTQPLPPPPPPQPAQLSVQQAAQPTRWV APRNRGSGFGHNGVDGNGVGQSQAGSGSTPSEPHPVLEKLRSIN NYNPKGSFGHNGVFFIIKSYSEDDIHRSIKYNIWCSTEHGNK RLDAAYRSMNGKGPVYLLFSVNGSGHFGGVAEMKSAVDYNTCAG VWSQDKWKGRFFDVRWIFVKDVPNSCDLRHIRLENNENKPYTNSRD	1			WKGNLLTHQRTHSGEKPFVCNVCGQGFSWKRSLTRHHWRIHSKE
TYSKHLREHIREKRECTGSVGEASS TKVSELLGGSQRLFFLPLWRRLCRCGLGPRVSPMAGPRVEVDGS IMEGGGQSLRVSTGLSWLLSLPWRAQRIRAGRSYA 6227 2581 890 MSASSLLEGGPRKGQGNKVQNGSVHQKDGLNDDDFEPYLSPQARP NNAYTAMSDSYLPSYYSPSIGFSYSLGEAWSTGGDTAMPYLTS YGQLSNGEPHFLPDAMFQQPGALGSTPFLQQHGFNFFPSGIDFS AWGNNSSQGQSTQSSGYSSNYAYAPSSLGGAMIDGQSAFANETL NKAPGMNTIDQGMAALKLGSTEVASNVPKVVGSAVGSGSITSNI VASNSLPPATIAPPKPASWADIASKPAKQQPKLKTKNGIAGSSL PPPPIKHNMDIGTWDNKGPVAKAPSQALVQNIGQPTQGSPQPVG QQANNSPPVAQASVGQQTQPLPPPPPQPAQLSVQQAAQPTRWV APRNRGSGFGHNGVDGNGVGQSQAGSGSTPSEPHPVLEKLRSIN NYNPKDTDWNLKHGRVFIIKSYSEDDIHRSIKYNIWCSTEHGNK RLDAAYRSMNGKGPVYLLFSVNGSGHFGGVAEMKSAVDYNTCAG VWSQDKWKGRFDVRWIFVKDVPNSCDRHIRLENNENKPVTNSRD	1		ļ	KPFVCQECKRGYTSKSDLTVHERIHTGERPYECQECGRKFSNKS
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NNAYTAMSDSYLPSYYSPSIGFSYSLGEAMWSTGGDTAMPYLTS YGQLSNCEPHFLPDAMFGQPGALGSTPFLGQHGFN*PPSGIDFS AWGNNSSQGQSTQSSGYSSNYAYAPSSLGGAMIDGQSAFANETL NKAPGMNTIDQGMAALKLGSTEVASNVPKVVGSAVGSGSITSNI VASNSLPPATIAPPKPASWADIASKPAKQQPKLKTKNGIAGSSL PPPPIKHNMDIGTWDNKGPVAKAPSQALVQNIGQPTQGSPQPVG QQANNSPPVAQASVGQQTQPLPPPPPQPAQLSVQQQAAQPTRWV APRNRGSGFGHNGVDGNGVGQSQAGSGSTPSEPHPVLEKLRSIN NYNPKDFDWNLKHGRVFIIKSYSEDDIHRSIKYNIWCSTEHGNK RLDAAYRSMNGKGPVYLLFSVNGSGHFCGVAEMKSAVDYNTCAG VWSQDKWKGRFDVRWIFVKDVPNSOLRHIRLENNENKPVTNSRD	6227			IMEGGGQSLRVSTGLSWLLSLPWRAQRIRAGRSYA
NNAYTAMSDSYLPSYYSPSIGFSYSLGEAAWSTGGDTAMPYLTS YGQLSNGEPHFLPDAMFQQPGALGSTPFLQQHGFN*PPSGIDFS AWGNNSSQGSTQSSGYSSNYAYAPSSLGGAMIDGQSAFANETL NKAPGMNTIDQGMAALKLGSTEVASNVPKVVGSAVGSGSITSNI VASNSLPPATIAPPKPASWADIASKPAKQOPKLKTKNGIAGSSL PPPPIKHNMDIGTWDNKGPVAKAPSQALVQNIGQPTQGSFQPVG QQANNSPPVAQASVGQQTQPLPPPPPQPAQLSVQQQAAQPTRWV APRNRGSGFGHNGVDGNGVGQSQAGSGSTPSEPHPVLEKLRSIN NYNPKDFDWNLKHGRVFIIKSYSEDDIHRSIKYNIWCSTEHGNK RLDAAYRSMNGKGPVYLLFSVNGSGHFGGVAEMKSAVDYNTCAG VWSQDKWKGRFDVRWIFVKDVPNSOLRHIRLENNENKPVTNSPD	044/	2581	890	MSASSLLEQRPKGQGNKVQNGSVHQKDGLNDDDFEPYLSPQARP
YGQLSNGEPHFLPDAMFGQPGALGSTPFLGQHGFNFFPSGIDFS AWGNNSSQGQSTQSSGYSSNYAYAPSSLGGAMIDGQSAFANETL NKAPGMNTIDQGMAALKLGSTEVASNVPKVVGSAVGSGSITSNI VASNSLPPATIAPPKPASWADIASKPAKQQPKLKTKNGIAGSSL PPPPIKHNMDIGTWDNKGPVAKAPSQALVQNIGQPTQGSPQPVG QQANNSPPVAQASVGQQTQPLPPPPPPQPAQLSVQQAAQPTRWV APRNRGSGFGHNGVDGNGGGGGGGSTPSEPHPVLEKLRSIN NYNPKGDFDWNLKHGRVFIIKSYSEDDIHRSIKYNIWCSTEHGNK RLDAAYRSMNGKGPVYLLFSVNGSGHFGGVAEMKSAVDYNTCAG VWSQDKWKGRFDVRWIFVKDVPNSOLRHIRLENNENKPVTNSPD			ļ	NNAYTAMSDSYLPSYYSPSIGFSYSLGEAAWSTGGDTAMPYLTS
AWGNNSSQGQSTQSSGYSSNYAYAPSSLGGAMIDGQSAFANETL NKAPGMNTIDQGMAALKLGSTEVASNVPKVVGSAVGSGSITSNI VASNSLPPATIAPPKPASWADIASKPAKQQPKLKTKNGIAGSSL PPPPIKHNMDIGTWDNKGPVAKAPSQALVQNIGQPTQGSPQPVG QQANNSPPVAQASVGQTQPLPPPPPQPAQLSVQQQAAQPTRWV APRNRGSGFGHNGVDGNGVGQSQAGSGSTPSEPHPVLEKLRSIN NYNPKDFDWNLKHGRVFIIKSYSEDDIHRSIKYNIWCSTEHGNK RLDAAYRSMNGKGPVYLLFSVNGSGHFCGVAEMKSAVDYNTCAG VWSQDKWKGRFDVRWIFVKDVPNSOLRHIRLENNENKPVTNSPD	1 1		1	YGQLSNGEPHFLPDAMFGQPGALGSTPFLGQHGFNFFPSGIDFS
NKAPGMNTIDQGMAALKLGSTEVASNVPKVVGSAVGSGSITSNI VASNSLPPATIAP PKPASWADIASKPAKQQPKLKTKNGIAGSSL PPPP I KHNMDIGTWDNKGPVAKAPSQALVQNIGQPTQGSPQPVG QQANNSPPVAQASVGQQTQPLPPPPPPQPAQLSVQQQAAQPTRWV APRNRGSGFFGHNGVVGNGVGQSQAGSGSTPSEPHPVLEKLRSIN NYNPKDFDWNLKHGRVFIIKSYSEDDIHRSIKYNIWCSTEHGNK RLDAAYRSMNGKGPVYLLFSVNGSGHFCGVAEMKSAVDYNTCAG VWSQDKWKGRFDVRWIFVKDVPNSOLRHIRLENNENKPVTNSPD	; l	[ļ	AWGNNSSQGQSTQSSGYSSNYAYAPSSLGGAMIDGOSAFANRTI.
VASNSLPPATIAPPKPASWADIASKPAKQQPKLKTKNGIAGSSL PPPPIKHNMDIGTWDNKGPVAKAPSQALVQNIGQPTQGSPQPVG QQANNSPPVAQASVGQQTQPLPPPPPQPAQLSVQQQAAQPTRWV APRNRGSGFGHNGVDGNGVGQSQAGSGSTPSEPHPVLEKLRSIN NYNPKDFDWNLKHGRVFIIKSYSEDDIHRSIKYNIWCSTEHGNK RLDAAYRSMNGKGPVYLLFSVNGSGHFCGVAEMKSAVDYNTCAG VWSQDKWKGRFDVRWIFVKDVPNSOLRHIRLENNENKPVTNSRD	1 . [j	,	NKAPGMNTIDQGMAALKLGSTEVASNVPKVVGSAVGSGSITSNI
PPPPIKHNMDIGTWDNKGPVAKAPSQALVQNIGQPTQGSPQPVG QQANNSPPVAQASVGQQTQPLPPPPPQPAQLSVQQQAAQPTRWV APRNGSGFGHNGVDGNGVGSQAGSGSTPSEPHPVLEKLRSIN NYNPKDFDWNLKHGRVFIIKSYSEDDIHRSIKYNIWCSTEHGNK RLDAAYRSMNGKGPVYLLFSVNGSGHFCGVAEMKSAVDYNTCAG VWSQDKWKGRFDVRWIFVKDVPNSOLRHIRLENNENKPVTNSPD	j			VASNSLPPATIAPPKPASWADIASKPAKQOPKLKTKNGIAGSSI.
QQANNSPPVAQASVGQQTQPLPPPPPQPAQLSVQQQAAQPTRWV APRNRGSGFGHNGVDGNGVGQSQAGSGSTPSEPHPVLEKLRSIN NYNPKDFDWNLKHGRVFIIKSYSEDDIHRSIKYNIWCSTEHGNK RLDAAYRSMNGKGPVYLLFSVNGSGHFCGVAEMKSAVDYNTCAG VWSQDKWKGRFDVRWIFVKDVPNSOLRHIRLENNENKPVTNSRD]	Į.	ļ	PPPPIKHNMDIGTWDNKGPVAKAPSQALVONIGOPTOGSPOPVG
APRNRGSGFGHNGVDGNGVGQSQAGSGSTPSEPHPVLEKLRSIN NYNPKDTDWNLKHGRVFIIKSYSEDDIHRSIKYNIWCSTEHGNK RLDAAYRSMNGKGPVYLLFSVNGSGHFCGVAEMKSAVDYNTCAG VWSQDKWKGRFDVRWIFVKDVPNSOLRHIRLENNENKPVTNSRD	1 1	ĺ	ĺ	QQANNSPPVAQASVGQQTQPLPPPPPQPAQLSVOOQAAOFTRWV
NYNPKDFDWNLKHGRVFIIKSYSEDDIHRSIKYNIWCSTEHGNK RLDAAYRSMNGKGPVYLLFSVNGSGHFCGVAEMKSAVDYNTCAG VWSQDKWKGRFDVRWIFVKDVPNSOLRHIRLENNENKDVTNSRD	[APRNRGSGFGHNGVDGNGVGQSQAGSGSTPSEPHPVLEKLRSIN
RLDAAYRSMNGKGPVYLLFSVNGSGHFCGVAEMKSAVDYNTCAG VWSQDKWKGRFDVRWIFVKDVPNSOLRHIRLENNENKPVTNSRD		1		NYNPKDFDWNLKHGRVFIIKSYSEDDIHRSIKYNIWCSTEHGNK
VWSQDKWKGRFDVRWIFVKDVPNSOLRHIRLENNENKPVTNSRD	1 1	j	[RLDAAYRSMNGKGPVYLLFSVNGSGHFCGVAEMKSAVDYNTCAG
TQEVPLEKAKQVLKIIASYKHTTSIPDDFSHYEKRQ				THIS CONTINUED DOWN THE THIS CONTINUE TO THE THIS C
] !	1	ŀ	VWSQDKWKGRFDVRWIFVKDVPNSQLRHIRLENNENKPVTNSRD

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	i	Glutamic Acid, F=Phenylalanine, G=Glycine,
- 1	corresponding	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	to first	to first	L=Leucine, M=Methionine, N=Asparagine,
į.	amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine,
- 1		residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /-possible nucleotide deletion
	sequence		\=possible nucleotide insertion)
6228	47	1978	GRRCRRGAVMELAQEARELGCWAVEEMGVPVAARAPESTLRRL
ł	1		CLGQGADIWAYILQHVHSQRTVKKIRGNLLWYGHQDSPQVRRKL
			ELEAAVTRLRAEIQELDQSLELMERDTEAQDTAMEQARQHTQDT
i			QRRALLLRAQAGAMRRQQHTLRDPMQRLQNQLRRLQDMERKAKV
1	1		DVTFGSLTSAALGLEPVVLRDVRTACTLRAQPLQNLLLPQAKRG
	1		SLPTPHDDHFGTSYQQWLSSVETLLTNHPPGHVLAALEHLAAER
	1		EAEIRSLCSGDGLGDTEISRPQAPDQSDSSQTLPSMVHLIQEGW
j			RTVGVLVSQRSTLLKERQVLTQRLQGLVEEVERRVLGSSERQVL
ŀ	· I		ILGLRRCCLWTELKALHDQSQELQDAAGHRQLLLRELQAKQQRI
1			THE POLICE OF THE PROPERTY OF
1			LHWRQLVEETQEQVRLLIKGNSASKTRLCRSPGEVLALVQRKVV
	i		PTFEAVAPQSRELLRCLEEEVRHLPHILLGTLLRHRPGELKPLP
			TVLPSIHQLHPASPRGSSFIALSHKLGLPPGKASELLLPAAASL
1	1		RODLLLLQDQRSLWCWDLLHMKTSLPPGLPTQELLQIQASQEKQ
ľ	1		QKENLGQALKRLEKLLKQALERIPELQGIVGDWWEQPGQAALSE
6229	1571	560	ELCQGLSLPQWRLRWVQAQGALQKLCS
	1 13/1	200	GPSLLGTRGTPNPARTLQIFFLIIGRRLTGRMAAVDDLQFEEFG
	1		NAATSLTANPDATTVNIEDPGETPKHQPGSPRGSGREEDDELLG
	1		NDDSDKTELLAGQKKSSPFWTFEYYQTFFDVDTYQVFDRIKGSL
	j		LPIPGKNFVRLYIRSNPDLYGPFWICATLVFAIAISGNLSNFLI
Ì	1		HLGEKTYHYVPEFRKVSIAATIIYAYAWLVPLALWGFLMWRNSK
ı			VMNIVSYSFLEIVCVYGYSLFIYIPTAILWIIPHKAVRWILVMI
	i		ALGISGSLLAMTFWPAVREDNRRVALATIVTIVLLHMLLSVGCL
6230	1 22 2		AYFFDAPEMDHLPTTTATPNQTVAAAKSS
0230	1723	600	SKMSGRSGKKKMSKLSRSARAGVIFPVGRLMRYLKKGTFKYRIS
			VGAPVYMAAVIEYLAAEILELAGNAARDNKKARIADRHILLAVA
			NDEELNQLLKGVTIASGGVLPRIHPELLAKKRGTKGKSETTLSP
i	1		PPEKRGRKATSGKKGGKKSKAAKPRTSKKSKPKDSDKEGTSNST
İ			SEDGPGDGFTILSSK\$LVLGQKLSLTOSDISHIGSMRVEGTVHP
1 .	1 1		TTAEIDLKEDIGKALEKAGGKEFLETVKELRKSOGPLEVAEAAV
1	1 1		SQSSGLAAKFVIHCHIPQWGSDKCEEOLEETIKNCLSAARDKKI.
1	1 1		KSVAFPPFPSGRNCFPKQTAAQVTLKAISAHFDDSSASSLKNVY
			FLLFDSESIGIYVQEMAKLDAK
6231	149	870	LIFSSSTMDRSLRNVLVVSFGFLLLFTAYGGLQSLQSSLYSEEG
}	1 1		LGVTALSTLYGGMLLSSMFLPPLLIERLGCKGTIILSMCGVVAF
1	[]		SVGNFFASWYTLIPTSILLGLGAAPLWSAOCTYLTITGNTHAEK
1.	i i		AGKRGKDMVNQYFGIFFLIFQSSGVWGNLISSLVFGQTPSQETL
1 .]		PEEQLTSCGASDCLMATTTTNSTQRPSQQLVYTLLGIYTGSGVL
		1	AVLMIAAFLQPIRDVQRESE
6232	3679	1476	FVAGTTMAGFWVGTAPLVAAGRRGRWPPQQLMLSAALRTLKHVL
	•		YYSRQCLMVSRNLGSVGYDPNEKTFDKILVANRGEIACRVIRTC
			KKMGIKTVAIHSDVDASSVHVKMADEAVCVGPAPTSKSYLNMDA
			IMEAIKKTRAQAVHPGYGFLSENKEFARCLAAEDVVFIGPDTHA
			IQAMGDKIESKLLAKKAEVNTIPGFDGVVKDAEEAVRIAREIGY
1			PVMIKASAGGGGKGMRIAWDDEKTRDGFRLSSQEAASSFGDDRL
1 1	1	}	LIEKFIDNPRHIEIQVLGDKHGNALWLNERECSIQRRNQKVVEE
		Ì	APSIFLDAETRRAMGEQAVALARAVKYSSAGTVEFLVDSKKNFY
1 1	1		FLEMNTRLQVEHPVTECITGLDLVQEMIRVAKGYPLRHKQADIR
]		1	INGWAVECRYYAEDPYKSFGLPSIGRLSQYQEPLHLPGVRVDSG
<u>].</u> [1]	TOPGSDICTVVDDMICKLITUGGDDDDAY
] [1	IQPGSDISIYYDPMISKLITYGSDRTEALKRMADALDNYVIRGV
			THNIALLREVIINSRFVKGDISTKFLSDVYPDGFKGHMLTKSEK
			NQLLAIASSLFVAFQLRAQHFQENSRMPVIKPDIANWELSVKLH
[1	ļ	DKVHTVVASNNGSVFSVEVDGSKLNVTSTWNLASPLLSVSVDGT
1 1	,	1	QRTVQCLSREAGGNMSIQFLGTVYKVNILTRLAAELNKFMLEKV
j .			TEDTSSVLRSPMPGVVVAVSVKPGDAVAEGQEICVIEAMKMQNS
6233	1	2654	MTAGKTGTVKSVHCQAGDTVGEGDLLVELE
·		2654	HSTRENLNAGNPNFPSEGHLVRSTGPGGSFAKHMVAQCVSPKGP

Deginning No:	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Not nucleotide location corresponding to first amino acid residue of amino acid residue of amino acid sequence sequence		beginning		
Coction Corresponding Co first anino acid amino acid residue of amino acid amino	NO:		location	
corresponding to first amino acid residue of amino acid residue of amino acid sequence and control of the control of the control of amino acid sequence and control of the control of amino acid sequence and control of the control of amino acid sequence ac		_	4	
to first amino acid residue of amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid sequence ### PFPTOIDE ### P				
amino acid residue of amino acid sequence S=Serine, T=Threonine, V=Valine, S=Serine, T=Threonine, V=Valine, S=Ser	1		1	
residue of amino acid sequence Nathyptophan, Yatyrosine, Xathknown, *-Stop Codon, *-possible nucleotide deletion,			1	
amino acid sequence Codon, /-possible nuclectida insertion				N-Trembers V M V II-leave t Cl
Appossible nucleotide insertion			P	w=irypcopnan, i=iryrosine, k=unknown, *=Stop
LACCRITYFGATHUPYLGGGELLEKKTTQURLGGYTANDYAL LACLACYANTS LITKARZWAROTLAGGLASPHLEGYTALGRAW LACLACYANTS LITKARZWAROTLAGGLASPHLEGYTALGRAW LACLACYANTS LITKARZWAROTLAGGLASPHLEGYTALGRAW LACLACYANTS LITKARZWAROTLAGGLASPHLEGYTALGRAW VENNEVKLSKRYROAWGGESFLOTYLTGGGGATLAGVERGW EGOWIFFSSGLLESHCHRGSI I SKORWHAISSINGWI EGOWIFFSSGLLESHCHRGSI I SKORWHAISSINGWI EGOWIFFSSGLLESHCHRGSI I SKORWHAISSINGWI EGOWIFFSSGLLESHCHRGSI I SKORWHAISSINGWI EGOWIFFSSGLLESHCHRGSI I SKORWHAISSINGWI EKSSLKLISARUEDURFUGHGSSBYEMIALFPRAKITVARTSEVY SLAKQODNSGISLAVIQEDGLSVEQKRHISSAQKLFSALSQPAG EXKSSLKLISARUEDLBWICHFAISSINGEVWITHHREGGRY MYVRQIMOSSECFHANHFORLISTSINGEVWARITVELLOQ AEINTTHRISSKVI ISIVTULOCICLASELCAFIUTHHREGGRY MYVRQIMOSSECFHANHFORLISTSINGGVARYIKKT RLUVULQYTDVIDUVQALQCHPDDSNVKASFTIGAITACVBPMS CYMERREIPRECOGCQULSWVVYTSTHTROERICHOQUSSI IRAANBAAAFILABRIGIVTREDIELLISSSSSPBMARSRVI, MYPGWERKLANGSVYPIMVQICVWGPQPLEXTRYDLOQGSL IRAANBAAAFILABRIGIVTREDIELLISSSSSPBMARSRVI, KOKPORKALKTRGMITORGEPLETTRYDGEPQEVHDLE EGOPPPDSKSVGODSSGQCCVLUF IGCSLKEGE KIMBLOQUSA KOKPORKALKTRGMITORGEPLETTRYDGELOQGVHDLE EGOPPPDSKSVGODSSGQCCVLUF IGCSLKEGE KIMBLOQUSA KOKPORKALKTRGMITORGEPLETTRYDELEQGYHDLE ELKP 6234 1731 404 PEWERDHMISPGNKGSLVYAGITSIVKSSLGMWESSRIMMSGL DKGSDIOMINBERILAJOLCGHIKKGTDVYQPEHASLUVGGSVHDLE ELKP FORGWITHERAGUNGTAS YOMIGGSPLOULANDAGGYT DECNSLINBERICSTURJOLANDYLCVWPRAYTEBETGSVDGVLIBS NAVARDRAPACKELSSTOLANTY ISILATEBETGSVDGVLIBS VAVARDRAPACKELSSTOLANTY ISILATEBETGSVDGVLIBS VAVARDRAPACKELSSTOLANTY ISILATEBETGSVDGVLIBS VAVARDRAPACKELSSTOLANTY ISILATEBETGSVDGVLIBS VAVARDRAPACKELSSTOLANTY ISILATEBETGSVDGVLIBS VAVARDRAPACKELSSTOLANTY ISILATEBETGSVDGVLIBS VAVARDRAPACKELSSTOLANTY ISILATEBETGSVDGVLIB VAVARDRAPACKELSSTOLANTY ISILATEBETGSVDGVLIB VAVARDRAPACKELSSTOLANTY ISILATEBETGSVDGVLIB VAVARDRAPACKELSSTOLANTY ISILATEBETGSVDGVLIB VAVARDRAPACKELSSTOLANTY ISILATEBETGSVDGVLIB ISICATALIDOU DKRUEDVINKAKRQI IKKRARIVAGGGFLLIDIGLARGGVVQT UNGGVGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	1		sequence	
LAGIACYAKTSLITKAREWASOTLOSGILDSFELIFF PRALEKSIN TFHINAVMORIUP LIDSBELSIS EVKTACMAYVDI PDLILGONGE LGSVVFSESPLTSQILVKEKDGTVTTETSSVULTAAVPRECSUL VENDEWILSEKTHOVLOVGGESPLTVALVGGGGAVLYSSKLIGGWP EEGNVIFFSGILFSHCRIGGILISKUDINGTSTVA ALLIDFKSSLLPHLPVHYHGSINFLMIALFPKSKITQAFTSETVA ALLIDFKSSLLPHLPVHYHGSINFLMIALFPKSKITQAFTSETVA ALLIDFKSSLLPHLPVHYHGSINFLMIALFPKSKITQAFTSETVA ALLIDFKSSLLPHLPVHYHGSINFLMIALFPKSKITQAFTSETVA ALLIDFKSSLLPHLPVHYHGSINFLMIALFPKSKITQAFTSETVA EKRSSLKALDSAKLPFLDWYLGFTASSISGEVWRTHLEVALOG AEINTTHRIESDKYILISTVTGLEGGASELCAFUTHREGGRM HVYRQIMDSSECFHAAHFQRTLSSLLEAQONSGARQSAYIRKT RLUVYLGYTDVIDVOALQTHDENSVRASFTIGATTACVEPMS CYMERRELPPKCLDQCSQGLVSHVVDTSHTTTGRRPPLLVOUQGS LTRAMPAAPILERGTVTRNEDIE LILISPNSFSSPBMLGRRYL MYPGWYBSKLNAGSVYPIMVQICVWFGRPLEKTRPVAKKKAIQS SIKPSFSGNITHLIGKVFSDSERTMEVVYTTHASIHPVL EGFTPPPDSKSVSDDSSGGQGCTLVFIGGSLKEDS IXDHALQSA KOKPGRALKTRGMITQGNISHTHEKVRHIJPELPGYFYNGTOPV NFFGOKTDFPLMOOPMDYVERANREIEXTNQELEQQEYHDLF ELKP 6234 1731 404 PRIVEEDMOHNSPGNKGSLVYJAGIKSTVESSLGWUESSRHINNSGL DKRSDIQNINBERILALQLCGNIKKGTDVTVOFFLHSILVGSERS KOKPGRALKTRGMITQOLISHTKARHIJGENGSSEKGDLLAVVAMALGSTT DENNSLAREKGSTURQLNNFYLCVWFAFITSETGSS DGVLYNG KVAVENDRVAFACKELBOTQLNRYT IKKLINBMERGSHOLGSILTG LTDGVDLMSSVVDRYGDVGTASYOM-QGSPLDVIKDERVQYMI ENTRALLDAMRFWIKAREFDTHASKLDDSSKELAGONISHLITG LTDGVDLMSSVVDRYGDVGTASYOM-QGSPLDVIKDERVQYMI ENTRALLDAMRFWIKAREFDTHASKLDDSSKELAGONISHLITG LTDGVDLMSSVVDRYGDVGTASYOM-QGSPLDVIKDERVQYMI ENTRALLDAMRFWIKAREFDTHASKLDDSSKELAGONINGTHON-PAETV OP DYSSDDSTRYLULITETARRHQWMRVVGKISGGRYNMFTKCHN CRIGGHAGMMLSWFROHASCPVSACTCKCMQLDTTONLVPAETV OP DYSSDDSTRYLULITETARRHQWRAVVGKISGGRANTENPPP DYSSDDSTRYLULITETARRHQWRAVVGKISGGRANTENPPP DYSSDDSTRYLULITETARRHQWRAVVGKISGGRANTENPPP DYSSDDSTRYLULITETARRHQWRAVVGKISGGRYNMFTKCHN KNEKAKRUSTUSTICHTARRHQWRAVVGKISGGRYNMFTKKNAGV SNDATLKYMBEGVAGCHUNDAVALGPPTLUDYCOMPRINSTTT LTTPQNQVONLLQBADDEAGLDLMNELPQCOTGSVGTSVASABQ DELSGRAALCULAS SLANDKEREIGPTLOTGTOMPRINSTTT LTTPQNQVONLLQBADDEAGLDLMNELPQCOTGSVGTSVASABQ DELSGRAALCULAS CKK KKANATUKSDPEGERMYKVPYGKACACHGHILLKYDDMKLL GEWOLKCHURNALUKARTLANA		sequence		
TFHIHAYMOGRITYPLDSEDSLSFYKTACHAVYDIPPLICSCOML LGSVVYSESSITIOLIVEKENGTVITTETSSVUTAAPRECSWL VEDNEVKLSEKTHOAVKODESFLOTVITGGGATYLYSSHLOGE BEGONVIPPSSGLISHERGHGITISKURMSTYPYDDGTSTVA ALLIDPKSSLLPHLDVIPFIGGSMFMINIALPYCKIYYSSHLOGE SLAWCODNSGILSKYTOLOGUSVYGKHISSAGKLFSALSQRAG EKRSSLKLLSAKLPELDWFLOHFAISSISGEVWRTHIBVILDOQ ABINTITRIBSDKYIISIVTOLOGGATAYSSYLVA ALLIDPKSSLLPHDWFLOHFAISSISGEVWRTHIBVILDOQ ABINTITRIBSDKYIISIVTOLOGGALSWYVTHIBVILOGA ABINTITRIBSDKYIISIVTOLOGGALSWYVTHIBVILOGA ABINTITRIBSDKYIISIVTOLOGGALSWYVTHIBVILOGA ABINTITRIBSDKYIISIVTOLOGGALSWYVTHIBVILOGAGAYIKKKY RILUVILOGITDVIOVQALQTHPDSNYKASFTIGAITACVSWR MYKRGHORSACFRAHFURTUSALBAQNORSAGAYIKKXY RILUVILOGITDVIOVQALQTHPDSNYKASFTIGAITACVSWR CYMERRELIFKCLOGGACLSWYVTHTANSISIRYVI MYGGYBGKLANGSVYPILNVQICVMGGPLENETRYPLLVOLQGS SIKPSPFSGNIYHILGKVKPSDSERTMSVCYNTLANSISIRYVI MYGGYBGKLANGSVYPILNVQICVMGGPLEVITANSISIRYVI LGGYPPDSKSVYGDSSQQCCTVHIGGSLEVSSIEDMLRQSA KQKPGKKALKTRGMLYQGS HSIHVKAHLEPLPAGYSYMGTQFV NFGROKTDFHILDAQVARDPHOLYTGARSETETNYCHAGGSPHOLY NFGROKTDFHILDAQVARDPHOLYTGARSETETNYCHAGGSPHOLY NFGROKTDFHILDAQVARDPHOLYTGARSETETNYCHAGGSPHOLYTGARGYBYDL ELKP 6234 1731 404 PRVEEDMCHKSFGNKGSLVYAGIKSIVKSSLGMVESSRINWSGL DKQSDIQMINEBRILALQLCGWIKKGTDVYQPFHASLOYGOGYHOLY NFGROKTDFHILDAGARAGASEGGILANAVAMALGGYY DENSLAREKCSTLRQLANPYLCWWFAPITSETGSYDGVYHOLY RVANPAVAFACKHSTANDYLCGWARAGASEGGILANAVAMALGGYY DENSLAREKCSTLRQLANPYLCWWFAPITSETGSYDGVYHOLY ENYRHALDAMRYWHKARAFDININISHLINMENERGANUSSILLTG LTCGGGHAGHMLSWFROHBSCVYGAGTKSDKALDSKALDLAYVAMALGGYY ENYRHALDAMRYWHKARAFDININISHLINMENERGANUSSILLTG LTCGGGHAGHMLSWFROHBSCVYGAGTKSDKALDSKALDAGVYCHOCK KSISYSCSAVPHQGGGFSYOVGGSFYKSKYTSCOCKPUPRC KSISYSCSAVPHQGGGFSGGGTKSDEKALDSKALDAGARAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA	ļ			
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CYMERIFLEPEKCLDOCSOGLIVENVPTSHITTOGRIPLLVOLOGSL IRANDRAAPILAENGIVITNEDIELISENSFSSEBMLRSRYI MYPGWYEGKLMAGSVYPLMVQICVWFGRPLEKTRVAKCKAIQS SIKPSFFSGNIYHLLGKVKFSDSERTMEVCYNTLANSLSIMPUL EGFTPPPDSKSVSQDSSOGQCETULFGLKEDISKUMLGSA KOKPORKALKTRGMLYQGEIRSIHVKHHLEPLPAGYFYNGTQFV NFFCDKTDFHPLMDQFMNDTVEEARREIEKYNQELEQQEYHDLF ELKP 6234 1731 404 PRVREDMDHKSPGNKGSLVYAGIKSIVKSSLGMVESSRHNWSGL DKQSDIQNINEERILALQLCGWIKKGTDVDVQPFLNSLVQEGEW ERAAAVALFNLDIRRATQILMEGASSEKGDLMINVVAMALSGYT DEKNELMREMCSTLRLQLNNPYLCVMFAPITSTGSYDGVLYEN KVAVRDRVAFACKFLSDTQLNRYIEKLTHEMKEAGNLEGILLTG LTKOGVDLMESYVDRYGDVQTASYCMYGGSPLDVLMOERQYWI ENTANLDAMFPHKRAEPDIHRSKLDPSSKPLAQVFVSCONFOG KSISYSCSAVPHQGRGFSOYGVSGSPTKSKVTSCFGCRKPLPRC ALCLIMMTPYWSCCPGGTKSDEKVDLKOERQYWI ENTANLDAMFPHKRAEPDIHRSKLDPSSKPLAQVFVSCNFGG KSISYSCSAVPHQGRGFSOYGVSGSPTKSKVTSCFGCRKPLPRC ALCLIMMTPYWSCCPGGTKSDEKVDLKOERQYWI CRHGGHAGHMLSWFRDHAECPVSACTCKCMQLDTTGMLVPAETV OP EKEDHELPSWFRAALKVPGRGGRVGTTPELAAGGIMATRNPPPO DYESDDDSYEVLDLTEYARRHQWNRRVPGHSSGPWKKYSVATO IVMGGVTOWCAGFLFQKVGKLAATAVGGGFLLQIASHGYVQI DWKRVEKDVNKAARGIKKRAANAAPETINLIEEATBEIKQNIVI SSGFVGGFLLGLAS ### MODNKGAAAGSGITLPSLPSARFSAGPPTGRSRPTMSNMEKHLF NLFFAAKBLSRSAKKCDKEEKAEKAKKKALQKSGMBVARTHAE NAIRQNOAVNFLRMSARVDAVAARVQTAVTMGKVIKSMAGVVK SHDATLKTMINLEKISALMDKFENGFETLDVOTQOMEDTMSSTIT LTTPQNQVDMLLQBMADEGLDLMMELPQQQTGSVGTSVASAEQ DELSQRLARLBDQV ### DELSQRLARLBDQV ### PAMAEEGIAAGGVMDVNTALGBVLKTALTHGGLARGIREAKA LDKRQAHLCVLASNCDEPMYVKLVEALCAENGINLIVDDNKKL GEWVGLCKIDRECKPRKVVGCSCVVWGYKESQAKDVIEEYFK CKK ### TIPEETASSTAHLWEKKTKTKLWELTLEESNETEKIAPTTELVP KGEMKNNIDSIFIVLEGGIGHRTVPMLLAKSRFSGGGKNWSSL INLHCOLELEVHYYMENGVVKRLLAKARSRFSKGGKNWSSL INLHCOLELEVHYYMENGFUWBLLEUFLDTOFDPPPWINLIKK MKKAKAMAIVESDPEEENYKVPEYKTVISFISKDQLNITISKCG LWMLKNLVKAFTZAATGSSADFVKDLAPPMILIAKSCTSLSK DSFSVLLIVMAESSLAMDTLERSKETADTELLOFT DSFSVLLIVMAGESSLAMDTLERKNDTHLGHTISKSF DSFSVLLIVMAGESSLAMDTTRKDDMIPNMTSLSSK ### DESTSVLLIVMAGESSLAMDTTRKDDMIPNMTSLSSK DSFSVLLIVMAGESSLAMDTTRKDDMIPNMTSLSSK ### DESTSVLLIVMAGESSLAMDTRKDDATENDTRANGLISK MKKAKARMAIVESDPEEENYKVPEYKTVISFISKDQLNITISKSSPS *	1			
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NLKFAAKELSRSAKKCDKEEKAEKAKIKKAIQKGNMEVARTHAE NAIRQKNQAVNFLRMSARVDAVAARVQTAVTMGKVTKSMAGVVK SMDATLKTMNLEKISALMDKFEHQFETLDVQTQQMEDTMSSTTT LTTPQNQVDMLLQEMADEAGLDLNMELPQGQTGSVGTSVASAEQ DELSQRLARLBDQV 6237 312 720 PTAMAEEGIAAGGVMDVNTALQEVLKTALIHDGLARGIREAAKA LDKRQAHLCVLASNCDEPMYVKLVEALCAEHQINLIKVDDNKKL GEWGLCKIDREGKPRKVVGCSCVVVKDYGKESQAKDVIEEYFK CKK 6238 2 4666 EEVPTQESVKWEINVIIKNPEIVPVADMTKNDAPALVITTQCEI CYKGNLENSTMTAAIKDLQVRACPFLPVKRKGKITTVLQPCDLP YQTTQKGTDPQVIDMSVKSLTLKVSPVIINTMITITSALYTTKE TIPEETASSTAHLWEKKDTKTLKMWFLEESNETEKIAPTTELVP KGEMIKMNIDSIFIVLEAGIGHRTVPMLLAKSRFSGEGKNWSSL INLHCQLELEVHYYNEMFGWWEPLLEPLEIDQTEDFRPWNIGIK MKKKAKMAIVESDPEEENYKVPEYKTVISFHSKDQLNITLSKCG LVMLNNLVKAFTZAATGSSADPVKDLAPFMILNSLGLTISVSPS DSFSVLNIPMAKSYVLKNGESLSMDYIRTKDNDHFNAMTSLSSK	6236	1	703	WDONKGAAAGSGLTLPSLPSARFSAGPPTORSRPTMSNMEKHLF
NAIRQKNQAVNFLRMSARVDAVAARVQTAVTMGKVTKSMAGVVK SMDATLKTMNLEKISALMDKFEHQFETLDVQTQQMEDTMSSTTT LTTPQNQVDMLLQEMADEAGLDLNMELPQGQTGSVGTSVASAEQ DELSQRLARLRDQV 6237 312 720 PTAMAEEGIAAGGVMDVNTALQBVLKTALIHDGLARGIREAAKA LDKRQAHLCVLASNCDEPMYVKLVEALCABHQINLIKVDDNKKL GEWVGLCKIDREGKPRKVVGCSCVVVKDYGKESQAKDVIEEYFK CKK 6238 2 4666 EEVPTQESVKWEINVIIKNPETVPVADMTKNDAPALVITTQCEI CYKGNLENSTMTAAIKDLQVRACPFLPVKRKGKITTVLQPCDLP YQTTQKGTDPQVIDMSVKSLTLKVSPVIINTMITITSALYTTKE TIPEETASSTAHLWEKKDTKTLKMWFLEESNETEKIAPTTELVP KGEMIKMNIDSIFIVLEAGIGHRTVPMLLAKSRFSGEGKNWSSL INLHCQLELEVHYYNEMFGWWEPLLEPLEIDQTEDFRPWNIGIK MKKKAKMAIVESDPEEENYKVPEYKTVISFHSKDQLNITLSKCG LVMLNNLVKAFTZAATGSSADPVKDLAPFMILNSLGLTISVSPS DSFSVLNIPMAKSYVLKNGESLSMDYIRTKDNDHFNAMTSLSSK	1		•	-
SMDATLKTMNLEKISALMDKFEHQFETLDVQTQQMEDTMSSTTT LTTPQNQVDMLLQEMADEAGLDLNMELPQGQTGSVGTSVASAEQ DELSQRLARLBDQV 6237 312 720 PTAMAEEGIAAGGWMDVNTALQEVLKTALIHDGLARGIREAAKA LDKRQAHLCVLASNCDEPMYVKLVEALCABHQINLIKVDDNKKL GEWVGLCKIDREGKPRKVVGCSCVVVKDYGKESQAKDVIEEYFK CKK 6238 2 4666 EEVPTQESVKWEINVIIKNPETUPVADMTKNDAPALVITTQCEI CYKGNLENSTMTAAIKDLQVRACPFLPVKRKGKITTVLQPCDLP YQTTQKGTDPQVIDMSVKSLTLKVSPVIINTMITITSALYTTKE TIPEETASSTAHLWEKKDTKTLKMWFLEESNETEKIAPTTELVP KGEMIKMNIDSIFIVLEAGIGHRTVPMLLAKSRFSGEGKNWSSL INLHCQLELEVHYYNEMFGWWEPLLEPLEIDQTEDFRPWNIGIK MKKKAKMAIVESDPEENYKVPEYKTVISFHSKDQLNITLSKCG LVMLNNLVKAFTEAATGSSADFVKDLAPFMILNSLGLTISVSPS DSFSVLNIPMAKSYVLKNGESLSMDYIRTKDNDHFNAMTSLSSK	1			
LTTPQNQVDMLLQEMADEAGLDLNMELPQGQTGSVGTSVASAEQ DELSQRLARLRDQV 6237 312 720 PTAMAEEGIAAGGVMDVNTALQBVLKTALIHDGLARGIREAAKA LDKRQAHLCVLASNCDEPMYVKLVEALCABHQINLIKVDDNKKL GEWVGLCKIDREGKPRKVVGCSCVVVKDYGKESQAKDVIEEYFK CKK 6238 2 4666 ERVPTQESVKWEINVIIKNPEIVFVADMTKNDAPALVITTQCEI CYKGNLENSTMTAAIKDLQVRACPFLPVKRKGKITTVLQPCDLP YQTTQKGTDPQVIDMSVKSLTLKVSPVIINTMITITSALYTTKE TIPEETASSTAHLWEKKDTKTLKMWFLEESNETEKIAPTTELVP KGEMIKNNIDSIFIVLEAGIGHRTVPMLLAKSRFSGEGKNMSSL INLHCQLELVHYYNEMFGVWEPLLEPLEIDQTEDFRPWNLGIK MKKKAKMAIVESDPEEENYKVPEYKTVISFHSKDQLNITLSKCG LVMLNNLVKAFTZAATGSSADFVKDLAPFMILNSLGLTISVSPS DSFSVLNIPMAKSYVLKNGESLSMDYIRTKDNDHFNAMTSLSSK	ļ	ļ		
DELSQRLARLRDQV 6237 312 720 PTAMAEEGIAAGGVMDVNTALQBVLKTALIHDGLARGIREAAKA LDKRQAHLCVLASNCDEPMYVKLVEALCABHQINLIKVDDNKKL GEWVGLCKIDREGKPRKVVGCSCVVVKDYGKESQAKDVIEEYFK CKK 6238 2 4666 ERVPTQESVKWEINVIIKNPETVPVADMTKNDAPALVITTQCEI CYKGNLENSTMTAAIKDLQVRACPFLPVKRKGKITTVLQPCDLP YQTTQKGTDPQVIDMSVKSLTLKVSPVIINTMITITSALYTTKE TIPEETASSTAHLWEKKDTKTLKMWFLEESNETEKIAPTTELVP KGEMIKNNIDSIFIVLEAGIGHRTVPMLLAKSRFSGEGKNWSSL INLHCQLELEVHYYNEMFGVWEPLLEPLEIDQTEDFRPWNLGIK MKKKAKMAIVESDPEENYKVPEYKTVISFHSKDQLNITLSKCG LVMLNNLVKAFTZAATGSSADPVKDLAPFMILNSLGLTISVSPS DSFSVLNIPMAKSYVLKNGESLSMDYIRTKDNDHFNAMTSLSSK]			
6237 312 720 PTAMAEEGIAAGGVMDVNTALQBVLKTALIHDGLARGIREAAKA LDKRQAHLCVLASNCDEPMYVKLVEALCABHQINLIKVDDNKKL GEWVGLCKIDREGKPRKVVGCSCVVVKDYGKESQAKDVIEEYFK CKK 6238 2 4666 ERVPTQESVKWEINVIIKNPEIVPVADMTKNDAPALVITTQCEI CYKGNLENSTMTAAIKDLQVRACPFLPVKRKGKITTVLQPCDLP YQTTQKGTDPQVIDMSVKSLTLKVSPVIINTMITITSALYTTKE TIPEETASSTAHLWEKKDTKTLKMWFLEESNETEKIAPTTELVP KGEMIKMNIDSIFIVLEAGIGHRTVPMLLAKSRFSGEGKNWSSL INLHCQLELEVHYYNEMFGWWEPLLEPLEIDQTEDFRPWNIGIK MKKKAKMAIVESDPEENYKVPEYKTVISFHSKDQLNITLSKCG LVMLNNLVKAFTZAATGSSADPVKDLAPFMILNSLGLTISVSPS DSFSVLNIPMAKSYVLKNGESLSMDYIRTKDNDHFNAMTSLSSK	[i			
LDKRQAHLCVLASNCDEPMYVKLVEALCABHQINLIKVDDNKKL GEWVGLCKIDREGKPRKVVGCSCVVVKDYGKESQAKDVIEEYFK CKK 6238 2 4666 EBVPTQESVKWEINVIIKNPEIVPVADMTKNDAPALVITTQCEI CYKGNLENSTMTAAIKDLQVRACPFLPVKRKGKITTVLQPCDLP YQTTQKGTDPQVIDMSVKSLTLKVSPVIINTMITITSALYTTKE TIPEETASSTAHLWEKKDTKTLKMWFLEESNETEKIAPTTELVP KGEMIKMNIDSIFIVLEAGIGHRTVPMLLAKSRFSGEGKNWSSL INLHCQLELEVHYYMEMFGVWEBPLLEPLEIDQTEDFRPWNIGIK MKKKAKMAIVESDPEENYKVPEYKTVISFHSKDQLNITLSKCG LVMLNNLVKAFTZAATGSSADPVKDLAPFMILNSLGLTISVSPS DSFSVLNIPMAKSYVLKNGESLSMDYIRTKDNDHFNAMTSLSSK	6237	312	720	
GEWGLCKIDREGKPRKVVGCSCVVVKDYGKESQAKDVIEEYFK CKK 6238 2 4666 EEVPTQESVKWEINVIIKNPETUPVADMTKNDAPALVITTQCEI CYKGNLENSTMTAAIKDLQVRACPFLPVKRKGKITTVLQPCDLP YQTTQKGTDPQVIDMSVKSLTLKVSPVIINTMITITSALYTTKR TIPEETASSTAHLWEKKDTKTLKMWFLEESNETEKIAPTTELVP KGEMIKMNIDSIFIVLEAGIGHRTVPMLLAKSRFSGEGKNWSSL INLHCQLELEVHYYNEMFGWWEPLLEPLEIDQTEDFRPWNIGIK MKKKAKMAIVESDPEENYKVPEYKTVISFHSKDQLNITLSKCG LVMLNNLVKAFTZAATGSSADFVKDLAPFMILNSLGLTISVSPS DSFSVLNIPMAKSYVLKNGESLSMDYIRTKDNDHFNAMTSLSSK	"~"	314	120	FINITE COLLEGE AND ANTALOUS VERTALIHOGLARGIREAAKA
CKK 6238 2 4666 EBVPTQESVKWEINVIIKNPEIVPVADMTKNDAPALVITTQCEI CYKGNLENSTMTAAIKDLQVRACPFLPVKRKGKITTVLQPCDLP YQTTQKGTDPQVIDMSVKSLTLKWSPVIINTMITITSALYTTKE TIPEETASSTAHLWKKDTKTLKMWFLEESNETEKIAPTTELVP KGEMIKMNIDSIFIVEAGIGHRTVPMLLAKSRFSGEGKNWSSL INLHCQLELEVHYYNEMFGVWBPLLEPLEIDQTEDFRPWNLGIK MKKAKMAIVESDPEEBNYKVPEYKTVISFHSKDQLNITLSKCG LVMLNNLVKAFTZAATGSSADFVKDLAPFMILNSLGLTISVSPS DSFSVLNIPMAKSYVLKNGESLSMDYIRTKDNDHFNAMTSLSSK	[PDVKCAHPCATASUCDERMAAKPAESTCARHGINFIKADDNKKF
6238 2 4666 EEVPTQESVKWEINVIIKNPEIVFVADMTKNDAPALVITTQCEI CYKGNLENSTMTAAIKDLQVRACPFLPVKRKGKITTVLQPCDLF YQTTQKGTDPQVIDMSVKSLTLKVSPVIINTMITITSALYTTKE TIPEETASSTAHLWEKKDTKTLKMWFLEESNETEKIAPTTELVP KGEMIKMNIDSIFIVLEAGIGHRTVPMLLAKSRFSGEGKNNSSL INLHCQLELEVHYYNEMFGVWEPLLEPLEIDQTEDFPWNLGIK MKKKAKMAIVESDPEEENYKVPEYKTVISFHSKDQLNITLSKCG LVMLNNLVKAFTZAATGSSADFVKDLAPFMILNSIGLTISVSPS DSFSVLNIPMAKSYVLKNGESLSMDYIRTKDNDHFNAMTSLSSK			İ	
CYKGNLENSTMTAAIKDLQVEACPFLPVKRKGKITTULQPCDLP YQTTQKGTDPQVIDMSVKSLTLKVSPVIINTMITITSALYTTKE TIPEETASSTAHLWEKKDTKTLKMWFLEESNETEKIAPTTELVP KGEMIKMNIDSIFIVLEAGIGHRTVPMLLAKSRFSGEGKNWSSL INLHCQLELEVHYYNEMFGVWEPLLEPLEIDQTEDFRPWNIGIK MKKKAKMAIVESDPEENYKVPEYKTVISFHSKDQLNITLSKCG LVMLNNLVKAFTZAATGSSADPVKDLAPFMILNSLGLTISVSPS DSFSVLNIPMAKSYVLKNGESLSMDYIRTKDNDHFNAMTSLSSK	<u></u>			
YQTTQKGTDPQVIDMSVKSLTLKVSPVIINTMITITSALYTTKE TIPEETASSTAHLMEKKDTKTLKMWFLEESNETEKIAPTTELVP KGEMIKNNIDSIFIVLEAGIGHRTVPMLLAKSRFSGEGKNMSSL INLHCQLELEVHYYNEMFGVWEPLLEPLEIDQTEDFPWNLGIK MKKKAKMAIVESDPEEENYKVPEYKTVISFHSKDQLNITLSKCG LVMLNNLVKAFTZAATGSSADFVKDLAPFMILNSLGLTISVSPS DSFSVLNIPMAKSYVLKNGESLSMDYIRTKDNDHFNAMTSLSSK	6238	3	4666	
YQTTQKGTDPQVIDMSVKSLTLKVSPVIINTMITITSALYTTKE TIPEETASSTAHLMEKKDTKTLKMWFLEESNETEKIAPTTELVP KGEMIKNNIDSIFIVLEAGIGHRTVPMLLAKSRFSGEGKNMSSL INLHCQLELEVHYYNEMFGVWEPLLEPLEIDQTEDFPWNLGIK MKKKAKMAIVESDPEEENYKVPEYKTVISFHSKDQLNITLSKCG LVMLNNLVKAFTZAATGSSADFVKDLAPFMILNSLGLTISVSPS DSFSVLNIPMAKSYVLKNGESLSMDYIRTKDNDHFNAMTSLSSK	1]		
TIPEETASSTAHLWEKKDTKTLKMWFLEESNETEKIAPTTELVP KGEMIKMNIDSIFIVLEAGIGHRTVPMLLAKSRFSGEGKNWSSL INLHCQLELEVHYYNEMFGWWEPLLEPLEIDQTEDFRPWNIGIK MKKKAKMAIVESDPEENYKVPEYKTVISFHSKDQLNITLSKCG LVMLNNLVKAFTZAATGSSADFVKDLAPFMILNSLGLTISVSPS DSFSVLNIPMAKSYVLKNGESLSMDYIRTKDNDHFNAMTSLSSK	1		•	
KGEMIKMNIDSIFIVLEAGIGHRTVPMLLAKSRFSGEGKNWSSL INLHCQLELEVHYYNEMFGVWEPLLEPLEIDQTEDFRPWNLGIK MKKKAKMAIVESDPEEENYKVPEYKTVISFHSKDQLNITLSKCG LVMLNNLVKAFTZAATGSSADFVKDLAPFMILNSLGLTISVSPS DSFSVLNIPMAKSYVLKNGESLSMDYIRTKDNDHFNAMTSLSSK				
INLHCQLELEVHYYNEMFGVWEPLLEPLEIDQTEDFRPWNLGIK MKKKAKMAIVESDPEEENYKVPEYKTVISFHSKDQLNITLSKCG LVMLNNLVKAFTZAATGSSADFVKDLAPFMILNSLGLTISVSPS DSFSVLNIPMAKSYVLKNGESLSMDYIRTKDNDHFNAMTSLSSK	1	[
MKKKAKMAIVESDPEEENYKVPEYKTVISFHSKDQLNITLSKCG LVMLNNLVKAFTZAATGSSADFVKDLAPFMILNSLGLTISVSPS DSFSVLNIPMAKSYVLKNGESLSMDYIRTKDNDHFNAMTSLSSK]			
LVMLNNLVKAFTZAATGSSADFVKDLAPFMILNSIGLTISVSPS DSFSVLNIPMAKSYVLKNGESLSMDYIRTKDNDHFNAMTSLSSK		1		
DSFSVLNIPMAKSYVLKNGESLSMDYIRTKDNDHFNAMTSLSSK	1 1	}		
		1		
DEFILIBLE PARTS TAUKT PUT TVANKES GVERS I VCQI	i I]		
	<u></u>			DEFIDDIFYMESTADKIPDTKVGRRDYTVRHRESGVERSIVCQI

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A-Alanine, C-Cysteine, D-Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ŀ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ı	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	•	\=possible nucleotide insertion)
			DTVEGSKKVTIRSPVQIRNHFSVPLSVYEGDTLLGTASPENEFN
İ			IPLGSYRSFIFLKPEDENYQMCEGIDFEEIIKNDGALLKKKCRS
İ			KNPSKESFLINIVPEKDNLTSLSVYSEDGWDLPYIMHLWPPILL
1			RNLLPYKIAYYIEGIENSVFTLSEGHSAQICTAQLGKARLHLKL
	1	•	LDYLNHDWKSEYHIKPNQQDISFVSFTCVTEMEKTDLDIAVHMT
i	Ì		YNTGQTVVAFHSPYWMVNKTGRMLQYKADGIHRKHPPNYKKPVL
			FSFQPNHFFNNNKVQLMVTDSELSNQFSIDTVGSHGAVKCKGLK
	l		MDYQVGVTIDLSSFNITRIVTFTPFYMIKNKSKYHISVAEEGND
1			KWLSLDLEQCIPFWPEYASSKLLIQVERSEDPPKRIYFNKQENC
			ILLRLDNELGGIIAEVNLAEHSTVITFLDYHDGAATFLLINHTK
			NELVQYNQSSLSEIEDSLPPGKAVFYTWADPVGSRRLKWRCRKS
			HGEVTQKDDMMMPIDLGEKTIYLVSFFEGLQRIILFTEDPRVFK
1	1		VTYESEKAELAEQEIAVALQDVGISLVNNYTKQEVAYIGITSSD
1			VVWETKPKKKARWKPMSVKHTEKLEREFKBYTESSPSEDKVIOL
1			DTNVPVRLTPTGHNMKILQPHVIALRRNYLPALKVEYNTSAHQS
1			SFRIQIYRIQIQNQIHGAVFPFVFYPVKPPKSVTMDSAPKPFTD
			VSIVMRSAGHSQISRIKYFKVLIQEMDLRLDLGFIYALTDLMTE
			ABVTENTEVELFHKDIEAFKEEYKTASLVDQSQVSLYEYFHISP
J	j		IKLHLSVSLSSGREEAKDSKQNGGLIPVHSLNLLLKSIGATLTD
			VQDVVFKLAFFELNYQFHTTSDLQSEVIRHYSKQAIKQMYVLIL
			GLDVLGNPFGLIREFSEGVEAFFYEPYQGAIQGPEEFVEGMALG
			LKALVGGAVGCLACAASKITGAMAKGVAAMTMDEDYQQKRREAM
1			NKOPAGFREGITRGGKGLVSGFVSGITGIVTKPIKGAOKGGAAG
			FFKGVGKGLVGAVARPTGGIIDMASSTFQGIKRATETSEVESLR
			PPRFFNEDGVIRPYRLRDGTGNQMLQKIQFYREWIMTHSSSSDD
			DDDDDDDDESDLNH
6239	2108	634	KPGMAGKGSSGRRPLLLGLLVAVATVHLVICPYTKVERSFNLQA
			THOLLYHWOOLEGYDHLEFPGVVPRTFLGPVVLAVFSSPAVYVL
1 1			SLLEMSKFYSQLIVRGVLGLGVIFGLWTLQKEVRRHFGAMVATM
1			FCWVTAMQFHLMFYCTRTLPNVLALPVVLLALAAWLRHEWARFI
			WLSAFAIIVFRVELCLFLGLLLLALGNRKVSVVRALRHAVPAG
			ILCLGLTVAVDSYFWRQLTWPEGKVLWYNTVLNKSSNWGTSPLL
1			WYFYSALPRGLGCSLLFIPLGLVDRRTHAPTVLALGFMALYSLL
			PHKBLRFIIYAF?MLNITAARGCSYLLNNYKKSWLYKAGSLLVI
]	·	!	GHLVVNAAYSATALYVSHFNYPGGVAMQRLHQLVPPQTDVLLHI
1 1	•		DVAAAQTGVSRFLQVNSAWRYDKREDVQPGTGMLAYTHILMEAA
			PGLLALYRDTHRVLASVVGTTGVSLNLTQLPPFNVHLQTKLVLL
 			ERLPRPS
6240	2202	1176	HERGDSLKEPTSIAESSRHPSYRSEPSLEPESFRSPTFGKSFHF
1 I			DPLSSGSRSSSLKSAQGTGFELGQLQSIRSEGTTSTSYKSLANQ
	·		TRNGSLSYDSLLTPSDSPDFESVQAGPEPDPPLGYTSPFLSARL
			AQQREAERHPRLVPTGPTHREPSPVRYDNLSRHIVASLQEREKL
1	•		LRQSPPLPGREEEPGLGDSGIQSTPGSGHAPRTSSSSDDSKRSP
, ,		İ	LGKTPLGRPAVPRFGKPDGLRGRGVGSPEPGPTAPYLGRSMSYS
1	İ		9QKAQPGVSETEEVALQPLLTPKDEVQLKTTYSKSNGQPKSLGS
J			ASPGPGQPPLSSPTRGGVKKVSGVGGTTYEISV
6241	3	1341	RNAEEKKRLSLQREKI IARVS I DNRTRALVQALRRTTDPKLCIT
1 . 1			RVEELTFHLLEFPEGKGVAVKERIIPYLLRLRQIKDETLQAAVR
'			EILALIGYVDPVKGRGIRILSIDGGGTRGVVALQTLRKLVELTQ
			KPVHQLFDYICGVSTGAILAFMLGLFHMPLDECBELYRKLGSDV
1 1	ł	i	FSQNVIVGTVKMSWSHAFYDSQTWENILKDRMGSALMIETARNP
1 1	Ì	ŀ	TCPKVAAVSTIVNRGITPKAFVFRNYGHFPGINSHYLGGCQYKM
1	!	-	WQAIRASSAAPGYFAEYALGNDLHQDGGLLLNNPSALAMHECKC
	ļ	j	LWPDVPLECIVSLGTGRYESDVRNTVTYTSLKTKLSNVINSATD
	1		TEEVHIMLDGLLPPDTYFRFNPVMCENIPLDESRNEKLDQLQLE
<u> </u>			GLKYIERNEQKMKKVAKILSQEKTTLQKINDWIKLKTDMYEGLP

SEQ	Predicted	Predicted end	lamino agid gogmont contribution
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F-Phenylalanine, G-Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ł	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ĺ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ŀ	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	•	\=possible nucleotide insertion)
			FFSKL
6242	198	1310	QHFLPGAETWSPGAAVCTARRFPGRSLAAFPRPAAPRRAVEMGE
			SSEDIDOMPSTLLGENDLLTQSLGVDTLPPPDPNPPRAEFNYSV
			GFKDLNESLNALEDQDLDALMADLVADISEAEQRTIQAQKESLQ
1	ł		NOHHSASLQASIFSGAASLGYGTNVAATGISQYEDDLPPPPADP
1			VLDLPLPPPPPEPLSQEEEEAQAKADKIKLALEKLKEAKVKKLV
1 .			VKVHMNDNSTKSLMVDERQLARDVLDNLFBKTHCDCNVDWCLYB
1			IYPELQIERFFEDHENVVEVLSDWTRDTENKILFLEKEEKYAVF
			KNPQNFYLDNRGKKESKETNEKMNAKNKESLLEVRLILQSGRKE
			KDVCSIFKSFASENNGKI
6243	1509	614 .	RSASRFSGCWSRDSTCCCCPSTCWSRSSASCPRARWPPSSAPAT
			TSRASSRRLACGPQTRAGAETRSTAMIRANSAARDTRRATCRSA
			AGTPSPTTMTCLTDVPTGCAAVEPTARLPAAAWASTITTGCCPA
			MGQAGAGPAGRKGSEAGGGPGRAHHAHPSPLPREPRVRTGPPAH
i			SPTPGSIDPSPELSWGSAGVTQESPLLDPVDFLLFRTRAVDPLR
			RVFFFFYQHLTFFSIQPQPPPCHAFHPRDPPAGTKRQLILVPLK
6244	2119		GPPILAPILSLTPILSRWSCYFPRSRIAQGWHLS
0244	2119	1745	FEHAYASQFGTFLGNNESERCKLKLQQKTMSLWSWVNQPSELSK
1			FTNPLFEANNLVIWPSVAPQSLPLWEGIFLRWNRSSKYLDEAYE
6245	81	1140	EMVNIIEYNKELQAKVNILRRQLAELETEDGMQESP
}	0.1	1148	LSLRNAKYSFPQELISLFSMTDLNDNICKRYIKMITNIVILSLI
1			ICISLAFWIISMTASTYYGNLRPISPWRWLFSVVVPVLIVSNGL
1	· .		KKKSLDHSGALGGLVVGFILTIANFSFFTSLLMFFLSSSKLTKW
			KGEVKKRLDSEYKEGGQRNWVQVFCNGAVPTELALLYMIENGPG
1	,		EIPVDFSKQYSASWMCLSLLAALACSAGDTWASEVGPVLSKSSP RLITTWEKVPVGTNGGVTVVGLVSSLLGGTFVGIAYFLTQLIFV
1			NDLDISAPQWPIIAFGGLAGLLGSIVDSYLGATMQYTGLDESTG
1			MVVNSPTNKARHIAGKPILDNNAVNLFSSVLIALLLPTAAWGFW
1 }			PRG
6246	1177	359	SLWPWILMDDSLMQISLQLLCVYTANFPNGCSSLCWSSCGQHPV
	1	•	QATHRGAVSNSLMLCILKLASQMPLENTTVQQMVFMLLSNLALS
[]	J		HDCKGVIQKSNFLQNFLSLALPKGGNKHLSNLTILWLKLLLNIS
1 . 1			SGEDGQQMILRLDGCLDLLTEMSKYKHKSSPLLPLLIFHNVCFS
			PANKPKILANEKVITVLAACLESENQNAQRIGAAALWALIYNYO
]]	1		KAKTALKSPSVKRRVDEAYSLAKKTFPNSEANPLNAYYLKCLEN
<u> </u>			LVQLLNSS
6247	3	1678	NSRVWGPWTEPSAGSLRPMARKQNRNSKELGLVPLTDDTSHAGP
			PGPGRALLECDHLRSGVPGGRRRKDWSCSLLVASLAGAFGSSFL
	Ī		YGYNLSVVNAPTPYIKAFYNESWERRHGRPIDPDTLTLLWSVTV
	Í		SIFAIGGLVGTLIVKMIGKVLGRKHTLLANNGFAISAALLMACS
ļ			LQAGAFEMLIVGRFIMGIDGGVALSVLPMYLSBISPKEIRGSLG
·			QVTAIFICIGVFTGQLLGLPELLGKESTWPYLFGVIVVPAVVQL
			LSLPFLPDSPRYLLLEKHNEARAVKAFQTFLGKAHVSQEVBEVL
	ļ		AESRVQRSIRLVSVLELLRAPYVRWQVVTVIVTMACYQLCGLNA
		i	IWFYTNSIFGKAGIPPAKIPYVTLSTGGIETLAAVFSGLVIEHL
			GRRPLLIGGFGLMGLFFGTLTITLTLQDHAPWVPYLSIVGILAI
	j	j	IASFCSGPGGIPFILTGEFFQQSQRPAAFIIAGTVNWLSNPAVG
		ĺ	LLFPFIQKSLDTYCFLVFATICITGAIYLYFVLPETKNRTYAEI
6248	56	1773	SQAFSKRNKAYPPEEKIDSAVTDGKINGRP
		1/13	VPPPRMMAAVPPGLEPWNRVRIPKAGNRSAVTVQNPGAALDLCI
{	İ	.	AAVIKECHLVILSLKSQTLDAETDVLCAVLYSNHNRMGRHKPHL
1	i	1	ALKQVEQCLKRLKNMNLEGSIQDLFELFSSNENQPLTTKVCVVP
}	1	I	SQPVVELVLMKVLGACKLLLRLLDCCCKTFLLTVKHI.GLQEFII
		1	LNLVMVGLVSRLWVLYKGVLKRLILLYEPLFGLLQEVARIQPMP
			YFKDFTFPSDITEFLGQPYFEAFKKKMPIAFAAKGINKLLNKLF LINEQSPRASEETLLGISKKAKQMKINVQNNVDLGQPVKNKRVF
			

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
İ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	aedneuce	Codon, /-possible nucleotide deletion.
	sequence		\=possible nucleotide insertion)
1			KEESSEFDVRAFCNQLKHKATQETSFDFKCSQSRLKTTKYSSQK
i			VIGTPHAKSFVQRFREAESFTQLSEEIQMAVVWCRSKKLKAQAI
		1	FLGNKLLKSNRLKHLEAQGTSLPKKLECIKTSICNHLLRGSGIK
1			TSKHHLRQRRSQNKFLRRQRKPQRKLQSTLLREIQQFSQGTRKS
į.			ATDTSAKWRLSHCTVHRTDLYPNSKQLLNSGVSMPVIQTKEKMI
6249	56	1773	HENLRGIHENETDSWTVMQINKNSTSGTIKETDDIDDIFALMGV
1 00.5]	1//3	VPPPRMMAAVPPGLEPWNRVRIPKAGNRSAVTVQNPGAALDLCI
ĺ			AAVIKECHLVILSLKSQTLDARTDVLCAVLYSNHNRMGRHKPHL
	ļ		ALKQVEQCLKRLKNMNLEGSIQDLFELFSSNENQPLTTKVCVVP
	<u> </u>		SQPVVELVLMKVLGACKLLLRLLDCCCKTFLLTVKHLGLQEFII LNLVMVGLVSRLWVLYKGVLKRLILLYBPLFGLLQEVARIQPMP
1			YFKDFTFPSDITEFLGQPYPEAFKKKMPIAFAAKGINKLLNKLF
			LINEQSPRASEETLLGISKKAKQMKINVQNNVDLGQPVKNKRVF
1			KEESSEFDVRAFCNQLKHKATQETSFDFKCSQSRLKTTKYSSQK
1			VIGTPHAKSFVQRFREAESFTQLSEEIQMAVVWCRSKKLKAQAI
	ì		FLGNKLLKSNRLKHLEAQGTSLPKKLECIKTSICNHLLRGSGIK
1	٠.		TSKHHLRQRRSQNKFLRRQRKPQRKLQSTLLREIQQFSQGTRKS
1			ATDTSAKWRLSHCTVHRTDLYPNSKQLLNSGVSMPVIQTKEKMI
4.5			HENLRGIHENETDSWTVMQINKNSTSGTIKETDDIDDIFALMGV
6250	232	1306	LAALHIMALPFRKDLEKYKDLDEDELLGNLSETELKOLETVLDD
İ			LDPENALLPAGFRQKNQTSKSTTGPFDREHLLSYLEKEALEHKD
1	i		REDYVPYTGEKKGKIFIPKQKPVQTFTEEKVSLDPELEEALTSA
1 .			SDTELCDLAAILGMHNLITNTKFCNIMGSSNGVDQEHFSNVVKG
			EKILPVFDEPPNPTNVEESLKRTKENDAHLVEVNLNNIKNIPIP
			TLKDFAKALETNTHVKCFSLAATRSNDPVATAFAEMLKVNKTLK
			SLNVESNFITGVGILALIDALRDNETLAELKIDNQRQQLGTAVE
ļ			LEMAKMLEENTNILKFGYQFTQQGPRTRAANAITKNNDLVRKRR VEGDHO
6251	62	972	TPGSGPMSAWAAASLSRAAARCLLARGPGVRAAPPRDPRPSHPE
1 .	·		PRGCGAAPGRTLHFTAAVPAGHNKWSKVRHIKGPKDVBRSRIFS
			KLCLNIRLAVKEGGPNPEHNSNLANILEVCRSKHMPKSTIETAL
			KMBKSKDTYLLYEGRGPGGSSLLIEALSNSSHKCQADIRHILNK
	i		NGGVMAVGARHSFDKKGVIVVEVEDREKKAVNLERALEMAIEAG
			AEDVKETEDEBERNVFKFICDASSLHQVRKKLDSLGLCSVSCAL
			EFIPNSKVQLAEPDLEQAAHLIQALSNHEDVIHVYDNIE
6252	27	1897	EEFCTWIAVRVGEMETAPKPGKDVPPKKDKLQTKRKKPRRYWEE
1 1			ETVPTTAGASPGPPRNKKNRELRPQRPKNAYILKKSRISKKPQV
['		PKKPREWKNPESQRGLSGAQDPFPGPAPVPVEVVQKFCRIDKSR
	}		KLPHSKAKTRSRLEVABAEEEETSIKAARSELLLAEEPGFLEGE
			DGEDTAKICQADIVEAVDIASAAKHFDLNLRQFGPYRLNYSRTG
			RHLAFGGRRGHVAALDWVTKKLMCBINVMEAVRDIRFLHSEALL
			AVAQNRWLHIYDNQGIELHCIRRÇDRVTRLEFLPFHFLLATASE
			TGFLTYLDVSVGKIVAALNARAGRLDVMSQNPYNAVIHLGHSNG
	J		TVSLWSPAMKEPLAKILCHRGGVRAVAVDSTGTYMATSGLDHQL
			KIFDLRGTYQPLSTRTLPHGAGHLAFSQRGLLVAGMGDVVNIWA
			GOGKASPPSLEQPYLTHRLSGPVHGLQFCPFEDVLGVGHTGGIT
			SMLVPGAGEPNFDGLESNPYRSRKQRQEWEVKALLEKVPARLIC LDPRALAEVDVISLEQGKKEQIERLGYDPQAKAPFQPKPKQKGR
			SSTASLVKRKRKVMDEEHRDKVRQSLQQQHHKEAKAKPTGARPS
			ALDREVAR ALD
6253	27	1897	EEFCTWIAVRVGEMETAPKPGKDVPPKKDKLQTKRKKPRRYWEE
	į.		ETVPTTAGASPGPPRNKKNRELRPQRPKNAYILKKSRISKKPQV
	1	ľ	PKKPREWKNPESQRGLSGAQDPFPGPAPVPVEVVQKFCRIDKSR
			KLPHSKAKTRSRLEVAEABEEETSIKAARSELLLAEEPGFLEGE
			DGEDTAKICQADIVEAVDIASAAKHFDLNLRQFGPYRLNYSRTG
			RHLAFGGRRGHVAALDWVTKKLMCEINVMEAVRDIRFLHSEALL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion.
<u> </u>	sequence	<u></u>	\=possible nucleotide insertion)
1	•		AVAQNRWLHIYDNQGIELHCIRRCDRVTRLEFLPFHFLLATASE
		ĺ	TGFLTYLDVSVGKIVAALNARAGRLDVMSQNPYNAVIHLGHSNG
1			TVSLWSPAMKEPLAKILCHRGGVRAVAVDSTGTYMATSGLDHQL
1	i		KIFDLRGTYQPLSTRTLPHGAGHLAFSQRGLLVAGMGDVVNIWA
1	ł		GQGKASPPSLEQPYLTHRLSGPVHGLQFCPFEDVLGVGHTGGIT
1			SMLVPGAGEPNFDGLESNPYRSRKQRQEWEVKALLEKVPAELIC
1.			LDPRALAEVDVISLEQGKKEQIERLGYDPQAKAPFQPKPKQKGR
1		•	SSTASLVKRKRKVMDEEHRDKVRQSLQQQHHKEAKAKPTGARPS ALDRFVR
6254	155	1139	HALGREGGSQELSAAACGCFALRLEAPGSGRPALAPGAAAFAGL
		. 1133	GGAPRFPPRGSAAGRTMLLKEYRICMPLTVDEYKIGQLYMISKH
1			SHEQSDRGEGVEVVQNEPFEDPHIGNGQFTEKRVYLNSKLPSWA
			RAVVPKIFYVTEKAWNYYPYTITEYTCSFLPKFSIHIETKYEDN
]]		KGSNDTIFDNEAKDVEREVCFIDIACDEIPERYYKESEDPKHFK
1			SEKTGRGQLREGWRDSHQPIMCSYKLVTVKFEVWGLQTRVEQFV
			HKVVRDILLIGHRQAFAWVDEWYDMTMDDVREYEKNMHEQTNIK
			VCNQHSSPVDDIESHAQTST
6255	1	1444	PTRPQQELLVSLATVIFVASQKALSVESKAVIKQQLESVSNGWT
	ļ		VYRIARQASRMGNHDMAKELYQSLLTOVASKHFYFWLNSLKEFS
1			HAEQCLTGLQEENYSSALSCIAESLKFYHKGIASLTAASTPIND
1			LSFQCEFVKLRIDLLQAFSQLICTCNSLKTSPPPAIATTIAMTI
Į .			GNDLQRCGRISNQMKQSMEEFRSLASRYGDLYQASFDADSATLR
1			NVELQQQSCLLISHAIEALILDPESASFQEYGSTGTAHADSEYE
			RRMMSVYNHVLEEVESLNGKYTPVSYMHTACLCNAIIALLKVPL
			SFQRYFFQKLQSTSIKLALSPSPRNPAEPIAVQNNQQLALKVEG
1 ,	,		VVQHGSKPGLFRKIQSVCLNVSSTLQSKSGQDYKIPIDNMTNEM EQRVEPHNDYFSTQFLLNFAILGTHNITVESSVKDANGIVWKTG
1 1			PRTTIFVKSLEDPYSQQIRLQQQQAQQPLQQQQQRNAYTRF
6256	1	1542	CRGAGAEPAANPRSPRSLVPSLESTSTSVPPAPGTMATDSWALA
!	Ì		VDEQEAAAESLSNLHLKEEKIKPDTNGAVVKTNANAEKTDEEEK
1 1	İ		EDRAAQSLLNKLIRSNLVDNTNQVEVLQRDPNSPLYSVKSFEEL
, ,			RLKPQLLQGVYAMGFNRPSKIQENALPLMLAEPPQNLIAQSQSG
1 1			TGKTAAFVLAMLSQVEPANKYPQCLCLSPTYELALQTGKVIEQM
ł I			GKFYPELKLAYAVRGNKLERGQKISEQIVIGTPGTVLDWCSKLK
			FIDPKKIKVFVLDEADVMIATQGHQDQSIRIORMLPRNCOMLLF
[j		SATFEDSVWKFAQKVVPDPNVIKLKREEETLDTIKOYYVLCSSR
			DEKFQALCNLYGAITIAQAMIFCHTRKTASWLAAELSKEGHOVA
]	ľ		LLSGEMMVEQRAAVIERFREGKEKVLVTTNVCARGIDVEQVSVV
1			INFOLPYDKOGNPONETYLHRIGRTGRFGKRGLAVNMVDSKHSM
6257	210	615	NILNRIQEHFNKKIERLDTDDLDEIEKIAN
		0.72	AFIPAMAELIQKKLQGEVEKYQQLQKDLSKSMSGRQKLEAQLTE
1		ł	NNIVKEELALLDGSNVVFKLLGPVLVKQELGEARATVGKRLDYI
	}	,	TAEIKRYESQLRDLERQSEQQRETLAQLQQEFQRAQAAKAGAPG KA
6258	210	615	
	1		AFIPAMAELIQKKLQGEVEKYQQLQKDLSKSMSGRQKLEAQLTE NNIVKEELALLDGSNVVFKLLGPVLVKQELGEARATVGKRLDYI
1			TAEIKRYESQLRDLERQSEQQRETLAQLQQEFQRAQAAKAGAPG
	ł		KA INDIANIES OD KIDLEK Ó SKO Ó KELL PÓL Ó Ó EL Ó KVAGY BARANTAR A LA CHARLAS A CHARLA
6259	2	1540	ILEKGFPSQCHPERKWKVDDVLESSQENEDDHFWELLFHNNKTV
	J		SVENGDRGSKTFNLGTDPVSLRNYPYKICDSCEMNLKNISGLII
		[SKKNCSRKKPDEFNVCEKLLLDIRHEKIPIGEKSYKYDQKRNAI
	.	1	NYHQDLSQPSFGQSFEYSKNGQGFHDEAAFFTNKRSQIGETVCK
	·	ł	YNECGRIFIESLKLNISQRPHLEMEPYGCSICGKSFCMNLRFGH
		ĺ	QRALTKDNPYEYNEYGEIFCDNSAFIIHQGAYTRKILREYKVSD
			KTWEKSALLKHQIVHMGGKSYDYNENGSNFSKKSHLTOLRRAHT
			GEKTFECGECGKTFWEKSNLTQHQRTHTGEKPYECTECGKAFCQ
			

SEQ	Predicted	Predicted end	Buring acid coment contribute simple
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1.0.	location	1	Glutamic Acid, F=Phenylalanine, G=Glycine,
		corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	_	\=possible nucleotide insertion)
			KPHLTNHQRTHTGEKPYECKQCGKTFCVKSNLTEHQRTHTGEKP
			YECNACGKSFCHRSALTVHQRTHTGEKPFICNECGKSFCVKSNL
i			THUADTUTOPEDANGARECOVERGENCAL TOUR THEORY
ĺ			IVHORTHTGEKPYKCNECGKTFCEKSALTKHORTHTGEKPYECN
6260	2002		ACGKTFSQRSVLTKHQRIHTRVKALSTS
0200	2081	1436	GTGPEIHACAHASARAPGSRAMALRELKVCLLGDTGVGKSSIVW
1	1		RFVEDSFDPNINPTIGASFMTKTVQYQNELHKFLIWDTAGQERF
			RALAPMYYRGSAAAIIVYDITKEETFSTLKNWVKELRQHGPPNI
}	1		VVAIAGNKCDLIDVREVMERDAKDYADSIHAIFVETSAKNAINI
j	!		NELFIEISRRIPSTDANLPSGGKGFKLRRQPSEPKRSCC
6261	3	1188	FWYRLGPGTRSRWPRRGSWAASLVPRGPSPAALVTSPCPPDPLR
			SPACEPCRPDFAPRPALLLRSGPRSAPAVTGKPALKGQPGPWPG
1			MAEVSIDQSKLPGVKEVCRDFAVLEDHTLAHSLQEQEIEHHLAS
Į.			NVQRNRLVQHDLQVAKQLQEEDLKAQAQLQKRYKDLEQQDCBIA
	!		QEIQEKLA1EAERRRIQEKKDEDIARLLQEKELQEEKKRKKHFP
1	ł i		EFPATRAYADSYYYEDGGMKPRVMKEAVSTPSRMAHRDQEWYDA
			EIARKLQEBELLATQVDMRAAQVAQDEEIARLLMAEEKKAYKKA
	i		KEREKSSLDKRKODPEWKPKTAKAANSKSKESDEPHHSKNERPA
			RPPPPIMTDGEDADYTHFTNQQSSTRHFSKSESSHKGFHYKH
6262	2	1759	PECHSOGLCSVHRPGKVPQARMSGLVLGQRDEPAGHRLSQEEIL
1			GSTRLVSQGLEALRSEHQAVLQSLSQTIECLQQGGHEEGLVHEK
			ARQLRRSMENIELGLSEAQVMLALASHLSTVESEKQKLRAQVRR
ĺ	l l		LCQENQWLRDELAGTQQRLQRSBQAVAQLEEEKKHLEFLGQLRQ
}]		YDEDGHTSBEKEGDATKDSLDDLFPNEEEEDPSNGLSRGQGATA
1	ĺ		100CCVETTARI DELL'AND AND AND AND AND AND AND AND AND AND
1			AQQGGYEIPARLRTLHNLVIQYAAQGRYEVAVPLCKQALEDLER
			TSGRGHPDVATMLNILALVYRDQNKYKEAAHLLNDALSIRESTL
			GPDHPAVAATLNNLAVLYGKRGKYKEAEPLCQRALEIREKVLGT
]			NHPDVAKQLNNLALLCQNQGKYEAVERYYQRALAIYEGQLGPDN
			PNVARTKNNLASCYLKQGKYAEABTLYKEILTRAHVQEFGSVDD
			DHKPIWMHAEEREEMSKSRHHEGGTPYAEYGGWYKACKVSSPTV
	i		NTTLRNLGALYRROGKLEAAETLEECALRSRROGTDPISQTKVA
l i			ELLGESDGRRTSQEGPGDSVKFEGGEDASVAVEWSGDGSGTLQR
J I	i i		SGSLGKIRDVLRR
6263	1	2408	RELDSLADLPERIKPPYANGLSTSHLRSSSVEDVKLIISEGRPT
	1		TEVERCEMPSVICENTKOPOTICPPENIOCOTY MURCHWEST
] }	İ		IEVRRCSMPSVICEHTKQFQTISBESNQGSLLTVPGDTSPSPKP
1 . 1	 		EVFSNVPERDLSNVSNIHSSFATSPTGASNSKYVSADRNLIKNT
J			APVNTVMDSPVHLEPSSQVGVIQNKSWEMPVDRLETLSTRDFIC
	. [PNSNIPDQESSLQSFCNSENKVLKENADFLSLRQTELPGNSCAQ
			DPASFMPPQQPCSFPSQSLSDAESISKHMSLSYVANQEPGILQQ
			KNAVQIISSALDTDNESTKDTENTFVLGDVQKTDAFVPVYSDST
	İ		IQEASPNFEKAYTLPVLPSEKDFNGSDASTQLNTHYAFSKLTYK
1 1	i		SSSGHEVENSTTDTQVISHEKENKLESLVLTHLSRCDSDLCEMN
			AGMPKGNLNEQDPKHCPESEKCLLSIEDEESQQSILSSLENHSQ
			QSTQPEMHKYGQLVKVELEENABDDKTENQIPQRMTRNKANTMA
1 1			NQSKQILASCTLLSEKDSESSSPRGRIRLTEDDDPQIHHPRKRK
1 1	1		VSDVDODVOVGDGI.I.ON VEVTOOOT NATIONAL VIDE VIDE VIDE VIDE VIDE VIDE VIDE VIDE
[VSRVPQPVQVSPSLLQAKEKTQQSLAAIVDSLKLDEIQPYSSER
] }			ANPYFEYLHIRKKIEEKRKLLCSVIPQAPQYYDEYVTFNGSYLL
			DGNPLSKICIPTITPPPSLSDPLKELFRQQEVVRMKLRLQHSIE
			REKLIVSNEQBVLRVHYRAARTLANQTLPFSACTVLLDAEVYNV
			PLDSQSDDSKTSVRDRFNARQFMSWLQDVDDKFDKLKTCLLMRQ
			QHEAAALNAVQRLEWQLKLQELDPATYKSISIYEIQEFYVPLVD
<u>. </u>			VNDDFELTPI
6264	143	1960	KHRQENNALDMAPEIHMTGPMCLIENTNGELVANPEALKILSAI
	1		TQPVVVVAIVGLYRTGKSYLMNKLAGKNKGFSLGSTVKSHTKGI
ļ [į	WWW.CABHDAADAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
ļ <u>†</u>	•		WMWCVPHPKKPEHTLVLLDTEGLGDVKKGDNQNDSWIFTLAVLL
		1	SSTLVYNSMGTINQQAMDQLYYVTELTHRIRSKSSPDENENEDS
<u> </u>			ADFVSFFPDFVWTLRDFSLDLEADGQPLTPDEYLEYSLKLTQGT

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1.0.	location	corresponding	With the diagram of t
1	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first	1	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	amino acid residue of	P=Proline, Q=Glutamine, R=Arginine,
İ	i e		S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			SQKDKNFNLPRLCIRKFFPKKKCFVFDLPIHRRKLAQLEKLQDE
			ELDPEFVQQVADFCSYIFSNSKTKTLSGGIKVNGPRLESLVLTY
	1		INAISRGDLPCMENAVLALAQIENSAAVQKAIAHYDQQMGQKVQ
1	1		LPAETLQELLDLHRVSEREATEVYMKNSFKDVDHLFQKKLAAQL
ļ			DKKRDDFCKQNQEASSDRCSALLQVIFSPLEEEVKAGIYSKPGG
1			YCLFIQKLQDLEKKYYEEPRKGIQAEEILQTYLKSKESVTDAIL
1	l		QTDQILTEKEKEIEVECVKAESAQASAKMVEEMQIKYQQMMEEK
1			EKSYQBHVKQLTEKMERERAQLLEEQEKTLTSKLQEQARVLKER
1			CQGESTQLQNEIQKLQKTLKKKTKRYMSHKLKI
6265	143	1960	KHRQENNALDMAPEIHMTGPMCLIENTNGELVANPEALKILSAI
		2200	
			TOPVVVVAIVGLYRTGKSYLMNKLAGKNKGFSLGSTVKSHTKGI
	j		WMWCVPHPKKPEHTLVLLDTEGLGDVKKGDNQNDSWIFTLAVLL
			SSTLVYNSMGTINQQAMDQLYYVTELTHRIRSKSSPDENENEDS
			ADFVSFFPDFVWTLRDFSLDLEADGQPLTPDEYLEYSLKLTQGT
Į.			SQKDKNFNLPRLCIRKFFPKKKCFVFDLPIHRRKLAQLEKLQDE
			ELDPEFVQQVADFCSYIFSNSKTKTLSGGIKVNGPRLESLVLTY
ł			INAISRGDLPCMENAVLALAQIENSAAVQKAIAHYDQQMGQKVQ
			LPAETLQELLDLHRVSEREATEVYMKNSFKDVDHLFQKKLAAQL
			DKKRDDFCKQNQEASSDRCSALLQVIFSPLEEEVKAGIYSKPGG
			YCLFIQKLQDLEKKYYEEPRKGIQAEEILQTYLKSKESVTDAIL
			QTDQILTEKEKEIEVECVKAESAQASAKMVEEMQIKYQQMMEEK
1			EKSYQEHVKQLTEKMERERAQLLEEQEKTLTSKLQEQARVLKER
			CQGESTQLQNEIQKLQKTLKKKTKRYMSHKLKI
6266	276	1421	GSHQKQMLVPCFLYSLQNRKPSLYGSLTCQGIGLDGIPEVTASE
ļ			GFTVNEINKKSIHISCPKENASSKFLAPYTTFSRIHTKSITCLD
İ			ISSRGGLGVSSSTDGTMKIWQASNGELRRVLEGHVFDVNCCRFF
1			PSGLVVLSGGMDAQLKIWSAEDASCVVTFKGHKGGILDTAIVDR
			GRNVVSASRDGTARLWDCGRSACLGVLADCGSSINGVAVGAADN
1			SINLGSPEQMPSEREVGTEAKMLLLAREDKKLQCLGLQSRQLVF
}			LFIGSDAFNCCTFLSGFLLLAGTQDGNIYQLDVRSPRAPVQVIH
ł i			RSGAPVLSLLSVRDGFIASQGDGSCFIVQQDLDYVTELTGADCD
			PVYKVATWEKQIYTCCRDGLVRRYQLSDL
6267	3	622	LGMMKKNNSAKRGPQDGNQQPAPPEKVGWVRKFCGKGIFREIWK
	·		NRYVVLKGDQLYISEKEVKDEKNIQEVFDLSDYEKCEELRKSKS
			RSKKNHSKFTLAHSKQPGNTAPNLIFLAVSPEEKESWINALNSA
1	·		ITRAKNRILDEVTVEEDSYLAHPTRORAKIQHSRRPPTRGHLMA
1 1	ļ	•	VASTSTSDGMLTLDLIQEEDPSPEEPTSLC
6268	160	1368	
		~~00	HRELCONLPAGLSSALIDNPLTLLLSIDTYVMLQEPVTFQDVAV
]			DFSREEWGLLGPTQRTEYRDVMLETFGHLVSVGWETTLENKELA
j i			PNSDIPEEEPAPSLKVQESSRDCALSSTLEDTLQGGVQEVQDTV
] [}		LKQMESAQEKDLPQKKHFDNRESQANSGALDTNQVSLQKIDNPE
] [1		SQANSGALDTNQVLLHKIPPRKRLRKRDSQVKSMKHNSRVKIHQ
1			KSCERQKAKEGNGCRKTFSRSTKQITFIRIHKGSQVCRCSECGK
]	j		IFRNPRYFSVHKKIHTGERPYVCQDCGKGFVQSSSLTQHQRVHS
[GERPFECQECGRTFNDRSAISQHLRTHTGAKPYKCQDCGKAFRQ
			SSHLIRHQRTHTGERPYACNKCGKAFTQSSHLIGHQRTHNRTKR
			KKKQPTS
6269	2886	1449	HASAPTRRNMAAASPLRDCHAWKDARLPLSTTSNEACKLFDATL
{	ļ		TQYVKWTNDKSLGGIEGCLSKLKAADPTFVMGHAMATGLVLIGT
1			GSSVKLDKELDLAVKTMVEISRTQPLTRREQLHVSAVETFANGN
			FPKACELWEQILQDHPTDMLALKFSHDAYFYLGYQEQMRDSVAR
} }	į		IYPFWTPDIPLSSYVKGIYSFGLMETNFYDQAEKLAKEALSIND
	j		TDAWSVHTVAHIHEMKAEIKDGLEFMQHSETLWKDSDMLACHNY
[WHWALYLIEKGEYEAALTIYDTHILPSLQANDAMLDVVDSCSML
			YRLQMEGVSVGQRWQDVLPVARKHSRDHILLFNDAHFLMASLGA
[]			HDPQTTQELLTTLRDASESPGENCQHLLARDVGLPLCQALVEAE
		i	The state of the s

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SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
i	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
]	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence		\=possible nucleotide insertion)
			DGNPDRVLELLLPIRYRIVQLGGSNAQRDVFNQLLIHAALNCTS
L			SVHKNVARSLLMERDALKPNSPLTERLIRKAATVHLMQ
6270	23	2086	SVTVTLGSEGDGRPPTYHLEEMEQEPQNGEPAEIKITREAYKKA
İ	· ·	•	FLFVNKGLNTDELGQKEEAKNYYKQGIGHLLRGISISSKESEHT
			GPGWESARQMQQKMKETLQNVRTRLEILEKGLATSLQNDLQEVP
			KLYPEFPPKDMCEKLPEPQSFSSAPQHAEVNGNTSTPSAGAVAA
ļ			PASLSLPSQSCPAEAPPAYTPQAAEGHYTVSYGTDSGEFSSVGE
1			EFYRNHSQPPPLETLGLDADELILIPNGVQIFFVNPAGEVSAPS
1	1 .		YPGYLRIVRFLDNSLDTVLNRPPGFLOVCDWLYPLVPDRSDVIK
1			CTAGAYMFPDTMLQAAGCFVGVVLSSELPEDDRELFEDLI.ROMS
'			DLRLQANWNRAEEENEFQIPGRTRPSSDOLKEASGTDVKOLDOG
	1		NKDVRHKGKRGKRAKDTSSEEVNLSHIVPCEPVPREKPKELDEW
1 .			SEKVAHNILSGASWVSWGLVKGAEITGKAIOKGASKLRERTODE
1			EKPVEVSPAVTKGLYIAKQATGGAAKVSOFLVDGVCTVANCVGK
i			ELAPHVKKHGSKLVPESLKKDKDGKSPLDGAMVVAASSVQGFST
]		VWQGLECAAKCIVNNVSAETVQTVRYKYGYNAGEATHHAVDSAV
1	1		NVGVTAYNINNIGIKAMVKKTATQTGHTLLEDYQIVDNSQRENQ
6271	32	1058	EGAANVNVRGEKDEQTKEVKEAKKKDK
1		1030	GCGVKTAGMVGREKELSIHFVPGSCRLVBBEVNIPNRRVLVTGA
Ī			TGLLGRAVHKEFQQNNWHAVGCGFRRARPKFEQVNLLDSNAVHH
			IIHDFQPHVIVHCAAERRPDVVENQPDAASQLNVDASGNLAKEA AAVGAFLIYISSDYVFDGTNPPYREEDIPAPLNLYGKTKLDGEK
			AVLENNLGAAVLRIPILYGEVEKLEESAVTVMFDKVQFSNKSAN
		•	MDHWQQRFPTHVKDVATVCRQLAEKRMLDPSIKGTFHWSGNEQM
J	4.4		TKYEMACAIADAFNLPSSHLRPITDSPVLGAQRPRNAQLDCSKL
<u> </u>			ETLGIGQRTPFRIGIKESLWPFLIDKRWRQTVFH
6272	1136	528	GAVMEDAAAPGRTEGVLERQGAPPAAGQGGALVELTPTPGGLAL
	1		VSPYHTHRAGDPLDLVALAEQVQKADEFIRANATNKLTVIAEQI
1		•	QHLQEQARKVLEDAHRDANLHHVACNIVKKPGNIYYLYKPESGO
1	1		QYFSIISPKEWGTSCPHDFLGAYKLOHDLSWTPYEDIEKODAKI
6273			SMMDTLLSQSVALPPCTEPNFQGLTH
02/3	256	843	SCPRVSPECRSLGCQVMFSLPLNCSPDHTRRGSCWGPPODIKIA
			SAAWNSKCHPGAGAAMARQHARTLWYDRPRYVFMEFCVEDSTDV
			HVLIEDHRIVFSCKNADGVELYNEIEFYAKVNSKDSODKRSSRS
'			ITCFVRKWKEKVAWPRLTKEDIKPVWLSVDFDNWRDWEGDEEME
6274	56	17/0	LAHVEHYAEVRDNTYCVLPT
		1142	AAAAMAAAAGGGAGAARSLSRFRGCLAGALLGDCVGSFYEAHDT
[]		· .	VDLTSVLRHVQSLEPDPGTPGSERTEALYYTDDTAMARALVQSL
			LAKEAFDEVDMAHRFAQEYKKDPDRGYGAGVVTVFKKLLNPKCR
			DVFEPARAQFNGKGSYGNGGAMRVAGISLAYSSVQDVQKFARLS
i 1	1	,	AQLTHASSLGYNGAILQALAVHLALQGESSSKHFLKQLLGHMED LEGDAQSVLDARELGMEERPYSSRLKKIGELLDQASVTREEVVS
	·	İ	ELGNGIAAFESVPTAIYCFLRCMEPDPEIPSAFNSLQRTLIYSI
	į		SLGGDTDTIATMAGAIAGAYYGMDQVPESWQQSCEGYEETDILA
L			QSLHRVFQKS
6275	20	565	SRRGRARCLARGSRRPVFRPAKTMAFMVKTMVGGQLKNLTGSLG
		-	GGEDKGDGDKSAAEAQGMSREEYEEYQKQLVEEKMERDAQFTQR
l	1	[KAERATLRSHFRDKYRLPKNETDESQIQMAGGDVELPRELAKMI
			EEDTEEEEEKASVLGQLASLPGLNLGSLKDKAQATLGDLKQSAE
			KCHVM
6276	797	97	TLLPLPPLPDTEGMILLNTGLEGTVAENPVPIVHTPSGMILTLE
	1	l.	SCLQQLATHPGHWGIHLQIAEPAALRPSLALLARI.SSLGLLHWD
1			VWVGAKISHGSFSVPGHVAGRELLTAVAEVFPHVTVAPGWPREV
1		l l	LGSGYREQLLTDMLELCQGLWQPVSFOMOAMLLGHSTAGATGRI.
İ	İ	1	LASSPRATVTVEHNPAGGDYASVRTALLAARAVDRTRVYYRLPO
			GYHKDLLAHVGRN

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
İ	amino acid	sequence	Codon, /=possible nucleotide deletion.
	sequence		\=possible nucleotide insertion)
6277	4600	2744	MAFRTEMGLYYSYPKTIVEAPSFLNGVWMIMNDKLTEYPLVINT
İ			LKRFNLYPEVILASWYRIYTKIMDLIGIQTKICNTVTIGEGLSP
			TESCEGLGDPACFYVAVIFILNGLMMALFFIYGTYLSGSRLGGL
ŀ			VTVLCFFFNHGECTRVMWTPPLRESFSYPFLVLQMLLVTHILRA
i			TKLYRGSLIALCISNVFFMLPWQFAQFVLLTQIASLFAVYVVGY
			IDICKLRKIIYIHMISLALCFVLMFGNSMLLTSYYASSLVIIWG
	1		ILAMKPHFLKINVSELSLWVIQGCFWLFGTVILKYLTSKIFGIA
i			NDAHIGNLLTSKFFSYKDFDTLLYTCAAEFDFMEKETPLRYTKT
	}		LLLPVVLVGFVAIVRKIISDMWGVLAKQQTHVRKHQFDHGELVY
	1		HALQLLAYTALGILIMRLKLFLTPHMCVMASLICSRQLFGWLFC
ſ	·		KVHPGAIVFAILAAMSIQGSANLQTQWNIVGEFSNLPQEELIEW
] .	1		IKYSTKPDAVFAGAMPTMASVKLSALRPIVNHPHYEDAGLRART KIVYSMYSRKAAEEVKRELIKLKVNYYILEESWCVRRSKPGCSM
			PEIWDVEDPANAGKTPLCNLLVKDSKPHFTTVFQNSVYKVLEVV
1			KE
6278	3	823	ILFRLVLLSLVYLLNSVATEERKPAEVLIVEGQQYAVVGTVLLL
1			IRIILEYCQGVDNIPSVTTDMLTRLSDLLKYFNSKSCQLVLGAG
1			ALOVVGLKTITTKNLALSSRCLQLIVHYIPVIRAHFEARLPPKQ
			YSMLRHFDHITKDYHDHIAEISAKLVAIMDSLFDKLLSKYEVKA
İ			PVPSACFRNICKOMTKMHEAIFDLLPEEQTOMLFLRINASYKLH
			LKKQLSHLNVINDGGPQNGLVTADVAFYTGNLQALKGLKDLDLN
6279	127		MARIWEQXR
62/3	121	1687	GGAMASDGARKQFWKRSNSKLPGSIQHVYGAQHPPFDPLLHGTL
			LRSTAKMPTTPVKAKRVSTFQEFESNTSDAWDAGEDDDELLAMA
			AESLINSEVVMETANRVLRNHSQRQGRPTLQEGPGLQQKPRPEAE
1 :			PPSPPSGDLRLVKSVSESHTSCPAESASDAAPLQRSQSLPHSAT VTLGGTSDPSTLSSSALSEREASRLDKFKQLLAGPNTDLEELRR
1 1	•		LSWSGIPKPVRPMTWKLLSGYLPANVDRRPATLQRKQKEYFAFI
1			EHYYDSRNDEVHQDTYRQIHIDIPRMSPEALILQPKVTEIFER:
1 1			LFIWAIRHPASGYVQGINDLVTPFFVVFICEYIEABEVDTVDVS
i l	<u>.</u>		GVPAEVLCNIEADTYWCMSKLLDGIQDNYTFAQPGIQMKVKMLE
1			ELVSRIDEQVHRHLDQHEVRYLQFAFRWMNNLLMREVPLRCTIR
j			LWDTYQSEPDGFSHFHLYVCAAFLVRWRKEILEEKDFQELLLFL
			QNLPTAHWDDEDISLLLAEAYRLKFAFADAPNHYKK
6280	857	2515	ECCDQKMGSRNSSSAGSGSGDPSEGLPRRGAGLRRSEEEEEEDE
			DVDLAQVLAYLLRRGQVRLVQGGGAANLQFIOALLDSEEENDRA
]			WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGOLGLRRAA
]]			QKHSFPRMLHQRERGLCHRGSFSLGEQSRVISHFLPNDLGFTDS
	İ		YSQKAFCGIYSKDGQIFMSACQDQTIRLYDCRYGRFRKFKSIKA
] [1		RDVGWSVLDVAFTPDGNHFLYSSWSDYIHICNIYGEGDTHTALD
	,		LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRRTLQ
	ļ		IESHEDDVNAVAFADISSQILFSGGDDAICKVWDRRTMREDDPK
			PVGALAGHQDGITFIDSKGDARYLISNSKDQTIKLWDIRRFSSR
!			BGMEASRQAATQQNWDYRWQQVPKKAWRKLKLPGDSSLMTYRGH
1 1	. }	l	GVLHTLIRCRFSPIHSTGQQFIYSGCSTGKVVVYDLLSGHIVKK LTNHKACVRDVSWHPFEEKIVSSSWDGNLRLWQYRQAEYFQDDM
			PBSEECASAPAPVPQSSTPFSSPQ
6281	857	2515	ECCDQKMGSRNSSSAGSGSGDPSEGLPRRGAGLRRSEEBEEEDE
	f	-	DVDLAQVLAYLLRRGQVRLVQGGGAANLQFIQALLDSEBENDRA
	ļ		WDGRLGDRYNPPVDATPDTRELEFNEIKTQVBLATGQLGLRRAA
	İ		QKHSFPRMLHQRERGLCHRGSFSLGEQSRVISHFLPNDLGFTDS
			YSQKAFCGIYSKDGQIFMSACQDQTIRLYDCRYGRFRKFKSIKA
	}		RDVGWSVLDVAFTPDGNHFLYSSWSDYIHICNIYGEGDTHTALD
		Ī	LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRRTLQ
	ļ		IESHEDDVNAVAFADISSOILFSGGDDAICKVWDRRTMRRDDDK
		[PVGALAGHQDGITFIDSKGDARYLISNSKDQTIKLWDIRRFSSR

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ŀ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
j	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Ston
1	amino acid	sequence	Codon, /=possible nucleotide deletion.
	sequence	[\=possible nucleotide insertion)
ŀ			BGMEASRQAATQQNWDYRWQQVPKKAWRKLKLPGDSSLMTYRGH
	1		GVLHTLIRCRFSPIHSTGQQFIYSGCSTGKVVVYDLLSGHIVKK
1			LTNHKACVRDVSWHPFEEKIVSSSWDGNLRLWQYRQAEYFODDM
 			PESEECASAPAPVPQSSTPFSSPQ
6282	125	906	RMAACRALKAVLVDLSGTLHIEDAAVPGAQEALKRLRGASVIIR
İ			FVTNTTKESKQDLLERLRKLEFDISEDEIFTSLTAARSLLERKO
ł			VRPMLLVDDRALPDFKGIQTSDPNAVVMGLAPEHFHYOILNOAF
]			RLLLDGAPLIAIHKARYYKRKDGLALGPGPFVTALEYATDTKAT
1			VVGKPEKTFFLEALRGTGCEPEEAVMIGDDCRDDVGGAQDVGML
6283			GILVKTGKYRASDEEKINPPPYLTCESFPHAVDHILQHLL
0203	140	1043	LSLFGIHVMNPFWSMSTSSVRKRSEGEEKTLTGDVKTSPPRTAP
ł			KKQLPSIPKNALPITKPTSPAPAAQSTNGTHASYGPFYLEYSLL
ı			AEFTLVVKQKLPGVYVQPSYRSALMWFGVIFIRHGLYQDGVFKF
			TVYIPDNYPDGDCPRLVFDIPVFHPLVDPTSGELDVKRAFAKWR
i			RNHNHIWQVLMYARRVPYKIDTASPLNPEAAVLYEKDIQLFKSK
			VVDSVKVCTARLFDQPKIEDPYAISFSPWNPSVHDEAREKMLTQ
6284	1	2879	KKKPEEQHNKSVHVAGLSWVKPGSVQPFSKEEKTVAT
1	-	20/9	RSVIPGSTISSRWPGLSRPRFMAAHEWDWFQREELIGQISDIRV
			QNLQVERENVQKRTFTRWINLHLEKCNPPLEVKDLFVDIQDGKI
'			LMALLEVLSGRNLLHEYKSSSHRIFRLNNIAKALKFLEDSNVKL
]			VSIDAAEIADGNPSLVIGLIWNIILFFOIKELTGNLSRNSPSSS LAPGSGGTDSDSSFPPTPTAERSVAISVKDQRKAIKALLAWVQR
1			KTRKYGVAVQDFAGSWRSGLAFLAVIKAIDPSLVDMKQALENST
1			RENLEKAFSIAQDALHIPRLLEPEDIMVDTPDEQSIMTYVAQFL
]			ERFPELEAEDIFDSDKEVPIESTFVRIKETPSEQESKVFVLTEN
1			GERTYTVNHETSHPPPSKVFVCDKPESMKEFRLDGVSSHALSDS
			STEFMHQIIDQVLQGGPGKTSDISEPSPESSILSSRKENGRSNS
1 1			LPIKKTVHFEADTYKDPFCSKNLSLCFEGSPRVAKESLRQDGHV
1 1			LAVEVAEEKEQKQESSKIPESSSDKVAGDIFLVEGTNNNSQSSS
1			CNGALESTARHDEESHSLSPPGENTVMADSFQIKVNLMTVRALE
1 1	1		EGDYFEAIPLKASKFNSDLIDFASTSQAFNKVPSPHETKPDEDA
	1		EAFENHAEKLGKRSIKSAHKKKDSPEPOVKMDKHEPHODSGEEA
1 1	ľ		EGCPSAPEETPVDKKPEVHEKAKRKSTRPHYEEEGEDDDLOGVG
[]	j		EELSSSPPSSCVSLETLGSHSEEGLDFKPSPPLSKVSVIPHDLF
1 1	ľ		YFPHYEVPLAAVLEAYVEDPEDLKNEEMDLEEPEGYMPDLDSRE
			EEADGSQSSSSSSVPGESLPSASDQVLYLSRGGVGTTPASEPAP
	ļ		LAPHEDHOQRETKENDPMDSHQSQESPNLENIANPLEENVTKES
] []		ISSKKKEKRKHVDHVESSLFVAPGSVQSSDDLEEDSSDYSIPSR
6285	2157	1331	TSHSDSSIYLRRHTHRSSESDHFSLCSVEERSRSG
	-431	1221	SCKTENLLEMWWFQQGLSFLPSALVIWTSAAFIFSYITAVTLHII
			IDPALPYISDTGTVAPEKCLFGAMLNIAAVLCIATIYVRYKQVH
		ļ	ALSPEENVIIKLNKAGLVLGILSCLGLSIVANFQKTTLFAAHVS
			GAVLTFGMGSLYMFVQTILSYQMQPKIHGKQVFWIRLLLVIWCG
			VSALSMLTCSSVLHSGNFGTDLEQKLHWNPEDKGYVLHMITTAA EWSMSFSFFGFFLTYIRDFQKISLRVEANLHGLTLYDTAPCPIN
	1		NERTRLLSRDI
6286	1619	276	KAGASCCGSANPYVSVGKSCVLLAMAQLQTRFYTDNKKYAVDDV
	-		PFSIPAASEIADLSNIINKLLKDKNEFHKHVEFDFLIKGQFLRM
		1	PLDKHMEMENISSBEVVEIEYVEKYTAPQPEQCMFHDDWISSIK
	1		GAEEWILTGSYDKTSRIWSLEGKSIMTIVGHTDVVKDVAWVKKD
! [1		SLSCLLLSASMDQTILLWEWNVERNKVKALHCCRGHAGSVDSIA
		ł	VDGSGTKFCSGSWDKMLKIWSTVPTDEBDEMEESTNRPRKKQKT
\ \	ł	ļ	EQLGLTRTPIVTLSGHMEAVSSVLWSDAEEICSASWDHTIRVWD
i	į	!	VESGSLKSTLTGNKVFNCISYSPLCKRLASGSTDRHIRLWDPRT
		ļ	KDGSLVSLSLTSHTGWVTSVKWSPTHEQQLISGSLDNIVKLWDT
			RSCKAPLYDLAAHEDKVLSVDWTDTGLLLSGGADNKLYSYRYSP
			

WO 01/53312

SEQ	Predicted	Predicted end	T 3-2
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
[corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
İ	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
ļ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W-Trumbonhan V-Trumbonhan V-Trumbonhan
J	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide deletion,
			TTSHVGA
6287	278	1482	MOFFPNFQIGLRSTSGKEKYSGDAGFLGDALQLFLQCLALDEDF
-			APAKLOVOKILCOLLLPENLKEGLKESSWSSLPCTKNRPFDFHS
- {	1		VMEESQSLNEPSPKQSEEIPEVTSEPVKGSLNRAQSAQSINSTE
į		1	MPAREDCLKRVSSEPVLSVQEKGVLLKRKLSLLEQDVIVNEDGR
1		}	NKLKKQGETPNEVCMFSLAYGDIPEELIDVSDFECSLCMRLFFE
			PVTTPCGHSFCKNCLERCLDHAPYCPLCKESLKEYLADRRYCVT
1	1		QLLEELIVKYLPDELSERKKIYDEETAELSHLTKNVPIFVCTMA
1	1		YPTVPCPLHVFEPRYRLMIRRSIQTGTKQFGMCVSDTQNSFADY
			GCMLQIRNVHFLPDGRSVVDTVGGKRFRVLKRGMKDGYCTADIE
		. *	YLEDV
6288	1	743	VTLYPCRGLVGNLLLGASGMASGCKIGPSILNSDLANLGAECLR
1 .	: [MLDSGADYLHLDVMDGHFVPNITFGHPVVESLRKOLGODPFFDM
		,	HMMVSKPEQWVKPMAVAGANOYTFHLEATENPGALIKDIDENGM
			KVGLAIKPGTSVEYLAPWANQIDMALVMTVEPGFGGOKFMEDMM
	1.		PKVHWLRTQFPSLDIEVDGGVGPDTVHKCAEAGANMIVSGSAIM
6289	 		RSEDPRSVINLLRNVCSEAAQKRSLDR
0203	1	743	VTLYPCRGLVGNLLLGASGMASGCKIGPSILNSDLANLGAECLR
1	1.		MLDSGADYLHLDVMDGHFVPNITFGHPVVESLRKOLGODDFFDM
]			HMMVSKPEQWVKPMAVAGANOYTFHLEATENPGALTKDIPENGM
İ			KVGLAIKPGTSVEYLAPWANQIDMALVMTVBPGFGGQKFMEDMM
1	1		PKVHWLRTQFPSLDIEVDGGVGPDTVHKCAEAGANMIVSGSAIM
6290	3	1856	RSEDPRSVINLLRNVCSEAAQKRSLDR
	1 1	1929	TIGRWLIGVYETVAPTLACLPRPRLRRRRRRRRRRRRRRMISRYTRKA
}			VPQSLELKGITKHALNHHPPPEKLEEISPTSDSHEKDTSSQSKS
i	1		DITRESSFTSADTGNSLSAFPSYTGAGISTEGSSDFSWGYGELD
1	1 .		QNATEKVQTMFTAIDELLYEQKLSVHTKSLQEECQQWTASFPHL
	1		RILGRQIITPSEGYRLYPRSPSAVSASYETTLSQERDSTIFGIR GKKLHFSSSYAHKASSIAKSSSFCSMERDEEDSIIVSEGIIEEY
1	1		LAPDHIDIEEGFHGKKSEAATEKQKLGYPPIAPFYCMKEDVLAY
	.[VFDSVWCKVVSCMEQLTRSHWEGFASDDESNVAVTRPDSESSCV
1	1 1		LSELHPLVLPRVPQSKVLYITSNPMSLCQASRHQPNVNDLLVHG
1.	1		MPLQPRNLSLMDKLLDLDDKLLMRPGSSTILSTRNWPNRAVEFS
			TSSLSYTVQSTRRRNPPPRTLHPISTSHSCAETPRSVEEILRGA
		·	RVPVAPDSLSSPSPTPLSRNNLLPPIGTABVEHVSTVGPQRQMK
	[PHGDSSRAQSAVVDEPNYQOPOERLLI.PDFFPRPNTTOSFIJ.DT
		ļ	QYRRSCAVEYPHQARPGRGSAGPQLHGSTKSQSGGRPVSRTROG
6291	1770		P
1 0231	1732	602	LVAKMASSASARTPAGKRVINQEELRRLMKEKQRLSTSRKRIES
1			PFAKYNRLGQLSCALCNTPVKSELLWOTHVLGKOHPEKVAELKG
ł			AKEASQGSSASSAPQSVKRKAPDADDODVKRAKATI.VPOVODST
	1	1	SAWTTNFDKIGKEFIRATPSKPSGLSLLPDYEDEEEEEEEGD
		. 1	GERKRGDASKPLSDAQGKEHSVSSSREVTSSVLPNDFFSTNPDK
		1	APIIPHSGSIEKAEIHEKVVERRENTAEALPEGFFDDPEVDARV
[.		ĺ	RKVDAPKDQMDKEWDEFQKAMRQVNTISEAIVAEEDEEGRLDRQ
	[[IGEIDEQIECYRRVEKLRNRQDEIKNKLKEILTIKELQKKEEEN
6292	1835	1142	ADSDDEGELQDLLSQDWRVKGALL
			TCPGAMKMVAPWTRFYSNSCCLCCHVRTGTILLGVWYLIINAVV
ĺ			LLILLSALADPDQYNFSSSELGGDFEFMDDANMCIAIAISLLMI
			LICAMATYGAYKORAAWIIPFFCYQIFDFALNMLVAITVLIYPN
		İ	SIQEYIRQLPPNFPYRDDVMSVNPTCLVLIILLFISIILTFKGY
		i	LISCVWNCYRYINGRNSSDVLVYVTSNDTTVLLPPYDDATVNGA AKEPPPPYVSA
6293	2382		FWCTLGTVDVHPIGWCAINSKILVPPRTIHAKFTDWKGYLMKRL
1			VGSRTLPVDFHIKMVESMKYPFRQGMRLEVVDKSQVSRTRMAVV
		ì	DTVIGGRLRLLYEDGDSDDDFWCHMWSPLIHPVGWSRRVGHGIK

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A-Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
-	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
İ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown *=Ston
	amino acid	sequence	Codon, /=possible nucleotide deletion.
	sequence	<u></u>	\=possible nucleotide insertion)
]			MSERRSDMAHHPTFRKIYCDAVPYLFKKVRAVYTEGGWFEEGMK
			LEAIDPLNLGNICVATVCKVLLDGYLMICVDGGPSTDGLDwrcv
1	,		HASSHAIFPATFCQKNDIELTPPKGYEAOTFNWENYLEKTKSKA
ļ			APSRLFNMDCPNHGFKVGMKLEAVDLMEPRLICVATVKRVVHRI.
i	į	•	LSIHFDGWDSEYDQWVDCESPDIYPVGWCELTGYQLQPPVAAEP
1			ATPLKAKEATKKKKKQFGKKRKRIPPTKTRPLRQGSKKPLLEDD
			PQGARKISSEPVPGEIIAVRVKEEHLDVASPDKASSPELPVSVE
6294	354	1014	NIKQETDD
	334	1814	AQLTTRGRTVAGGVRWIPSPFPDLELYSCCLGTDRGFPELSHHC
			KNVIATASDYDMAEITNIRPSFDVSPVVAGLIGASVLVVCVSVT
1	}		VFVWSCCHQQAEKKHKNPPYKFIHMLKGISIYPETLSNKKKIIK
i			VRRDKDGPGREGGRRNLLVDAAEAGLLSRDKDPRGPSSGSCIDQ
	ì		LPIKMDYGEELRSPITSLTPGESKTTSPSSPEEDVMLGSLTFSV DYNFPKKALVVTIQEAHGLPVMDDQTQGSDPYIKMTILPDKRHR
1			VKTRVLRKTLDPVFDETFTFYGIPYSQLQDLVLHFLVLSFDRFS
1	١ ، ا		RDDVIGEVMVPLAGVDPSTGKVQLTRDIIKRNIQKCISRGELQV
1			SLSYQPVAQRMTVVVLKARHLQKMDIAGLSGNPYVKVNVYYGRK
1			RIAKKKTHVKKCTLNPIFNESFIYDIPTDLLPDISIEFLVIDFD
1		•	RTTKNEVVGRLILGAHSVTASGAEHWREVCESPRKPVAKWHSLS
			EY
6295	2795	617	VSSALLTGATSGSDAAKSEGASASPLSCTNAVAMDRPDEGPPAK
1			TRRLSSSESPORDPPPPPPPPPPLLRLPLPPPPOORPRIOEETEAA
1 1			QVLADMRGVGLGPALPPPPPYVILEEGGIRAYFTIGAECPGWDG
			TIESGYGEAPPPTESLEALPTPEASGGSLEIDFOVVOSSSEGGE
			GALETCSAVGWAPQRLVDPKSKEEAIIIVEDEDEDERESMBSSP
1 1			RRRRRRKQRKVKRESRERNAERMESILQALEDIQLDLEAVNI
1			KAGKAFLRLKRKFIQMRRPFLERRDLIIQHIPGFWVKAFLNHPR
1 1			ISILINRRDEDIFRYLTNLQVQDLRHISMGYKMKLYFQTNPYFT
1			NMVIVKEFORNRSGRLVSHSTPIRWHRGQEPQARRHGNQDASHS
1	1		FFSWFSNHSLPEADRIAEIIKNDLWVNPLRYYLRERGSRIKRKK QEMKKRKTRGRCEVVIMEDAPDYYAVEDIFSEISDIDETIHDIK
1			ISDFMETTDYFETTDNEITDINENICDSENPDHNEVPNNETTDN
! i			NESADDHETTONNESADDNNENPEDNNKNTDDNEENPNNNENTY
1 1			GNNFFKGGFWGSHGNNQDSSDSDNEADEASDDEDNDGNEGDNEG
1 1			SDDDGNEGDNEGSDDDDRDIEYYEKVIEDFDKDQADYEDVIEII
1 !			SDESVEEEGIEEGIQQDEDIYEEGNYEEEGSEDVWEEGEDSDDS
			DLEDVLQVPNGWANPGKRGKTG
6296	727	1199	RHCGCDAQGACDSLPPTGTSSPVTARNAIPEARCCVWLLDGTTV
	1		EAVRPARERLARKELROKRMOOFSRDSAYSSNKDSTCLLTRDDT
	ĺ		LGTSLQFPSPFSGTISFGSFSDSGIFPLGSQCCLGFQQFSISGK
6297	1		KWALIHKRVRLSVFGARWGRIYFGK
,	-	922	QRAAAAS PSSCGPRGAEYGALMAMEGYWRFLALLGSALLVGFLS
		}	VIFALVWVLHYREGLGWDGSALEFNWHPVLMVTGFVFIQGIAII
	ŀ	i	VYRLPWTWKCSKLLMKSIHAGLNAVAAILAIISVVAVFENHNVN
			NIANMYSLHSWVGLIAVICYLLQLLSGFSVFLLPWAPLSLRAFL
		1	MPIHVYSGIVIFGTVIATALMGLTEKLIFSLRDPAYSTFPPEGV
į į		Í	FVNTLGLLILVFGALIFWIVTRPQWKRPKEPNSTILHPNGGTEQ
6298	3	985	GARGSMPAYSGNNMDKSDSBLNNEVAARKRNLALDEAGQRSTM SVPLRPLSLSGTLOGAGGTTTVMANARY
		j	SVPLRRLSLSGTLQGAGTTTKMAVARLAAVAAWVPCRSWGWAAV
·]	1	f	PFGPHRGLSVLLARIPORAPRWLPACROKTSLSFLNRPDLPNLA YKKLKGKSPGIIFIPGYLSYMNGTKALAIEEFCKSLGHACIRFD
			YSGVGSSDGNSEESTLGKWRKDVLSIIDDLADGPQILVGSSLGG
- 1	<u> </u>		WLMLHAAIARPEKVVALIGVATAADTLVTKFNQLPVELKKEVEM
	1		KGVWSMPSKYSEEGVYNVQYSFIKEAEHHCLLHSPIPVNCPIRL
		į	LHGMKDDIVPWHTSMQVADRVLSTDVDVILRKHSDHRMREKADI
		1.	QLLVYTIDDLIDKLSTIVN

WO 01/53312

SEQ	Predicted	; Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A-Alanine, C-Cysteine, D-Aspartic Acid, E-
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	Lalouging Manager and Relysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
Ī	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ŀ		sequence	Codon, /=possible nucleotide deletion,
6299	sequence		\=possible nucleotide insertion)
6299	512	814	ECDLEGIMPNVTISLSLPTNGSPLQDILVHPCVTSLDSAILTSS
	Ī		SIDAMDDSAFSGPYKFPFTPPLESFNLCFYTSQVPVPPILGFYQ
	<u></u>		MKEEEVQLRNNH
6300	121	692	AAPSCWSQRGVPAAGTPSSPRLLVSRAAAPSAGPWGAWRQGARA
	l	1	AQSPFSIPNSSSVPYGSQDSVHSSPEDGGGGRDRPVGGSPGGPR
			LVIGSLPAHLSPHMFGGFKCPVCSKFVSSDEMDLHLVMCLTKPR
1			ITYNEDVLSKDAGECAICLEELQQGDTIARLPCLCIYHKGCIDE
			WFEVNRSCPEHPSD
6301	616	284	GKFVPVNWEPPQPLPFPKYLRCYRCLLETKELGCLLGSDICLTP
			AGSSCITLHKKNSSGSDVMVSDCRSKEQMSDCSNTRTSPVSGFW
Ĺ I			IFSQYCFLDFCNDPQNRGLYTP
6302	490	745	IFGFLHLFHMEHSFLLVCALFAHVFFSSSCGSSVALHSDPCLLS
L			PVLLNCLPGDLRPLDELYAQKLKYKAISEELDHALNDMTSL
6303	2	1961	YWNEYGGGLLWQSWQEXHPGQALSSEPWNFPDTKEEWEQHYSQL
1 1			YWYYLEQFQYWEAQGWTFDASQSCDTDTYTSKTEADDKNDEKCM
1 1			KVDLVSFLSSPIMGDNDSSGTSDKDHSEILDGISNIKLNSEEVT
1			QSQLDSCTSHDGHQQLSEVSSKRECPASGQSEPRNGGTNEESNS
			SGNTNTDPPAEDSQKSSGANTSKDRPHASGTDGDESEEDPPEHK
1 1			PSKLKRSHELDIDENPASDFDDSGSLLGFKYGSGQKYGGIPNFS
1 1		i	HRQVRYLEKNVKLKSKYLDMRRQIKMKNKHIFFTKESEKPFFKK
			SKILSKVEKFLTWVNKPMDEEASQESSSHDNGHDASTSCDSEEQ
1 1			DMSVKKGDDLLETNIPEPEKCQSVSSAGELETENYERDSLLATV
1 . 1			PDEQDCVTQEVPDSRQAETEAEVKKKNKKKNKKVNGLPPEIAA
1 1			VPELAKYWAQRYRLFSRFDDGIKLDREGWFSVTPEKIAEHIAGR
1 1			VSQSFKCDVVVDAFCGVGGNTIQFALTGMRVIAIDIDPVKIALA
1 1			RNNAEVYGIADKIEFICGDFLLLASFLKADVVFLSPPWGGPDYA
· 1			TARTEDIDTMMCDCCETERI CUNTONIA DONA DE LA CONTRACTORIO DE LA CONTRACTOR
1 1			TARTFDIRTMMSPDGFEIFRLSKKITNNIVYFLPRNADIDQVAS
6304	1	1438	LAGPGGQVEIEQNFLNNKLKTITAYFGDLIRRPASET
1	-	2170	HRARVDRSRESPGGDLRHPGRVRRDITLSGHPRLSTQHVVLLRE
1 1	1		DEVGDPGTKDLGHPQHGSPIQETQSEVVTLVSPLPGSDMAALPA
			NRATSGLTLWPHTAEGRDLLGAENRALTGGQQAEDPTLASGAYQ
1 1	1		WPGSVEKLQGSVWCDAETLLSSSRTGGQAPPWLTDHDVQMLRLL
]	j		AQGEVVDKARVPAHGQVLQVGFSTEAALQDLSSPRLSQLCSQGL
	i		CGLIKRPGDLPEVLSFHVDRVLGLRRSLPAVARRFHSPLLPYRY
			TDGGARPVIWWAPDVQHLSDPDEDQNSLALGWLQYQALLAHSCN
1 1	1		WPGQAPCPGIHHTEWARLALFDFLLQVHDRLDRYCCGFEPEPSD
			PCVEERLREKCRNPAELRLVHILVRSSDPSHLVYIDNAGNLQHP
1 1			EDKLNFRLLEGIDGF?ESAVKVLASGCLQNMLLKSLQMDPVFWE
6305	99		SQGGAQGLKQVLQTLEQRGQVLLGHIQKHNLTLFRDEDP
	, , ,	420	NMIWRGRSTYRPRPRRSVPPPELIGPMLEPGDEEPQQEEPPTES
			RDPAPGQEREEDQGAAETQVPDLEADLQELSQSKTGDECGDGPD
6306		<u>·</u>	VQGKILTKSEQFKMPEGR
0300	1	1874	PTRPSKVKVPHTFLIHSYTRPTVCQACKKLLKGLFRQGLQCKDC
) I	Ì		KFNCHKRCATRVPNDCLGEALINGDVPMEEATDFSBADKSALMD
1	J	!	ESEDSGVIPGSHSENALHASEEEEGEGGKAQSSLGYIPLMRVVO
		İ	SVRHTTRKSSTTLREGWVVHYSNKDTLRKRHYWRLDCKCITLFO
		{	NNTTNRYYKEIPLSEILTVESAQNFSLVPPGTNPHCFEIVTANA
1		j	TYFVGEMPGGTPGGPSGQGAEAARGWETAIRQALMPVILODAPS
1 1			APGHAPHRQASLSISVSNSQIQENVDIATVYQIFPDEVLGSGOF
1 1			GVVYGGKHRKTGRDVAVKVIDKLRFPTKQESQLRNEVAILOSLR
1 1	1	1	HPGIVNLECMFETPEKVFVVMEKLHGDMLEMILSSEKGRLPERL
[[Ī	TKFLITQILVALRHLHFKNIVHCDLKPENVLLASADPFPOVKLC
j	1	ľ	DFGFARIIGEKSFRRSVVGTPAYLAPEVLLNQGYNRSLDMWSVG
	1	J	VIMYVSLSGTFPFNEDEDINDQIQNAAFMYPASPWSHISAGAID
]	1		LINNLLQVKMRKRYSVDKSLSHPWLQEYQTWLDLRELEGKMGER
L			YITHESDDARWEQFAAEHPLPGSGLPTDRDLGGACPPQDHDMQG
			בייייייייייייייייייייייייייייייייייייי

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C-Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
I	corresponding	to first	H-Histidine, I=Isoleucine, K=Lysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
İ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W-Truntophan V Thursday V V
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
	sequence	acquence	\=possible nucleotide deletion,
		 	\=possible nucleotide insertion) LAERISVL
6307	2136	589	
		309	CFLLPRGRDPEPPEAGAAAPCAPGAPDMSFRKVVRQSKPRHVFG
ì		ł	QPVKNDQCYEDIRVSRVTWDSTFCAVNPKFLAVIVEASGGAPL
			VLPLSKTGRIDKAYPTVCGHTGPVLDIDWCPHNDEVIASGSEDC
ı			TVMVWQIPENGLTSPLTEPVVVLEGHTKRVGIIAWHPTARNVLL SAGCDNVVLIWNVGTAEELYRLDSLHPDLIYNVSWNHNGSLFCS
]		· ·	ACKDKSVRIIDPRRGTLVAEREKAHEGARPMRAIFLADGKVFTT
İ			GFSRMSERQLALWDPENLEEPMALQELDSSNGALLPFYDPDTSV
]		VYVCGKGDSSIRYFEITEEPPYIHFLNTFTSKEPQRGMGSMPKR
1			GLEVSKCEIARFYKLHERKCEPIVMTVPRKSDLFQDDLYPDTAG
i			PEAALEAEEWVSGRDADPILISLREAYVPSKQRDLKISRRNVLS
			DSRPAMAPGSSHLGAPASTTTAADATPSGSLARAGEAGKLEEVM
1			QELRALRALVKEQGDRICRLEEQLGRMENGDA
6308	2	1118	GRPTRPEKMLLSLVLHTYSMRYLLPSVVLLGTAPTYVLAWGVWR
			LLSAFLPARFYQALDDRLYCVYQSMVLFFFENYTGVQILLYGDL
1			PKNKENIIYLANHQSTVDWIVADILAIRQNALGHVRYVLKEGLK
1			WLPLYGWYFAQHGGIYVKRSAKFNEXEMRNKLQSYVDAGTPMYL
1		•	VIPPEGTRYNPEQTKVLSASQAFAAQRGLAVLKHVLTPRIKATH
ł			VAFDCMKNYLDAIYDVTVVYEGKDDGGQRRESPTMTEFLCKECP
1			KIHIHIDRIDKKDVPEEQEHMRRWLHERFEIKDKMLIEFYESPD
			PERRKRFPGKSVNSKLSIKKTLPSMLILSGLTAGMLMTDAGRKL
<u> </u>			YVNTWIYGTLLGCLWVTIKA
6309	220	563	LVAEVKEPCSLPMLSVDMENKENGSVGVKNSMENGRPPDPADWA
			VMDVVNYFRTVGFEEQASAFQEQEIDGKSLLLMTRNDVLTGLQL
		•	KLGPALKIYEYHVKPLQTKHLKNNSS
6310	36	979	GPRCWKFLILSSVNCETLRIGKAWPOSSGOERYWTPRTHSSASE
1 1			AQRGSLAELNVAAAGLWADCDOPLYDCPMCGLICTNYHILOEHU
1 1		.	DLHLBENSFQQGMDRVQCSGDLOLAHOLOOEEDRKRRSEESROE
	Ì		IEEFQKLQRQYGLDN3GGYKQQOLRNMEIEVNRGRMPPSEFHRR
1 1	1		KADMMESLALGFDDGKTKTSGIIEALHRYYONAATDVRRVWLSS
	ĺ		VVDHFHSSLGDKGWGCGYRNFQMLLSSLLONDAYNDCLKGMLIP
i		•	CIPKIQSMIEDAWKEGFDPQGASQLIIRLQGTKAWIGACEVYIL
			LTSLRV
6311	1	675	PVWWNSCEGPRLAAAARTGHGVGRRARLACLGEPRVKAAVMLTL
			ASKLKRDDGLKGSRTAATASDSTRRVSVRDKLLVKEVAELEANI.
	ł		PCTCKVHFPDPNKLHCFQLTVTPDEGYYOGGKFOFETEVPDAYN
•			MVPPKVKCLTKIWHPNITETGBICLSLLREHSIDGTGWAPTRTI.
		.	KDVVWGLNSLFTDLLNFDDPLNIEAAEHHLRDKEDFRNKVDDYI
6312	213		KRYAR
0312	<i>2</i> 13	1400	GDELVKREAGMKMLPGVGVFGTGSSARVLVPLLRAEGFTVEALW
			GKTEEEAKQLAEEMNIAFYTSRTDDILLHQDVDLVCISIPPPLT
1 • 1	1		RQISVKALGIGKNVVCEKAATSVDAFRMVTASRYYPQLMSLVGN
! !	i		VLRFLPAFVRMKQLISEHYVGAVMICDARIYSGSLLSPSYGWIC
	, [DELMGGGGLHTMGTYIVDLLTHLTGRRAEKVHGLLKTFVRQNAA
	1	İ	IRGIRHVTSDDFCFFQMLMGGGVCSTVTLNFNMPGAFVHEVMVV
[]	i		GSAGRLVARGADLYGQKNSATQEELLLRDSLAVGAGLPEQGPQD
	j	ļ	VPLLYLKGMVYMVQALRQSFQGQGDRRTWDRTPVSMAASFEDGL
6313	2	3023	YMQSVVDAIKRSSRSGEWEAVEVLTEEPDTNQNLCEALQRNNL
	•	2071	QRSGAARLAFLPSPFSPACVHRSPLSFHGCWFYFVVVFMPLGVL
· 1	ļ	ļ	FHRRRAHGCTLSCSSFVEQPTAMEAEETMECLQEFPEHHKMILD
			RLNEQREQDRFTDITLIVDGHHFKAHKAVLAACSKFFYKPFQEF
		ļ	TOEPLVEIEGVSKMAFRHLIEFTYTAKLMIOGEEEANDVWKAAE
ĺ	}		FLOMLEAIKALEVRNKENSAPLEENTTGKNEAKKRKIAETSNVI
			TESLPSAESEPVEIEVEIAEGTIEVEDEGIETLEEVASAKQSVK
}			YIQSTGSSDDSALALLADITSKYRQGDRKGQIKEDGCPSDPTSK QVEGIEIVELQLSHVKDLFHCEKCNRSFKLFYHFKEHMKSHSTE
			OVEG LET VELOT SHOWNT, PUCKYCARO CEVT RVURKETMYOUGHO

Do beginning nucleotide location corresponding cofirst anino acid ani	SEQ	Predicted	Predicted end	Dring agid
NO: nucleotide corresponding to first amino acid residue of amino acid residue of amino acid sequence		4		(A=A)anine C-Cysteins Dube-outin Deid
corresponding to first amino acid amino acid residue of amino acid sequence sequen	NO:			Glutamic Acid E-Phenylalanian Cochesia
to first amino acid residue of amino acid sequence Serine, TeThreonine, VeValine, Vevaline, V				Halistidine Talsoleucine Valuetne
amino acid residue of amino acid residue of amino acid sequence Secrine, T-Mirenoine, V-Valine, W-Tryptophan, Y-Tyrosine, K-Unknown, *-stop Sequence		corresponding		LaLeucine, Mamethionine, Nahamaraine
amino acid residue of amino acid sequence Saserine, Tefhreonine, Vavaline, Sequence	1			P=Proline O=Glutamine D=Avaining
### ### ### ### ### ### ### ### ### ##	1	amino acid		Seserine, TeThreonine, V-Valine,
sequence seq			1	W=Tryptophan VaTyrosine Y-Unknown +-Sta-
Sequence Appossible nucleotide insertion	1	amino acid		Codon. /=possible nucleotide deletion
SFKCE_LONGY_LEESAMK_ORLING_THEERCAYSKKORTICK.THE OYCEKOFDHOFHERHIRARITIESEM_FECON_CHERRIST_LICH LIACOTIOUSAKKORKKI_YECOYCUSYFNSHOOPKOHLVI_HTSDW PRHCTLCLDIEMR_GELERRILI_SOUNT_SECUSYFTEVO TEPYTSMTI_IEOYGKYRU_PLI_QVQUDSAQUTYEQYMPDLLQDS OW_HDSHMSEL_BEQVQVSY_LEVEN_CTS_SECUSYFTEVO TEPYTSMTI_IEOYGKYRU_PLI_QVQUDSAQUTYEQYMPDLLQDS OW_HDSHMSEL_BEQVQVSY_LEVEN_CTS_SECUSYFTEVO TEPYTSMTI_IEOYGKYRU_PLI_QVQUDSAQUTYEQYMPDLLQDS OW_HDSHMSEL_BEQVQVSY_LEVEN_CTS_SECUSYFTEVEDHER ADDLETKPTVDSS_TAKABRDETTALPUS_ ADDLETKPTVDSS_TAKABRDETTALPUS_CADABABAREDHED ADDLETKPTVDSS_TAKABRDETTALPUS_CADABABARAREDHED ADDLETKPTVDSS_TAKABRDETTALPUS_CADABABARAREDHED ADDLETKPTVDSS_TAKABRDETTALPUS_CADABABARAREDHED ADDLETKPTVDSS_TAKABRDETTALPUS_CADABABARAREDHED TOBPL_SEL_SEL_SEL_SEL_SEL_SEL_SEL_SEL_SEL_SE	1	sequence	•	\=possible nucleotide insertion)
GYCRKOFDRIGHERKHIRKITGEKPFECONCHERFRARMSTILLED LIACOTGVGAKKRIKLIPGOVGVSYNSHONGO PRINTIHTICHE PRHCTLCLIAFMGGRELRRHLSDAHNI SERLVTEBVLSVETRU TEPVTSMTI IEQGKURVULJELLQVGVGSAVTUPELLQUE QVHDSHMSEL BEQVQVSYLEVGRIQTERGTEVHVEBLHVERVNO MPVEVOTELLEADLHVTPSIMNOPERESSGADARAEAREDHED AEDLETKPTVOSSARKAENBORTALDVLE FRANKAGCTISCSSFVEOPTAMBAECTMECLQE PREHIKMILD LINGOPEODRATDILLIVOGHHERALETMECLQE PREHIKMILD LINGOPEODRATDILLIVOGHHERALETMECLQE PREHIKMILD LINGOPEODRATDILLIVOGHHERALETMECLQE PREHIKMILD LINGOPEODRATDILLIVOGHHERALETYTAKUM QUEBENDOWKAGAE PLQULEAK KALBURVENISHA LEETYTAKUM QUEBENDOWKAGAE PLQULEAK KALBURVENISHA LEETYTAKUM QUEBENDOWKAGAE PLQULEAK KALBURVENISHA LEETYTAKUM QUEBENDOWKAGAE PLQULEAK KALBURVENISHA LEETYTAKUM QUEBENDOWKAGAE PLQULEAK KALBURVENISHA LEETYTAKUM QUEBENDOWKAGAE PLQULEAK KALBURVENISHA LEETYTAKUM QUEBENDOWKAGAE PLQULEAK KALBURVENISHA LEETYTAKUM QUEBENDOWKAGAE PLQULEAK KALBURVENISHA LEETYTAKUM QUEBENDOWKAGAE PLQULEAK KALBURVENISHA LEETYTAKUM QUEBENDOWKAGAE PLQULEAK KALBURVENISHA LEETYTAKUM QUEBENDOWKAGAE PLQULEAK KALBURVENISHA LEETYTAKUM QUEBENDOWKAGAE PLQULEAK KALBURVENISHA LEETYTAKUM QUEBENDOWKAGAE PLQULEAK KALBURVENISHA LEETYTAKUM QUEBENDOWKAGAE PLQULEAK KALBURVENISHA LEETYTAKUM QUEBENDOWKAGAE PLAGULEAK KALBURVAL LEETYTAKUM QUEBENDOWKAGAE QUEBENDOSALAALAD LEETYTAKUM AURUS KALBURVAL LUKUM PLAGULA LUKUM PLA				SFKCEICNKRYLRESAWKOHINCYHI.FFCGVSYVODTGVYTUUG
### LTACOTYCAKKGRKKIPEQUCNSVINSMODPKOHLVIHTODK PMHCTLCDLWPMGCNELRHISDAMINISENLEVLSVETIVO TEPVTSMTIIBQUCKVHULPLLQVGVDSAQVTVEQUSPDLLQDG QVHDSHMSELEPGVQVSVLEVGRIGTEGETEVELSVETIVO HPVEVOTELLEADLDHVTPEINMGERESSQADAAEAAREDHED AEDLETKPTVDSSERKARINESSADDAAEAAREDHED AEDLETKPTVDSSERKARINESSADDAAEAAREDHED AEDLETKPTVDSSERKARINESSADDAAEAAREDHED AEDLETKPTVDSSERKARINESSADDAAEAAREDHED AEDLETKPTVDSSERKARINESSADDAAEAAREDHED RICHERDAGUS ARDEN AEDLETKSTEVEN AEDLETKSTEVEL GEFTEVRIKHILD FIRRAHGCTLSCSSFVEQPTAMIREETHECLQSFPEHKHILD RICHERDAGUS ARDEN AEDLETKSTEVEN AERCH GEFTEVEN AERCK KYRKIAETSNVI TESLFSSESEVELEVELESHTVGINGREK KYRKIAETSNVI TESLFSSESEVELEVELESSATIVERGORKGOLEDGEGEDTISK QVEGIBLVELQLSHVADLFICEKCNRSPKLFYHFKEHKKSISTE SFKCELCKKRYLESSAMKQHKVILEGGGVAFTIKKRI LTACOTGVGAKKGRKKLYECOVGNSVNSKOPGTEKHVU QYEKGFDHFGHFKEHLEKHTGEKFFEONCHERFARNSTIKKRI LTACOTGVGAKKGRKKLYECOVGNSVNSKOPGTEKHVU QYEKGFDHFGHFKEHLEKHTGEKFFEONCHERFARNSTIKKRI LTACOTGVGAKKGRKKLYECOVGNSVNSKOPGTEKHVEH PRICTLCDLWFMGGNELERHLISDAMINISERLVTEEVLSVETRVO TEBVTSMTII EDGGKVHVLELUQVDSAQVTEVOHPDLLQDS QVHDSHMSELPEOVQVSSLEVGRIGTEEGTEVHVESHVEHVU QVEKGFDHFRGSHLERHINGVTSEONTEVEN AUGUSTALAREDHVEN MPVEVOTELLEADLDHVTPEINOGERESSADDAAEAAREDHED AEDLETKFIVLDSEAKKARKKIKLAGUTSEONTEVEN AUGUSTALAREDHVEN MPVEVOTELLEADLDHVTPEINOGERESSADDAAEAAREDHED AEDLETKPTVUSSEAKKARNDENTALPAUS AEDLETKPTVUSSEAKKARNDENTALPAUS AEDLETKPTVUSSEAKKARNDENTALPAUS 1 1015 LIGLAVAVTFULVISTYPTATERPAVTTULCALGGIFTYGSLDA AEDLETKPTVUSSEAKKARNDENTALPAUS AEDLETKPTVUSSEAKKARNDENTALPAUS AEDLETKPTVUSSEAKKARNDENTALPAUS AEDLETKPTVUSSEAKKARNDENTALPAUS AEDLETKPTVUSSEAKKARNDENTALPAUS AEDLETKRANDENTALPAUS 6316 1503 792 VSAGAGTSINGSTLAGUTSUNGERESSADDISTENTALPAUS AERLEKGRANDENTTEILELUALLPAUSFLOOTIVELGE AERLEKGRANDENTTEILELUALLPAUSFLOOTIVELGE AERLEKGRANDENTALPAUS AERLEMBELALEQAKKES EDGKRIKKGAKELDERGARAPGVALSSEBLANDARSGELALEQAKKES EDGKRIKKGAKELDERGARAPGVALSEBLANDARSGELALEGARSEND 792 VSAGAGTSINGSVGTSTSTRANDSSELKRENTVTVKGTRALSENVIDR KKRENTALDAGUTS AERLEKGRANDAGUTSTRANDSSILTATAVKGANGFILMTIN BESFANDOMSTON TINNGGRESSADDEN TINNGGARSUNSTENDEN PERFAU	1			OYCEKOFDHFGHFKEHLRKHTGRKDERCDNCHEDERDNGTI VCH
PRINCTICOLM/PROGNEL RRILLSDAINI SERILVITE DUIS VETTVO TEPTY SMIT I REQUENTIVO LIQUO VENDE LA COUNTRE DE COUNTR	1]		LTACOTGVGAKKGRKKLYECOVCNSVENSWDORKDULVILUTCDV
6314 2 2071				PNHCTLCDLWFMOGNELRRHLSDAHNISERIATEEVI.SVETDVO
GOVEDSHMSELPEQUOYSYLEVORIOTEESTEVHVEEHVERNO MPVEVOTELLEADLDHYPPI MNOGERESSORDAARAPREDHED AEDLETKPTVDSSAEKABNEDRTALPVIE GOSGARALBH-PSFFSACHSTENGERSSFENGENFYFVVVFRPLOV. FRERRAHGCTLSCSSFVEOPTAMBAEETMECLOSEPSHHKMILD RLNBORGEODFTDTILTUVOGHIFKAHKAVLAACSKFYTKFOGE TOPPLVBIEGVSKMAPRILLEFTYTAKLDIGGEBANDVWKAAR FLOMEALKALEVRNKBNSAPLEENTTGKNEAKKKKLASTSNYI TESLFSASSSFVEIVEVLASGTIEVEDEGIETLEEVASAKOSVK YIGSTGSSDDSALALLADITSKYRGGRKGOIKEDGCEPSDTSK GOVEGIEIVELLGSHWADIFFCEKCRSFFLUFYH KCHMKSHSTE SFKCEICKKRYLLESSAWGHLACYLLEEGGVSKKORTKKKKKKATSNYI TESLFSASSSFVEIVEVLASGTIEVEDEGIETLEEVASAKOSVK YIGSTGSSDDSALALLADITSKYRGGRKGOIKEDGCEPSDTSK GOVEGIEIVELLGSHWADIFFCEKCRSFFLUFYH KCHMKSHSTE SFKCEICKKRYLLESSAWGHLACYLLEEGGVSKKORTKKKKKATSNYI TESLFSASSSFVEIVEVLASGTEKKRKSKAPTUREVAKKORKSKKKHVC OYCEKGFDHOFGHFKEHLBKITGERFFENDENTENGERFESDTSK GOVEGIEIVELLGSHVADIFFCEKCKRSFFLUFH KCHMKSHSTE SFKCEICKKRYLLESSAWGHLACYHSEGGVSKAGRTKKKHVC OYCEKGFDHOFGKFEKHLBKLINGERFESCONDARARAREDHED LIACOTGVGAKKGRKKLYECOVCHSVFNSWODFFENDTILLOS OVHDSHMSGLE BEQVOVSYLEVENGTOTECTEVHTSCHLYPEVTHOK PRICTICLUM PROVENTALTEVLISTENGERFESSONDARARAREDHED AEDLETKFYUDSERKARANDENTLAPVLE 6315 1 1015 IGGANNOVTFILVISTENDERSCHOOTLAPVLE WYPUSAFGGATHMOVTTI LIEUKALLPVLOFIJGGVIFSCONFF HVILIGGGVGROSTIATORYSGMLARVUNTETGIALNY VPULSAFGGATHMOVTTI LIEUKALLPVLOFIJGGVIFSCONFF HVILIGGGVGROSTIATORYSGMLARVUNTETGIALNY VPULSAFGGATHMOVTTI LIEUKALLPVLOFIJGGVIFSCONFF HVILIGGGVGROSTIATORYSGMLARVUNTETGIALDIALLAND VPRKHECLYLLMGCVFRANVSOKLVVAHMTISSELYLGOTVELOF GLIFLDOYFNIN TIDSYVVLMMAMVISSFBMUTYNKKSATD VPRKHELTILLANDIALNAMVISSFBMUTYNKSHALLGONND VSAGGGTTIANGTTI DETYVULMAMVISSFBMUTYNKKSATD VPRKHELTILLANDIALNAMVISSFBMUTYNKSHALLGONND KKSSPSSGSKSGRYSGRYGGSVSOELKRAVABELALLQOAKKS EDOKKKAAREDENDATATUKKNATATOY MKSSSPSGSKSGRYSGRYGGSVSOELKRAVABELALLQOAKKS EDOKKKAAREDENDATATUKKNATATOY MKSSSPSGSKSGRYSGRYGGSVSOELKRAVABELALLQOAKKS EDOKKKAAREDENDATATUKKNATATOY MKSSSPSGSKSGRYGGRYGGAVSOELKRAVABELALDQOAKKSS EDOKKKAAREDENDATATOY TYKKEKRI KLQIMDTAQGRYKGULAPHTOYLKCALATOY MHOVHHAAQSMLEKG PRATAAQOMTSATATUKTSTPPPTORCAC 102 839 PRATAAQOMTSATAT	İ		•	TEPVTSMT1IEQVGKVHVLPLLOVOVDSAOVTVEOVHPDLLODS
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6314 2 2071 GRGGARLAFLFJESFESJCKURSPISFHGCOPFYVVVPRPIGVL FHRRAHGCTLSCSSFVEOPTAMBABETMECLQEFPEHHKMILD RINSORRODRFDITLIVOGHHFKAHKAVLAAGSKFYKFFQGE TQEPLVBIEGVSKGARHLIBFYTAKKHIQGEEBANDVMGABE FLQMLBAIKALEVBNRENSAFLEBTTTKURGEEBANDVMGABE FLQMLBAIKALEVBNRENSAFLEBTTTKVRNBAKKRIATSNVI TESSIPSASSEPVEIEVBLEGTTEVDEBGI STILEBVASAKOSVK YIGSTGSSDDSALALLADITSKKRGDRKGGIKEDGCPSDFTSK QVGEISIVELQLSHVKOLPHCEKKNSSYTHYKEHMKSISTE SFKCEICNRKYLRESAWKOHLNCYHLBEGGYSKKQFKKIHVC QYCEKOFDFHOFHKEHLRHKTGSKPPECHCHBERPANSTLKCH LTACQTGVCAKKGRKKLYSCQVCNSVFNSHDQPKCHLVHYTGKK PNHCTLCDLWFNQGNEIRRHLISDRHVTEVFKCHWORSTE SFKCEICNRKYLRESAWKOHLNCYHLBEGGYSKKQFKKIHVC QYCEKOFDFHOFHKEHLRHKTGSKPPECHCHBERPANSTLKCH LTACQTGVCAKKGRKKLYSCQVCNSVFNSHDQPKCHLVHYTGKK PNHCTLCDLWFNQGNEIRRHLSDRAWTGHEKYBFRQV QYBSHMSBLBEQVQVSYLEVGRIGTEGGTSVHVEELHVENVGN MPVEVOTELLEADLDRIVTPIEMMQGERESSADDARBAREHBD AEDLETKFYTUSSEAREARNEDRTALPVLE GLGAVWVTYTTLVISTSYCTPATERAPFWYTLLCAIGLFYYGSLDA LDGKQARRTNSCSPLGELPDHGCDSLSTVPMAVGASIAARLGTY PDWFSCSSFIGMFYFYCAHMGTVYSGMLFGKWVTVEIQIALVI VFULSAFGGATMMDYTIPLIEIKLLIPTLGFLGGVIFSGSNFF HVLIRGGVGNGSTTATGTSVLSSGHIGHLITLIAIMIKKSATD VFRKHELLYILMFGCVFAKNSQKLVVARMYSLSTLVODTVFLGP GLLFLDQYFNNFIDETVVLMNAWVISSFDHWITYSALCLGISKH HLHNIFKTACHQAPEQVUVJSSKSKQNING WKSSSFSGKSKGSVSGAVSGAVSAVSDBELKRAVARBLALEQAKKSS EQKRIKGAKELDREPAAANEQLTAAILERICSBEERAKKHL ARQLEEKDRYLKKQDAFYKEQLAFLERSSEFYTTVOKGRABENTIT WKSSSFSGKSKQFYSGAVGAVSDBELKRAVABELALEQAKKSS EQKRIKGAKELDREPAAANEQLTAAILERICSBEERAKKHL ARQLEEKDRYLKKQDAFYKEQLARLERSSEFYSTTYGYGKAA EEVEAKYKRYESHPVCADLQAKTLCCTRENTHGTLKCSALATQY MHCVMRAKQAMLEKGG PDMFKLLICIGNSSVGKTSLLFRYADDSFTSAFVSTVG1DFKKK TVFKNEKR IKIQJUDTAGGRYRTTTTATYTGYGKAA EEVEAKYRKYESHPVCADLQAKTLCCTRENTHGTLKCSALATQY MHCVMRAKQAMLEKGG OHLGGLGFFFTSAKNILATVKGTFERLOPTICOCKAA EEVEAKYRKYESHPVCADLGAKTLCCTRENTHGTLKCSALATQY MHCVMRAKQAMLEKGG OHLGGLGFFFTSAKNILATVKGTFERLOPTICHMKESLEFT OHATGAGARGHILTPRANNLA EESFAVQDWSTGILTVSKMTSLLFRYADDSFTSAFVSTVG1DFKKK TVFKNEKR IKIQJUDTAGGRYRTTTTATYTSAGAAPCTAGCHENTGT VGFKISKUTVGGLSVGKCILTHRYCKGTPTDNKAATIGDFEM ERFEULLITURGLANGLANGESLEFTITNAGAGACAGGRIFGT VGFKISKUTVG	1			MPVEVQTELLEADLDHVTPEIMNOEERESSOADAAEAAREDHED
6314 2 2071 ORSGARLEFUSDYSEACURESUSTHECKPYFVUVPRDIGUL FHRRANGCILSCSSYUGPTAMEABETMECLQEFPEHKMILD RLNEOREQDRPTDITLIVDGHHFKAHKAVLAACSKFYKFYGEF TQEPLVEIGGYSKAPRHLIGFTTAKLMIGGEERANDWKAAE FLONLEAIKALEVENRENSARLERTTEKNEAKKRIAETSNYI TESLPSARSSEVEIEVEIAEGTIEVEDEGISTLEEVASAKGSVK YIGSTGSSDBSALALLADITSKYRQGDRENGEKKORTGKKIHVC QVGEKOPDHFGHFKEHLRKHTGEKPFECONGERKRIKHVC QVGEKOPDHFGHFKEHLRSDANISERIVTEEVLSVERTYKKHVC QVGEKOPDHFGHFKEHLRSDANISERIVTEEVLSVETRVO TEVTIMTIIEQVSKVHULPLLQVQVDSAQVTVGVHDLLQDS QVHDSIMMSELPEQVQVSYLVEGGIGTEETSHVVEELHVERVNO MFVEVOTELLEADLDHVTPEIMMOBERESSOADABARAREDHED AEDLETKFYVDSSAREKANDERTALDVLE 6315 1 1015 LGGAVRVVTIVLISYCPTATEERFYWTYLLCALGLFIYQSLDA IDGKQARRTNSCSPLGELPDIGCDELSTVFMAVGASIAALGTY PDMFFSCSFIGMEVFYCAMMAVISSPDMVIYFSALCLGIFIYQSLDA IDGKQARRTNSCSPLGELPDIGCDELSTVFMAVGASIAALGTY PDMFFSCSFIGMEVFYCAMMAVISSPDMVIYFSALCLGIFIYQSLDA IDGKQARRTNSCSPLGELPDIGCDELSTVFMAVGASIAALGTY PVFNFFSCFIGMEVFYCAMMAVISSPDMVIYFSALCLGIFIYQSLDA HULLIKIGVGNGSTIAGTSVLSSGLHIGLILAMINKKSATD VFRKHPCLYILIMSCCFFAKVSQLUVAMMYISSPDMVIYFSALCLGISRH LHLNIFKTACHQABEQVQVLSSKSHQNNMD VSAGAGTGIMGGTTSTRRVTFEADDRENITVVKGGIRLSENVIDR MKSSSPSGSKGRYSGAGASVSDEBLKRAVABELALEQAKKES EQUKRIKQAKELDRERAAMEQLTTAILRERICSSEERAKKHL ARQLEEKDRYUKRQDAFFKGLALEFERSEAKKHL ARQLEEKDRYUKRQDAFFKGLALEFERSEAKKHL ARQLEEKDRYUKRQDAFFKGLALEFTSVATOSIPFKX TVFKEKEK IRLQIMDTAGGRYRTITTAYRATBETICSSEERAKKHL ARQLEEKDRYUKRQDAFFKGLARLEFTSVATOSIPFKX TVFKEKEK IRLQIMDTAGGRYRTITTAYRATBETUTDITN ESSFANQOMSTQIKTSVBMONAQVILVGNKCOMEDERVISTERQ QHILGGGLGFFFTSTAKNINNVGOTFERLUTCKMSESLETD PAITAAKONTRIKETPPPPOPNCAC 0HIGGGLGFFFTSTAKNINNVGOTFERLUTCKMSFSLETD PAITAAKONTRIKETPPPPOPNCAC 10HGGGLGFFFTSTAKNINNVGOTFERLUTCKMSFSLETD PAITAAKONTRIKETPPPPOPNCAC 10HGGGLGFFFTSTAKNINNVGOTFERLUTCKMSFSLETD PAITAAKONTRIKETPPPPOPNCAC 10HGGGLGFFFTSTAKNINNVGOTFERLUTCKMSFSLETD DVASLEHTKGNLADLKENDFSVILLEUNGKKOLSTPAQVALM EKDALQVAQSMKAEVMAVSLIGENVREPFFRVAALTTVANIA ELEKSGARRIGOVENINSDOMILITAKKKRPTCCP VGFKISKU VVYOLDLSVKKICLINTRECKOTFDUNYATGTGDPEM ERFEULGIFFSIQLLUNDFSSVILLEUNGKKOLSTPAQVALM EKDALQVAGGMKAEVMAVSLIGENVREPFFRVAALTTFANV				AEDLETKPTVDSEAEKAENEDRTALPVLE
FHRRAHGCTLSCSSFVEOPTAMBAETMECLQEFPEHKMILD RINDORGODFTDITLIVOGHHRAHKANCASKHPYKPYOET TQEPLVEIEGVSKWAPPHLIETTTAKKMIQGEEGANDVWKAAE FLQNLERIEGVSKWAPPHLIETTTAKKMIQGEEGANDVWKAAE FLQNLERIKALEVRNKENSAPLEENTTGKNEAKKRIKATSMVI TESLPÄÄRSEPEVEIEVEILEGTTEVEDEGISTILEEVASAKOSVK YIGSTGGSDDSALALLADITSKYRQDRKGGIKEDGEPDTEK QVEGIEIVELGLSHVKDIPHEKEKNISFKLYHFKEHMKSHSTE SFKCEICNKRYLRESAMKQHLNCYHLEEGGYSKKOFKKHVUC QYCEKGFDHFGHFKEHLKRIGSKPFECOHERPARNSTLKCH LTACOTGVGAKKGRKLYRCOVCNSYPNSMOORKDHUHTMCOK PNICTLCOLUMPROGNELRRHISGAMINGERPARNSTLKCH LTACOTGVGAKKGRKLYRCOVCNSYPNSMOORKDHUHTMCOK PNICTLCOLUMPROGNELRRHISGAMINGERPARNSTLKCH LTACOTGVGAKKGRKLYRCOVCNSYPNSMOORKDHUHTMCOK PNICTLCOLUMPROGNELRRHISGAMINGERPARNSTLKCH LTACOTGVGAKKGRKLYRCOVCNSYPNSMOORKDHUHTMCOK PNICTLCOLUMPROGNELRRHISGAMINGERPARNSTLKCH LTACOTGVGAKKGRKLYRCOVCNSYPNSMOORKDHUHTMCOK PNICTLCOLUMPROGNELRRHISGAMINGERVOVTEQUALUH TEVETSMTILLOVGKVHVLPLLQVQVDSAQVTVEQVHPDLLQDS QVHDSHMSELPSCVUSTLEVGRGIGTEGGTEVHVEELHVERVNO MPVEVOTELLEADLDNYTPITMKGGERFSSADAARAREHBD AEDLEKKPTUDSEARRABENDRTALPVLE 6315 1 1015 LGGAVNVYTTVLISVCYTARERFYTYLLCALGIFTYOSLDA LDGKQARRTNSCSPLGELPDMCCDSLSTVPMAVGASIARLGTY PDMFFSCSPIGMEVFYCAMMOTYVSGMIRGKVDVTETQIALNI VFULARGGORMANDTVSGTERRKVDVTETQIALNI VFULARGGORMANDTVSGTERRKVDVTETQIALNI VFULARGGORMANDTVSGTERRKVDTVEGAURTIKKSATU VFULARGGORMANDTVSGTERRAVSSELUGISTRIPTLERICTSSETENTYFLAD VFULARGGORMANDTVSGTERRAVSSELUGISTRIPTLOGGERVATHTATYVKGTILSENTIDR MKSSSPSGSKGNIGGGAGAVSVDBELKRRVABELALEQAKKSS EDQKRIKGAKELDRERAANEQLITATILRRICTSEETERAKKHL ARQLEEKBRYLKKODAFVKGLARLEERSSEFTYVTTEGYOKAA ECUBAKFKYESHVCALQARKIGCTRENTITGTLKCSALATQY MHCVNHAKQSMEKGG PRAMTAKTIGTHTATAGTTSTRATTFRANGTSLARGHIMDTIN ESEFANAVOMSTOILTYSMINAQVILVGNKCOMEDERVISTERQ OHLGRICAFGFFTSTAKNINIVKQTFERLYDTIOTLKCSALATQY VFKEKEK IKIQ JUDTAGGRYRTTTTAYNGAGPTIMSSLEDTO PATTAKONTRIKETPPPPOPRICAC 6318 1765 733 PHAPITATIPHINPRIPPRAGREGREGADSMSHLPGLERREPPPL LGPLLSPP PLPAGSSHROMESSLEPTYNAGAGATIGPHWALE ERFELLGIFFSLQLUMDTAGGERFKCTASTYNGAGATIGPHWALA ELEKSGARRIGOVRINSDDSNLLVLASKKKDICTPP VARGRIKELLUKHUNGLADLKKNODFSSVLLEUNGKKDLSTPAQYALM EKDALQVAGEMK	6314	2	2071	QRSGAARLAFLPSPFSFACVHRSPLSFHGCWFYFVVVFMPIGVI.
RLINGGREQORFTDITLIVOCHIFICHARKAVLAACSKFYKYFOGE TORFLUESEGVSKAMPRHLEFTYTAKUMIGGEERANDVWKAAE FLOMLENIKALEVENKENSAPLEENTTOKNEAKKRIAETSNVI TESLEPSABSEPVEIEVEIAGGTIEVEIDGEITEVERSAKOSVK YIQSTGSSDDSALALLADITSKYRGORKSOIKENGCESPTEK QVEGIEIVELGUSHVKOLFHCEKCRRSFKLPYHFKEHKKSHSTE SFKCEILORRYIRESAMKOHLKOYLEGVSKKORTKKHUC QYCEKOPDHFGHFKEHLEKHTGEKFFECPNCHERFARNSTIKCH LTAQOTGVGAKKGRKKJKEOCUNSUVEDOPTOKKKHUC QYCEKOPDHFGHFKEHLEKHTGEKFFECPNCHERFARNSTIKCH LTAQOTGVGAKKGRKKJKEOCUNSUVEDOPTOKHTÜRCK PNHCTLCOLMFMGGNELRRHLSDAHNISERLVTEEVLSVETRVQ TEPVTSMTIIEQVGKVHVLPLLQVOYDSAQTVTEQVHDDLLQDS QVHDSHMSELEPGQVQVSYLEVERIQTEEGTEVHVEELHVERVNG MPVEVOTELLEADLDHYTEINNOEREESSQADAAEAAREDHED AEDLETKFYTVDSEAKRABEDRTALPVTUCALGIFTYGSLDA HEDLETKFYTVDSEAKRABEDRTALPVTUCALGIFTYGSLDA AEDLETKFYTVDSEAKRABEDRTALPVTUCALGIFTYGSLDA IDGKQARRYNGSSIGEPHOCOSLETHAWAGASILARLGTY PDMPFSCSPIGMFYPYCAHMQTYVSGMLRFGKVDVTEIQTALVI VFVLSAFGGATMUDYTIPILERLKKILPVLGFLGGVIFSCSNYF HVLIHGGVGKNGSTIAGTSVLSGCHLFUTLAMTIKKSATD VFRKHPCLYILMFGCVFAKVSGKLVAMHTKSELVLODTVPLGP GLIFLDGVFNNFIDEVVLWMMMYISTVLYSALCLQISH LHINIFKTACHQAPEQVOULSKSHONNDD VFSKHPCLYILMFGCVFAKVSGKLVAMHTKSELVLODTVPLGP GLIFLDGVFNNFIDEVVLWMMMYISTVLYSALCLQISH LHINIFKTACHQAPEQVOULSKSHONNDD VFSKHPCLYILMFGCVFAKVSGKLVAMHTKSELVLODTVPLGP GLIFLDGVFNNFIDEVXLWMMMYISTVLYSALCLQISH LHINIFKTACHQAPEQVOULSKSHONNDD VFSKHPCLYILMFGCVFAKVSGRAVGAVSDEBLKRRVABELALEQAKKES EQKRIKQASELDRERAANSQLTRAILERSTCESERRAKHLL ARQLEEKGRVLKKQDAFKYEQLAALERSSEFTRVTTEGYOKAA EEVERKFKRYESHPVCADLQAKTLQCTRRTHTOTIKCSALATQY MHCVNEHAKQSHLEKGG HOLMGELOFEFFTSTAKNINKYGTTERSGTOKAS GHIGGULGFEFFTSTAKNINKYGTTERSGTOKAS UHGVNEHAKQSHLEKGG UHGGULGFEFFTSTAKNINKYGTTERSTYTGIDFKVK TVFKWEKRIKLQIWDTAGGERYRTITTATYRGAMGFILHYDITN EESFRAVQDMSTGIKTYSMDAAQVILVONKCOMEDERVISTERG GHIGGULGFEFFTSTAKNINKYGTTERYTTAQAPCKAAGRINI LAPVRRDRVLAELPGCLKKRADAFKCTASTYYRGAGATIVYOHLM EKSALPTURUHHDHPEPPPAGGREGADSKSILPGLEERRAPPL LGPLLSPFPLPAGGNEGADSKVILCTIPRCKTACAGERRTGT VGFKISKVILVOOLSVGKTGITTATYTAGARPCKAAGRINI LAPVRRDRVLAELPGCLKKRADAFKCTLATYTRGAAGTIVTOKACH EKSGARRIGDVVRINGDSNULFUTGACHTYNKATIGOVPEM ERFEULGIPFSLAUMTHURGHTERS				FHRRRAHGCTLSCSSFVEQPTAMBAEETMECLOEFPEHHKMILD
TOPPLUSTISOUSKAPPRILIETTYTAKIMIOGEBEANDVIKAABE FLONLEN KALEVRIKUNSAPLEENTTOKKEAKKKILASTINI TESLPSABSEPUTEVBIJABGITEVEDEGITTLEEVASAKOSVK YIQSTGSSDDSALALLADITSKYRGGDRKGOIKEGGESDTSK QVEGISIVBLOUSHVKOLPFICEKCIRSPKLFYHPKEHHKSHSTE SFKCEICNRRYLRESAMKOHLACYHLEEGGUSKKQRTCKKIHUC QYCEKOPOHFIGHFKEHLIKHTGEKPFSOKLERPARNSTILKCH LTACOTGVGAKKGRKKLYEGQUCNSVINSHODPKDHLVIHTGOK PNHCTLCDLWPMQGNELRRHLSDAHNISERLYTEEVLSVETRVQ TEPVTSMTIIEQVGKVHVLPLLQVQVDSAQVTVEQVHEDLLQDS QVHDSHMSELPEQUQVSYLEVGRIQTEEGTEVHVEELHVERVNOK MPUEVOTELLEADLDHYTPEINNORESAGDADAEARAREDHED AEDLETKPTUDSEAKKAENEDRTALPVLE LGLANWVITTULISYCPTATEBASPWTYLLCALGLFTYQSLDA IDGKQARRTNSCSPLGELPDHGCDSLSTVFMAVGASIAARLGTY PDHPFSCSFIGMFVFYCARWGTVYSGMLRFGKVDVTEIQIADJI VFULSAFGGATMMDYTT PLIETIKKLTHYSELTVLODTVFLOP GLLFLDOYFNNFIDESYVLWMAMVISSFDMVIYPSALCLQISRH LHLNIFKTACHQAPEQVOLUSKSHQNNMD FRKHPLCVILIMFGCVPKAVSGKUVAMTKSELTVLODTVFLOP GLLFLDOYFNNFIDESYVLWMAMVISSFDMVIYPSALCLQISRH LHLNIFKTACHQAPEQVOLUSKSHQNNMD FRKHPLCVILIMFGCVPKAVSGKUVAMTKSELTVLODTVFLOP GLLFLDOYFNNFIDESYVLWMAMVISSFDMVIYPSALCLQISRH LHLNIFKTACHQAPEQVOLUSKSHQNNMD FRKHPLCVILIMFGCVPKAVSGKUVAMTKSELTVLODTVFLOP GLLFLDOYFNNFIDESYVLWMAMVISSFDMVIYPSALCLQISRH LHLNIFKTACHQAPEQVOLUSKSHQNNMD FRKHPLCVILIMFGCVPKAVSGKUVAMTKSELTVLODTVFLOP GLLFLDOYFNNFIDESYVLWMAMVISSFDMVIYPSALCLQISRH LHLNIFKTACHQAPEQVOLUSKSHQNNMD FRKHPLCVILIMFGCVPKAVSGKUVAMTKSELTQDTVFLOP GLLFLDOYFNNFIDESYVLWMAMVISSFDMVIYPSALCLQISRH ARGUEKKORAPAVOMSTQIKTSFFRNDMASAQDARYGGKDSDON FYRKHELLIGNSSVKRYSGAVGASVSGBLKRRVABBLALEQAKKES EDQKRIKKQAKELDERFAANBGLITATHCKSALLATQY MCVNHAAKQNSTLIKTSHNDNASALTGARSTTTAYYRGAAGTILMCSALLATQY MCVNHAAQSNLEKGG 6317 102 839 PRAQTSAVLARERGEHDPVINTHEAPMOMASAQDARYGGKDSDON FYDMFKLILIGNSSVKRTSFFFRADDSTSTLFTUKCSALLATQY MCVNHAAQSNIKKSTFFPRADGREGADSNSHLPGLELRREAPPL LGPLLSPFPLAGSNIRGMMLRSSLRPPTTNSAGAPCKAAGRNNI LAPVRRDEVLAELPQCLRKEAALHGHKDFPHVTCACQCHRTGT VGFKISKVIVVGDLSVGKTCLIMPFCKDKKNLSTROVPEM ERFEVLGIPPSLJAHDHTAPGGERFKCLASTYYRGAQAIIIVFNIN DVASLEHTKOMALDALKRONPOSVLLIFUKKKNLSTIVVDEM EKDALQVARD VALEM EKDALQVARDKARETNAVSSLTGENVERPFRANALTIFEANVLA ELEKSGARA TODVET			•	RLNEQREQDRFTDITLIVDGHHFKAHKAVLAACSKFFYKFFOEF
FLONLENIRALEVENKENSAPLEENTGKNEAKKKIAETSNVI TESILPSASESPVEIEVENSGTIEVEDGGTETLEBVASAKOSVK YIQSTGSSDDSALALLADITSKYRGGDKGGIKEGCPSDPTSK OVGEIGTVELQLSHYKDLPHCEKCRKSPKLFYHFKEHKKSHSTE SFRCEICNRRYLRESAWKGHLKCYHLEGGVSKKQRTKKKIHVC QYCEKGFDHFGHFKEHLRKHTGEKFFECONCHERPARSTIKCH LTACQTGVCAKKGRKKJYEGOVCNSVYNSMODFKDHLVHTGKK PNHCTLCDLWFMGCNELRRHLSDAHNISERLVTEEVLSVETRYG TEDVTSMTITIEOVGKVUTJPLUQVOYSAYTVEOVHDDLUQDS QVHDSHMSELPFBQVQVSYLEVGRIQTEEGTEVHVEELHVERVNQ MPVEVQTELLEADLDHVTPIMNOERRESSQADAABAARCDHED AEDLETKFTVDSEAEKAENEDRTLDFVY PDWFFSCSFIGMFVFYCAHMOTYVSGHLRFGKVDVTEIQLALUJ VFVLSAFGGATMMDVTITJLSYCFFTATEBAPYWTYLLCALGLFTYQSLDA LDGKQARRINGSSIGEPHOHGOSLETPMAGGAIAALGFTY PDWFFSCSFIGMFVFYCAHMOTYVSGHLRFGKVDVTEIQLALUJ VFVLSAFGGATMMDVTITJLEIKLKILPVLGFLGGVIFSCSNYF HVILHGGVGKNGSTIAGTSVLSFGLHRGLIILLAIMTYKKSATD VFRKHPCLVILMFGCVFAKVSGKUVAHMTKSELYLDDTVFLGF GLIFLDGVFNNFIDEVVLWMAMMISSAMVIYFSALCLGISRH LHLNIFKTACKQAPEQVQVLSKSHQNNMD VSAGAGTINGGTTSFRRTVFFADDERBNTTVVKGTFLSENVTDR MKSSSFSGSKSGRYSGRYGASVSDEBLKRRVAEBLALEQAKKES EDQKRLKQAKELDRERAAANEQLTRAILRERICESERAKKHL ARQLEEKBRVLKKQDAFYKEQLARLEERSSEFTRVTTEQYQKAA EEVEAKFRRYESHPVCADLQAKILQCYRRNTHQTIKCSALATQY MHCVHRAKQSNLEKGG HOMONITLIGKTSFIFFRADDASTSALVSTVGIDPKVK TVFKNEKRIKLQIMDTAGQERYRTITTAYYRGAMGFILMYDITN EBSFRAVQDMSTGIKTYSMDNAQVILVONKCDMEDERVISTERG GHLGSCLOFEFFFTSAKONINNKQTTERSTAVSTVGIDPKVK TVFKNEKRIKLQIMDTAGQERYRTITTAYYRGAMGFILMYDITN EBSFRAVQDMSTGIKTYSMDNAQVILVONKCDMEDERVISTERG GHLGSCLOFEFFFTSAKNINNKQTTERTALVSTVGIDPKVK TVFKNEKRIKLQIMDTAGQERYRTITTAYYRGAMGFILMYDITN EBSFRAVQDMSTGIKTYSMDNAQVILVONKCDMEDERVISTERG GHLGSCLOFEFFFTSAKNINNKQTTERVICACQEHRROT LGPHLSPFPLAGREGRADSNSHLPGLEERRAPPL LGPLLSPFPLAGREGRADSNSHLPGLEERRAPPL LGPLLSPFPLAGRUPGAGREGRADSNSHLPGLEERRAPPL LGPLLSPFPLAGRUPGAGREGRADSNSHLPGLEERRAPPL LGPLLSPFPLAGRUPGAGREGRADSNSHLPGLEERRAPPL LGPLLSPFPLAGRUPGARGRADSNSLLPGLEERRAPPL LGPLLSPFPLAGRUPGAGRADSNSLLPTAACAGCHROT VGFKISKVIVVGDLSVGKTCLINFRCKOTCACCHERNOT VGFKISKVIVVGDLSVGKTCLINFRCKOTCACCHERNOT VGFKISKVIVVGDLSVGKTCLINFRCKOKKOLSTPANYATIGVANAL EKLEKGARRIODVRINGDSNLLPGIEWMKSEELQRLT ASEPLLTLEGSYANQCSMGEDADKCTIVL	i			TOEPLVBIEGVSKMAFRHLIEFTYTAKLMIOGEEEANDVWKAAE
TESLPSAESEPVEIEVEIAEGTIEVEDEGIETLEEVASAKOSVK YIGSTSSDSALALLAIDTISKYROPKGOIKEDGESPTSK OVEGIETVELOLSHVKDLPHCEKCNRSPKLPYHPKEHMKSHSTE SFKCEICNKRYLRESAMKQHMCYHLEBGGYGKKQRTGKKIHVC QYCEKOPDHFGHFKEHLRKHTGEKPKPECNCHERPARNSTLKCH LTACQTGVCAKKGRKKLYECQVCNSVYNSWDQPKDHLVIHTGEK PNHCTLCDLWFMCGELERHLISANIERISTERYSTEVGY TESVTSMTIIEOVGRVHVLPLLQVQVDSAQVTVEQVHPDLLQDS QVHDSHMSELPBOVQVSYLEVGRIGTEEGTEVHVEELHVERVNQ MPVEVOTELLEADLDHVTPEIMNGERESSQADAAEAARDHED AEDLETKPTVDSEAEKAENEDRTALDVLE 6315 1 1015 LIGLAVRUVTILVLISYCPTATEERSTYWTLLCALGLFTYQSLDA LDCKQARRTNSCSPLGELFPHGCDSLSTVFMAVGASIAARLGTY PDWFFSCSFIGMFVFYCAHWQTVYSGMLRFGKVUTVEIGIALVI VFVLSAFGGATMWYTTY ILEKILLIVLIGFLGGVIFFSCSNYF HVILHGGVGKNOSTIAGTSVLSGCHIGLIILLIMIYKKSATD VFERHFCLVILIMFGCVFAKVSGKLWVAHMTKSELYLDDTVFLGP GLLFLDQYSNNFIDEVVVLWMAWVISSFDMVIYSSALCLQISRH LHINIFKTACHQAPBQVQVLSSKSHQNIMD 6316 1503 792 VSAGAGTGIMGGTTSTRVTFFADDERNITVVKGIRLSENVIDR MKSSSPSGSKSGRYGAYGASVSDEELKRRVABELALEQAKKES EDQKRLKQAKELDBERGAANSQLTARLIRERICGSEERRAKHLL ARQLEEKORVLKKQDAFYKSGLARLEERSSFTRVTTEQYQKAA EEVEAKFKRYSSHPVCADLQAKILQCYRENTHQTLKCSALATQY MHCVNHAKQSMLEKGG PEAGTSAVLARRKGHLEFTMRHEAPMQMASAQDARYGGKDSSDQN FDYMFKLLIIGNSSVGKTSFLFRYADDSFTSAFVSTVGIDPKVK TVFKNEKRIKLQINDTAGGBRYRTTTTAYVRGAMGFILMYDITN EBSFANAVODMSTOLKTYSMDNAQVILVORKCDMEDERVISTERG OHLGEQLGFEFFTSAKDNINVKGTFERLVDIICDKMSSSLETD PAITAAKQNTRLKKFTPPPPOPRACC 6318 1765 733 PMHPLRTTLPLHHHPRPPPRAGGRGGADSMGHLFGLEIRREAPPL LGPLLSPFPLDAGSMRQMLRSSLEFPTTNSAGAPCXAAGRINI LADVRDRVLAELBQCLKREAALHGHKDFHRVTCACQEHRTGT VGFKISKVIVVUGLSVGKTCLINRFCKOTPTKNYKATIGVPFEM ERFEVLGIPFSLQLUMDTAGQRFKCLASTYRAQAAITUPNILA EKOALQVAQBKKAFWANSSLIGENVREFFFRAALTFPANVLA EKOALQVAQBKKAFWANSSLIGENVREFFFRAALTFPANVLA ELEKSGARR IGDVVR INSDERNILYLTVASKKULSTPAQAAI EKOALQVAQBKKAFWANSSLIGENVREFFFRAALTFPANVLA EKOALQVAQBKKAFWANSSLIGENVREFFFRAALTFPANVLA ELEKSGARR IGDVVR INSDERNILYLTVASKKULSTPAQAAI EKKAGARRICHTURINGTHENDERNILTTARKKERDFFENVLAGARGARGTEES CWGOVINIPTIDLEDHTINSDERNILTTARSKKRORQQFGATEES CWGOVINIPTIDLEDHTINGSPGCRGKGGTGRAVAM	ľ			FLQMLEAIKALEVRNKENSAPLEENTTGKNEAKKRKIAETSNVI
YIQSTGSSDDSALALLADITSKYRQCDREGGIKEDGCPSDPTSK QVEGIETVRLOGSHVRDLFHCEKCKNSPKLPYHFKEHNKSHSTE SFKCEICNKRYLRESAWKQHLNCYHLEEGGVSKXQRTGKKIHVC QYCEKGPTBEGFFKEHLRKHTGEKPPECPNECHEFPARNSTLKCH LTACQTGVGAKKGRKKYPCQVCNCHEFPARNSTLKCH LTACQTGVGAKKGRKKYPCQVCNCHEFPARNSTLKCH LTACQTGVGAKKGRKKYPCQVCNCHEFPARNSTLKCH LTACQTGVGAKKGRKKYPCQVCNGVFNEWDOPKDHLVIHTGKK PNHCTLCDLMFMQGELRRHLSDANHISERLYTEVLSVETRYQ TEPVTSMTIIEQVGKWHVPLLQVQVDSAQVTVEQVISVETRYQ TEVTSMTIIEQVGKWHVPLLQVQVDSAQVTVEQVISVETRYQ QVHDSHMSELPEQVQVSYLEVGRIGTEEGTEVHVEELHVERVNQ MPVEVOTELLEADLDHVTPEIMMGEREESGADAAEAAREDHED AEDLETKPTVDSEAREKAENDERTALDVLE 1015 1016 1016 1017 1018 1018 1019 1019 1019 1019 1019 1019	1			TESLPSAESEPVEIEVEIAEGTIEVEDEGIETLEEVASAKOSVK
OVEGIETVELQUSHWGLIFHCEKCNRSYRLEHYPKEHMKSHSTE SFKCELGNRYYLRESGWSHKQNGYCHLEEGGYSKKQRTKKIHVC QYCEKOPDHEGHFKEHLEKHTGEKPFECPNCHERFARNSTLKCH LTACQTGVGAKKGRKKLYECQVCRSYFNSWODGKDHLVIHTGEK PNHCTLCDLWFMCGRELRRHLSDAHNISERLVTEEVLSVETRVQ TEPVTSMTIIEQVGKVHVLPILQVQVDSAQVTVEQVHEDLLQDS QVHDSHMSELPREVQVSYSLEVGHGTEGTBWHVEELHVERVNO MPVEVOTELLEADLDHVTPEIMMGERESSQADAAEAAREDHED AEDLETKPTVDSEAEKAENEDRTALPVLE 1015 LGLAVRVVTILVLISYCPTATEEBFYWTTLLCALGLFIYQSLDA LDCKQARRTINSCSPLGSLFPHGCDSLSTVFMAVGASIAARLGTY PDWFFSCSTIGMFVYCAHMOTYSCHREFKKVDVTSIQIALVI VFVLSAFGGATWBVTTPILEIKLKILPVLGFLGGVIFSCSNYF HVILHGGVGKNGSTIAGTSVLSPGHHIGLIILIAIMIYKKSATD VFSKHPCLYILMFGCVFAKVSQGLVVALMMTKSEIYLDDTVFLGF GLLFLDQYFNNFIDEYVVLWMAWISSFBWVTYSALCLGISRH LHNINIKTACHQAPEQVQVLSSKSKNOMMD 6316 1503 792 VSAGAGTGIMGGTTSTRGVFFEADENENITVVKGIRLSENVIDR MKESSPSGSKSQRYSGAYGASVSDEBLRRRABELALEQAKKES EDQKRLKQAKELDBERAAANEQLITAAILREELSESFRAVHL ARQLEEKDRVLKKQDAFYKSQLARLEERSSEFTRVTTEQYQKAA EEVEARFKRYESHPVCADLQAKILQCYRENTHQTLKCSALATQY MHCVNRIAKGSHLEKGG 6317 102 839 PEAQTSAVLAREKGHLPTMRHEAPMQMASAQDARYGQKDSSDQN FDYMKYLLIIGNSSVGKTSFLRRYADDSFTSAFVSTVGIDFKVK TVFKNEKRIKLQINDTAGGBRRTTTTAYVRGMGFILMYDITN EESFINAVQOWSTOLKTYSBNDAQVINKCOMEDEDEVISTERG QHLGSCLGFEFFETSAKDNINVKQTFERLVDIICDKMSESLETD PAITAAKQNTRLKSTPPPPONCAC 6318 1765 733 PHHPLETTLPLHHPHPREPPRAGEGEGADSMSHLFGLELRREAPPL LGPLLSPPPLDAGSWHRQMLRSSLRFPITMSAGAPCKAAGRMNI LAPVRRDRVLAELFQCLRREAALHGHPFPRTCACQCHRTGT VGFKISKVIVVGDLSVGKTCLINRFCKDTPDKNYKATIGVPFEM ERFEVLGIPFSLQLWDTAGGRFKCLASTYTRAGAAIIVPFEM ERKPULGIPFSLQLWDTAGGRFKCLASTYTRAGAAIIVPFEM ERKPULGIPFSLQLWDTAGGRFKCLASTYTRAGAAIIVPFEM ERKPULGIPFSLQLWDTAGGRFKCLASTYTRAGAAIIVPFEM ERKDALQVAQBWKAFYWANSSITGENVREFFFRAALTTFEANVLA ELEKSGAR IGDVVR INSDBANLYLLFLVGSKKDLSTPRQVALM EKDALQVAQBWKAFYNANSSITGENVREFFFRAALTTFEANVLA ELEKSGAR IGDVVR INSDBANLYLLFLVGSKRUSTFPRAVILA ELEKSGAR IGDVVR INSDBANLYLLFLVGSKRUSTFPRAVILA ELEKSGAR IGDVVR INSDBANLYLLFLVGSKRUGAQPGATEES CWGOVINJFITDLEDLIFIABPSGROKGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG				YIQSTGSSDDSALALLADITSKYRQGDRKGOIKEDGCPSDPTSK
OYCEKOPDHFGHFKEHLRHTGEKPFECDNCHERPARNSTLKCH LTACOTOVGAKKRKLYSCOVCNSVYNSMODPKDHLVIHTGDK PNHCTLCDLWFMQGNELRRHLSDAHNISERLVTEEVLSVETRVQ TEVTSMTIIEQVGKVHVLPLLQVQVDSAQVTVEQVHPDLLQDS OVHDSHMSELPBCQVQVSILEVERQTVTEEGTEVHVEELHVERVNO MPVEVOTELLEADLDHVTPEIMNQERESSQADAAEAAREDHED AEDLETKFTVDSEAEKAENEDRTALPVLE 6315 1 1015 LGLAVNVVTTLVLISYCPTATEERPYWTYLLCRLGLFIYQSLDA IDGKQARRTMSCSPLGELPDHGCDSLSTVFMAVQASIAARLGTY PDWFFSCSFIGMFVYCAHWQTYVSGMLRFGKVDVTSIQIALVI VFVLSAFGGATMWDYTIPLIERLKKILPVLGFLGGVIFSCSNYF HVILHGGVGKNGSTIAGTSVLSSGLHIGLIILIAIMIYKKSATD VFBKHPCLVILIMFGCVFAKVSGKLVVAHMTKSELYLQDTVPLGP GLLFLDQYFNNFIDEYVVLWMAMVISSFDMVIYFSALCLQISRH LHLNIFKTACHQAPBQVQVLSSKSHQNND 6316 1503 792 VSAGAGTGIMGGTTSTRRVTFADENENTYVVKGIRLSENVIDR MKSSSPSGSKSQRYSGAVGASVSDEBLKRRVABELALEQAKKES EDQKRLKQAKELDRERAANEQLTRALIRERICSEEERAKKHL ARQLEEKORVLKKQDAFYKEQLARLERSSEFYRVTTEQYQGAA EEVEAKFKRYSSHPVCADLQAKILQCYRENTHOTLKCSALATQY MHCVNHAKQSMLEKGG 6317 102 839 PEAQTSAVLARREKGHLFTMRHEAPMQMASAQDARYGQXDSSDQN FDYMFKLLIGNSSVGKTSILFRYADDSTYSAFVSTVGIDFRVK TVFKMEKRIKLQIWDTAQGERYKRTITTAYYRGAMGFILMYDITN EBSFNAVQDWSTQIKTYSWDNAQVILVGNKCDMEDERVISTERG QHLGEQLGFFFFFTSAKONINVKQTFERLVDICCKMESSLETD PAITAAKQNTRLKSTPPPPQDACAC MUGEQLGFFFFTSAKONINVKQTFERLVDICCKMESSLETD VGFKISKVIVVGDLSVGKTCLINRFCKDTPDNYKATIGVDFEM LAPVRRDRVLAELBQCLKREAALHGHKDFHPRVTCACQEHRTGT VGFKISKVIVVGDLSVGKTCLINRFCKDTPDNYKATIGVDFEM ERFEULG IPFSLQUMDTAGGERFALAFYYRGAQAIIIVFNLN DVASLBHTKQMLADALKENDPSSVLLFLVGSKKOLSTPAQYALM EKDALQVAQEMKASYNAVSSLTCENNREFFFRVAALTFEANVLA ELEKSGARRIGDVVRINSDDSNLYTASKKKPTCCP 6319 88 717 AATMELNQNTELLIGKKVULVPYTSEHVPSRYHEMMKSEELQRLT ASGEPLTLEQEVAMQCSWGEDADKCTTIVLDAEKWQAQPGATEES CWGDVNLFTDLUBLTLGEIEVHLBPSCRKKGGGTANVAML				QVEGIEIVELQLSHVKDLFHCEKCNRSFKLFYHFKEHMKSHSTE
LTACQTGVGAKKGRKKLYECQVCNSVYNSPOPERDHLUTHTCDK PNHCTLCDLEMPGGNELRHLSDAHNISERLYTEGVLSVETRVQ TEPVTSMTIIEQVGKVHVPPLLQVQVDSAQVTVEQVHPDLLQDS QVHDSHMSELPEQVQVSYLEVGRIQTEEGTEVHVEELHVERVNO MPVEVQTELLEADLDHVTPEIMNGERESSQADAAEAAREDHED AEDLETKPTUDSEAEKAENEDRTALPVLE 6315 1 1015 LGLAVNVVTLVLISYCPTATEEAPPWTYLLCALGIFIYQSLDA DDGKQARRTNSCSPLGELPJMGCSLSTVFMAVGASIAARLGTY PDMFFSCSPIGMFVFYCAHWQTYVSGMLRFGKVDVTEIQIALVI VFVLSAFGGATWMDVTIPILEIKLKLPYLGFLGGVIFSCSNYF HVLLHGGVGKNGSTIAGTSVLPSGHVGYLGFLGGVIFSCSNYF HVLLHGGVGKNGSTIAGTSVLPSGHVIFVLGFLGGVIFSCSNYF HVLLHGGVGKNGSTIAGTSVLPSHVIYFSALCLGISRH LHLNIFKTACHGAPSQVQVLSKSHQNNMD 6316 1503 792 VSAGAGTGTMGGTTSTRRVFEADENENITVVKGIRLSENVIDR MKESSPSGSKSQRYSGAYGASVSDEELKRRVAEBLALQAKKES EQUARIKQAKELDERAAANSQLTRAILERRICSEEERAKAKL ARQLEEKDRVLKKQAELDRERAAANSQLTRAILERRICSEEERAKAKL ARQLEEKDRVLKKQAELDRERAAANSQLTRAILERRICSEEERAKAKL ARQLEEKDRVLKKQAELDRERAAANSQLTRAILERRICSEEERAKAKL ARQLEEKDRVLKKQAELDRERAAANSQLTRAILERRICSEEERAKAKL ARQLEEKDRVLKKQAEFBVCADLQAKILQCYRENTHOTLKCSALATQY MHCVNHAKQSMLEKGG MHCVNHAKQSMLEKGG 6317 102 839 PEAQTSAVLARRKGGILPTMHEAPMQMASAQDARYGOKDSSDON FDYMFKLLIIGNSSVGKTSLIFRYADDSFTSAFVSTVGIDPKVK TVFKNEKRIKLQIWDTAGQERYRTITTAYYRGAMGFILMYDITN EESFNAVQDWSTQIKTSWDNAQVILVGNKCDMEDERVISTERG OHLGSCLAGFFFFTSTAAKDNINVGTFELVDIICDKMSESLETD PAITAAKQNTRLKETPPPPQPNCAC 6318 1765 733 PHHPLETTLPLHHPHPEPPPAEGGEGADSMSHLDGLELRREAPPL LGPLLSPPFLPAGSNHRQMLRSSLRPPITNSAGAPCKAAGRMNI LAPVRRDRVLAELPQCLRKEAALHGHKDFHPRVTCACQEHRTGT VGFKISKVIVVGDLSVGKTCLINRFCKDTFDNYKATIGUPFEM EFFEVLGIPFSIGLWDTAGGGRSCLASTYVKRAGAGIIIVSNLN DVASLEHTKQWLADALKENDPSSVLLFLVGSKKDLSTPAQYALM EKDALQVAGEKABYWAVSSLTCENNYBEFFRVAALTPEANVLA ELEKSGARRIGDVVRINSDDSNILTJTASKKRPTCCP ASTMLNODTTLLGKVVVPYTSEHVPSRYHEWMKSEELQRLT ASEPLTLEQEYAMCSWQEDANCTFIVLABEWGAGAGGATEES CWGDVNIFLTDLEDLTLGEIEWIAEPSCRGKGGGTAVLAML	1			SFKCEICNKRYLRESAWKQHLNCYHLEEGGVSKKQRTGKKIHVC
PRHCTLCDLWFMCGNELRRHLISDAHNISERLUTEEVLSVETRVQ TEPVTSMTIIEQUGKUNVLPULQVQVDSAQVTVEQVHPDLLQDS QVHDSHMSELPEQUGVSYLEVGRIGTEGGTEVHVEELHVERVNQ MPVEVGTELLEADLDHVTFEIMNGERESSQADAABAREDHED AEDLETKPTUDSBERKEABERESSQADAABAREDHED AEDLETKPTUDSBERKEABERDRTALPVLE 1 1015 LGLAVNUVTTLVLISYCPTATEEAPYWTYLLCALGLFIYQSLDA LDGKQARRTMSCSPLGELPDHGCDSLSTVFMAVGASIAARLGTY PDMFFSCSPIGMFVYCAHWAQTVSGMLFGKRUDVTEQIALVI VFVLSASGGATMMDYTIPILEIKLKILPVLGFLGGVIFSCSNYF HVILHGGVGKNGSTIAGTSVLSPGLHIGLIIILAMIKKKSATD VFRKHPCLYILMFGCVFAKVSQKLVVAHMTKSELTVQDTVFLGGP GLLFLDQYFNNFIDEYVVLWMAWVISSFDMVIYFSALCLQISRH LHLNIFKTACHQAPEQVQVLSKSHQNNMD 6316 1503 792 VSAGAGTGMGGTTSTRRVTFEADENENITVVKGIRLSENVIDR MKESSPSGSKGRYSGAYGASVSDEELKRVABELALEQAKKES EDQKRIKQAREDDREAANBEQLTRAILERCSBEERAKHL ARQLEEKDRVLKKQDAFYKEQLARLEERSSEFYRVTTEQYGKAA EEVEARFKYESHPVCADLQAKILQCYRENTHOTLKCSALATQY MHCVNHAKQSMLEKGG 6317 102 839 PEAGTSAVLARERGHLDTWRHEAPMQMASAQDARYGQXDSSDQN FDYMFKLLIGNSSVGKTSFLFRYADDSFTSAFVSTVGIDFKVK TVFKMEKRIKLQIWDTAGGERYRTITTAYYRGAMGFILMYDITN EESFNAVODWSTQIKTYSWDNAQVILVGNKCDMEDERVISTERG QHLGEQLGFFFFTSAKDNINVKQTTBERUDIICDKMSESLETD PAITAAKQNTRLKETPPPPQENCAC 6318 1765 733 PHHPLRTLPLHHHPPPPHABGREGADDMSHLPGLEERREAPPL LGPLLSPFPLDAGSNHRQMLRSSLFPPITNSAGAPCKAAGRMNI LAPVRRDRVLAELPQCLRKEAALHGHKDFHPRVTCACQEHRTGT VGFKISKVIVVGDLSVGKTCLINRFCKLAFTYNKAGAGIIIVFNLN DVASLEHTKQWLADALKENDPSSVLLFLVGSKKDLSTPAGYALM EKDALQVAQEMKAEYNAVSSLTGENVERFFFRVAALITENNVLA ELEKSGARRIGDVVIINSDDNVILTASKKKPTCCP 6319 88 717 AATMELNONTYLLGKKVVLVPYTSEHVPSRYHEWMKSEELQRLT ASEPLTLEGGYAMGCSWGEDAKKTIVLDAEKRQAGGATEES CWWGDVNIFLTIDLEDLTLIGEITWAAPSPCRGKGGLGTEAVLAML	1			QYCEKQFDHFGHFKEHLRKHTGEKPFECPNCHERFARNSTLKCH
TEPVTSMTIIEQVGKVHVLPLLQVQVDSAQVTVEQVHPDLLQDS QVHDSHM9ELPEQVQVSYLEVGRIQTEEGTEVHVEELHVERVNQ MPVEVQTELLEADLDHVTPEIMNQEERESQADAAEAAREDHED AEDLETKPTVDSEAEKAENEDRTALPVLE 6315 1 1015 LIGLANNVTTILVLISYCPTATEEAPYWTYLLCALGLFIYQSLDA LDGKQARRTNSCSPLGELPHGCDSLSTVFMAVGASIAARLGTY PDWFFSCSFIGMFVFYCAHMQTVVSGMLRFGKVDVTEIQIALVI VFVLISAFGGATMMDYTTPILEIKLKILPPUGFLGGVIFSCSNYF HVILHGGVGKNGSTIAGTSVLSPGLHIGLIIILAIMIYKKSATD VFEKHPCLYILMFGCVFAKVSQKLVWAHMTKSELYLQDTVFLGP GLLFLDQYFNNFIDEYVVLWMAVVAHMTKSELYLQDTVFLGP GLLFLDQYFNNFIDEYVVLWMAVVAHMTKSELYLQDTVFLGP GLLFLDQYFNNFIDEYVVLWMAVVAHMTKSELYLQDTVFLGP HVILHGGVGKNGSTIAGTSVLSPGWIYJYFSALCLQISRH LHLNIFKTACHQAPEQVQVLSKSHQNNMD WSAGAGTIMGGTTSTRRTTFBADENENTVVKGTRLSENVIDR MKSSSPSGSKSQRYSGAYADEBELKRRVABBLALEQAKKES EDQKRLKQAKELDRERAAANEQLTRAILERSISFFYRVTTEQYQXAA EEVEAAFKFKYESHPVCADLAGNEERSSEFYRVTTEQYQXAA EEVEAAFKFKYESHPVCADLAGNLCYRENTHOTLKCSALATQY MHCWNIAKQSMLEKGG FDYMFKLLIGNSSVGKTSFLFRVADDSFTSAFVSTVGIDFKVK TVFKNEKRIKLQIWDTAGQERYRTITTAYYRGAMGFILMYDITN EESFNAVQDWSTQIKTYSWDNAQVILLVONKCDMEDERVISTERG OHLGGCLGFEFFFTSAKNNINVKQTFERLVDIICDKMSESLETD PAITAAKQNTRLKETPPPPQPNCAC 6318 1765 733 PWHPLKTLPHHHPPRPPRABGREGADSMSHLPGLELERREAPPL LGPLLSPFPLDAGSNHRQMLRSSLRFPITNSAGAPCKAAGRMNI LAPVRRDRVLAELPQCLRKEAALHGHKDFHPRVTCACQEHRTGT VGFKLSKVIVVGDLSVGKTCLINNFCKRTGAQAIITVSNIN DVASLBHTKQWLADALKRNDPSSVLLFLVGSKKDLSTPAQYALM EKDALQVAQEMKAEYMAVSSLTGENVRKGAGAIITVSNIN DVASLBHTKQWLAPPSSVLLFLVGSKKDLSTPAQYALM EKDALQVAQEMKAEYMAVSSLTGENVRKFFFRVAALITEANVLA ELEKSGARRIGDVVXINADSLKRNDFSRYHEWMKSEELQRLT ASSPLLLVARDRVILARKVVJLVPYTSEHVPSRYHEWMKSEELQRLT ASSPLLLVARDRCSWQEDADKCTFIVLDAEKRQAQFGATEES CWVGDVNLFLTDLEDLTLGEITVALASKKKPTCCP AATMRILNONTLLLGKKVVJLVPYTSEHVPSRYHEWMKSEELQRLT ASSPLLLEGGARAGCSWQEDADKCTFIVLDAEKRQAQFGATEES CWVGDVNLFLTDLEDLTLGEITVALASPKCRGKGLGTEAVLAML				LTACQTGVGAKKGRKKLYECQVCNSVFNSWDQFKDHLVIHTGDK
QVHDSHMSELPEQUQUSYLEVGRIQTESGTEWHVEELHVERUNQ MPVEVQTELLEADLIDHVTPEIMNQBERESSQADAAEAREDHED AEDLETKFTVDSEAEKAENEDRTALPVUE 6315 1 1015 1 1015 1 1015 1 1015 1 1015 1 1015 1 1016 1 1016 1 1017 1 1016 1 1017 1 1017 1 1017 1 1017 1 1018 1 1018 1 1019				PNHCTLCDLWFMQGNELRRHLSDAHNISERLVTEEVLSVETRVQ
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6315 1 1015 LGLAVNVTTLVLISYCPTATEEAPYWTYLLCALGLFIYQSLDA LDCKQARRTNSCSPLGELPDHGCDSLSTVFMAVGASLARRLGTY PDWFFSCSPIGMFVFYCAHWQTYVSGMLRFGKVDVTEIQIALVI VFVVLSAFGGATMWDYTIPILEIKKLKILPVLGFLGGVIFSCSNYF HVILHGGVGKNGSTIAGTSVLSPGLHIGLIILIAIMTYKKSATD VFBKHPCLYILMFGCVFAKVSQKLVVAHMTKSELYLQDTVFLGP GLLFLDQYFNNFIDEYVVLWMAMVISSFDMVIYFSALCLQISRH LHLNIFKTACRQAPFQVQVLSSKSHQNNMD 6316 1503 792 VSAGAGTGIMGGTTSTRRVTFEADENENTTVVKGYRLSENVIDR MKESSPSGSKSQRYSGAVASVSDELKRRVABELALEQAKKES EDQKRIKKQAKELDBERANBQLTRAILRERICSEEFRAKAKL ARQLEEKDRVLKKQDAFYKEQLARLEERSSEFYRVTTEQYQKAA EEVEAKFKRYESHVCADLQAKILQCYRENTHQTLKCSALATQY MHCNNHAKQSNLEKUG MHCVNHAKQSNLEKUG FPYMFKLLIIGNSSVGKTSFLFRYADDSFTSAFVSTYGIDFKVK TVFKNEKRIKLQIWDTAGQERYRTITTAYYRGAMGFILMYDITN EESFNAVQDMSTQIKTYSWDNAQVILVONKCDMEDERVISTERG OHLGEQLGFEFFTSAKDNINVKQTFERLVDIICDKMSESLETD PAITAAKQNTRLKETPPPPPQRACC OHLGEGLGFEFFTSAKDNINVKQTFERLVDIICDKMSESLETD PAITAAKQNTRLKETPPPPPRAGGREGADSMSHLPGLELRREAPPL LGPLLSPFPLPAGSWHRQMLRSSLRFPITNSAGAPCKAAGRMNI LAPVRRDRVLAELPQCLRKEAALHGHKDFHPRVTCACQERRTGT VGFKISKV LVVGDLSVGKCTLINFEKCHTFDKNYKATIGVDPEM ERFEVLGIPFSLQLWDTAGGERFKCIASTYYRGAQAIITVFNLN DVASLEHTKQWLADALKENDFSSVLLFIVGSKKDLSTPAQYALM EKDALQVAQEMKABYNAVSSLTGENVREFFFFVAALTFEANVLA ELEKSGARRIGDVR INSDSNLYLTASKKKPTCCP 6319 88 717 AATMRINONTLLLGKKVULVPYTSEHVPSRYHEWMKSEELQRIT ASEPLTLEQEYAMQCSWQEDADKCTFIVLDAEKWQAQFGATEES CMVGDVNLFLTDLEDLTLGEIFUM LABPSCRGGGGTEAVLAML	1			QVHDSHMSELPEQVQVSYLEVGRIQTEEGTEVHVEELHVERVNQ
1015 IGKANNUTTIVLISYCPTATEEAPYWTYLLCAIGLFIYQSLDA IDGKQARRTNSCSPLGEIPHGGSLSTVFMAVGASIAARLGTY PDWFFSCSPIGMFYPYCAHWQTYVSGMLRFGKVDVTEIQIALVI VFVLSAFGGATMWDYTIPILEIKLKILPVLGFLGGVIFSCSNYF HVILHGGVGKNGSTIAGTSVLSPGLHIGLIILIAIMIYKKSATD VFPKHPCLYILMFGCVFAKVSQKLVVAHMTKSELYLQDTVFLGP GLLFLDQYFNNFIDEYVVLWMMWISFFMVIJFSALCLQISRH LHLNIFKTACHQAPEQVQVLSSKSHQNNMD VSAGAGTGIMCGTTSTRRVTFEADENENTTVVKGYRLSENVJDR MKESSPSGSKSQRYSGAVGASVSDEELKRRVASELALEQAKKES EDQKRLKQAKELDRERAAANEQLTRAILRERICSEEERAKAKHL ARQLEEKDRVLKKQDAFYKEQLARLEERSSEFYRVTTEQYQKAA EEVEAKPKRYESHPVAQLAKILQCYRENTHQTLKCSALATQY MHCVNHAKQSMLEKGG MHCVNHAKQSMLEKGG MHCVNHAKQSMLEKGG FDYMFKLLIIGNSSVGKTSFLFRYADDSFTSAFVSTVGIDFKVK TVFKNEKRIKIQIMDTAQGERYRTITTAYYRGAMGFILMMDITN EESFNAVQDWSTQIKTYSWDNAQVILVGNKCDMEDERVISTERG QHLGBCLGFEFFTSAKONINVKQTFERLVDIICDKMSESLETD PAAITAAKQNTRLKETPPQPONCAC GHLGBCLGFEFFTSAKONINVKQTFERLVDIICDKMSESLETD PAAITAAKQNTRLKETPPQPONCAC GHLGBCLGFEFFTSAKONINVKQTFERLVDIICDKMSESLETD TVGKRSKVIVVGDLSVGKTCLINRFCKOTFDKNYKATIGYDFEM ERFEVLGIPFSLQLWDTAGQERFKCIASTYYRGAQAIIVVFNLN DVASLEHTKQWLADALKENDPSSVLLFLVGSKKADLSTPAQYALM EKDALQVALQBMKAESULFUNGSKKADLSTPAQYALM EKDALQVALQBMKAESULFUNGSKKADLSTPAQYALM EKDALQVALQBMKAESULFUNGSKKADLSTPAQYALM ELEKSGARRIGDVVRINSDDSNLYLTASKKRPTCCP AATMRLNQNTLLLIGKKVVVVPYTSEHVPSRYHEWMKSEELQRIT ASEPLTLEQEYAMQCSWQEDADKCTFIVLDAEKWQAQPGATEES CMVGDVNLFLTDLEDLTLGEIFUMIABPSCRGKGGTEAVLAML				MPVEVQTELLEADLDHVTPEIMNQEERESSQADAAEAAREDHED
IDCKQARTINSCSPLGELPDHGCDSLSTVFMAVGASIAARLGTY PDWFFSCSPIGMTVFYCAHWQTYVSGMLRFGKVDVTEIQIALVI VFVULSAFGGATMWDYTIPILEKLKILPVLGFLGGVIFSCSNYF HVILHGGVGKNGSTIAGTSVLSPGLHIGLIILLAHIYKKSATD VFEKHPCLYILMFGCVFAKVSQKLVVAHMTKSELYLQDTVFLGP GLLFLDQYFNNFIDEYVVLWMMMVISSFDMVIYFSALCLQISRH LHLNIFKTACHQAPFQVJSSKSHQNMMD 6316 1503 792 VSAGAGTGIMGGTTSTRRVTFEADENENTTVVKGYRLSENVIDR MKESSPSGSKSQRYSGAYGASVSDELKRRVABELALEQAKKES EDQKRIKKQAKELDBERAANBQLTRAILRERICSEEFRAKAKHL ARQLEEKDRVLKKQDAFYKEQLARLEERSSEFYRVTTEQYQKAA EEVEAKFKRYESHPVCADLQAKILQCYRENTHQTLKCSALATQY MHCNNHAKQSMLEKGG FPYMPKLLIIGNSSVGKTSFLFRYADDSFTSAFVSTYGIDFKVK TVFKNEKRIKLQIWDTAGQERYRTITTAYYRGAMGFILMYDITN EESFNAVQDMSTQIKTYSWDMAQVILVONKCDMEDERVISTERG OHLGEQLGFEFFTSAKDNINVKQTFERLVDIICDKMSESLETD PAITAAKQNTRIKETPPPPQROACC OHLGEQLGFEFFTSAKDNINVKQTFERLVDIICDKMSESLETD LGPLLSPFPLPAGSWHRQMLRSSLRFPITNSAGAPCKAAGRMNI LAPVRRDRVLAELPPQCLRKEAALHGHKDFHPRVTCACQEHRTGT VGFKISKV IVVOBLSVGKTCLINBFCKORTPKNYKATIGVDPEM ERFEVLGIPFSLQLWDTAGGERFKCIASTYYRGAQAIITVFNLN DVASLEHTKQWLADALKENDFSSVLLFIVGSKKDLSTPAQYALM EKDALQVAQEMKAEYNAVSSLTGENVREFFFFVAALTFEANVLA ELEKSGARRIGDVVR INSDDSNLYLTASKKRPTCCP 4ATMRINONTLLIGKKVVLVPYTSEHVPSRYHEWMKSEELQRIT ASEPLTLEQEYAMQCSWGEDADKCTFIVLDAEKWQAQFGATEES CMVGDVNLFLITDLEDLITLGEIFUM LABFSCRGKGIGTEAVLAML	6315		1015	
PDMFFSCSFIGMFVFYCAHMQTTYSGMLRFGKVDVTEIQIALVI VFVLSAFGGATMMDYTIPILEIKKILPVLOFLGGYJFSCSNYF HVILHGGYGKNGSTIAGTSVLSPGLHTGLITLAIMIYKKSATD VFBKHPCLYILMFGCVFAKVSQKLVVAHMTKSELYLQDTVPLGP GLLFLDQYFNNFIDETVVLWMAMVISSFDMVIYFSALCLQISRH LHLNIFKTACHQAPEQVQVLSKSHQNNMD SAGAGTGIMGGTTSTRRVTFEADENENITVVKGTRLSENVIDR MKESSPSGSKSGRYSGAYGASVSDEBLKRRVAEBLALEQAKKES EDQKRLKQAKELDRERAAANEQLTRAILREICSEEERAKAHL ARQLEBEKDRVLKKQDAFYKEQLARLEERSSEFYRVTTEQYQKAA EEVEAKFKRYESHPVCADLQAKILQCYRENHHQTLKCSALATQY MHCVNHAKQSMLEKGG 6317 102 839 PEAGTSAVLAREKGHLFTMRHEAPMQMASAQDARYGQKDSSDQN FDYMFKLLICINSSVGKTSFLFRYADDSFTSAFVSTVGIDPKVK TVFKNEKRIKLQIWDTAGQERYRTITTAYYRGAMGFILMYDITN EESFNAVQDMSTQIKTYSWDANQVILVGNKCDMEDERVISTERG QHLGEQLGFFFFTSAKDNINVKQTFERLVDIICDKMSESLETD PAITAAKQNTRLKETPPPPQPNCAC 6318 1765 733 PMHPLRTLPLHHPHPRPPRAEGREGADSMSHLPGLELRREAPPL LGPLLSPFPLDAGSWHRQMLRSSLRFPITMSAGAPCKAAGRMNI LAPVRRDRVLAELPQCLKKEAALHGHKDFHPRVTCACQEHRTGT VGFKISKVIVVGDLSVGKTCLINNFCKDTPDKNYKATIGVDFEM ERFEVLGIFFSLQLWDTAGQERFKCLASTYYRGAQAIIVFNLM DVASLEHTKQWLADALKENDPSSVLLFLVGSKKDLSTRAQYALM EKDALQVAQGMKAFYNAVSSLTGENNYREFFFRVAALTFEANVLA ELEKSGARRIGDVVRINSDDSNLYLTASKKKPTCCP 6319 88 717 AATMRLNQNTLLGKKVVLVPYTSEHVPSRYHEMMKSEELQRLT ASEPLTLEQEYAMQCSWGDADKCTFIVLDAEKWQAQPGATEES CMVGDVNLFLITDLEDLTLGEIEVMLAEPSCRGKGLGTEAVLAML			. 1013	IDCYOADDWAGGON GENERALIZATION CONTROL
VFVLSAFGGATMMDYTTPILEIKLKILPVLGFLGGVIFSCSNYF HVILHGGVGKNGSTIAGTSVLSPGLHIGLIIILAIMIYKKSATD VFBEHPCLYILMFGCVFAKVSQKLVVAHMTKSELYLQDTVFLGP GLLFLDQYFNNFIDEYVVLWMAMVISSFDMVIYFSALCLQISRH LHLNIFKTACHQAPEQVQVLSSKSHQNNMD VSAGAGTGIMGGTTSTRRVTFEADENENITVVKGIRLSENVIDR MKESSPSGSKSQRYGGAYGASVSDEBLKRRVAEBLALEQAKKES EDQKRLKQAKELDRERAAANEQLTRAILRERICSEEERAKAKHL ARQLEEKDRVLKKQDAFYKEQLARLEERSSEFYRVTTEQYQKAA EEVEAKFKRYESHPVCADLQAKILQCYRENTHQTLKCSALATQY MHCVNHAKQSMLEKGG 6317 102 839 PEAQTSAVLAREKGHLPTMRHEAPMQMASAQDARYGQKDSSDQN FDYMFKLLIIGNSSVGKTSFLFRYADDSFTSAFVSTVGIDPKVK TVFKNEKRIKQIWDTAGQERYRTITTAYYRGAMGFILMYDITN EESFNAVQDWSTQIKTYSWDNAQVILVGNKCDMEDERVISTERG QHLGEQLGFEFFETSAKDNINVKQTFERLVDIICDKMSESLETD PAITAAKQNTRLKETPPPPQNCAC 6318 1765 733 PWHPLRTLPLHHPHPRPFPRAEGREGADSMSHLPGLELRREAPPL LGPLLSFPLPDAGSWHRQMLRSSLRFPITNSAGAPCKAAGRMNI LAPVRRDRVLAELPQCLRKEAALHGHKDFHPRVTCACQEHRTGT VGFKISKVIVVGDLSVGKTCLINRFCKDTFDKNYKATIGVDPEM ERFEVLGIPFSLQLWDTAGQERFKCIASTYYRGAQAIIVFNIN DVASLSHTKOWLADALKGROPFSVLLFLVGSKKDLSTPAQYALM EKDALQVAQEMKAEYMAVSSLTGENVRRFFFRVAALITEANVLA ELEKSGARRIGDVVRINSDDSNLYLTASKKKPTCCP 6319 88 717 AATMRLNQNTLLLGKKVULVPYTSEHVPSRYHEWMKSEELORLT ASEPLTLEQEYAMQCSWGEDADKCTFIVLDAEKWQAQPGATEES CMVGDVNLFITDLEDLTLGEIEWMIAEFSCRGKGLGTBAVLAML				DDWPECCEPTCMEVENCEURODINGCON PROGRAMMENT
HVILHGGYGKNGSTIAGTSVLSPGLHIGLIIILAMIYKKSATD VFEKHPCLYILMFGCVFAKVSQKLVVAHMTKSELYLQDTVFLGP GLLFLDQVFNNFIDEYVVLWMAWISFDWVIYFSALCLQISRH LHLNIFKTACHQAPEQVQVLSSKSHQNNMD 792 VSAGAGTGIMGGTTSTRRUTFFADENENITVVKGTRLSENVIDR MKESSPSGSKSQRYSGAYGASVSDEBLKRRVAEBLALEQAKKES EDQKRLKQAKELDRERAAANSQLTRAILERSICSEERAKAKHL ARQLEEKDRVLKKQDAFYKEQLARLEERSSEFYRVTTEQYQKAA EEVEAKFKRYESHPVCADLQAKILQCYRENTHQTLKCSALATQY MHCVNHAKQSMLEKGG FDYMPKLLIIGNSSVGKTSFLFRYADDSFTSAFVSTVGIDFKVK TVFKNEKRIKLQIWDTAGQERYRTITTAYYRGAMGFILMYDITN EESFNAVQDWSTQIKTYSWDDNAQVILVGNKCDMEDRVISTERG OHLGEQLGFEFFETSAKDNINVKQTFERLVDIICDKMSESLETD PALTAAKQNTRLKETPPPPQPNCAC 6318 1765 733 PWHPLRTLPLHHPHPRPPRAEGREGADSMSHLPGLELRREAPPL LGPLLSPFPLPAGSWHRQMLRSSLRFPITNSAGAPCKAAGRMNI LAPVRRDRVLAELPQCLRKEAALHGHKDFHPRVTCACQEHRTGT VGFKISKVIVVGDLSVGKTCLINRFCKDTFDKNYKATIGVDPEM ERFEVLGIPFSLQLWDTAGGERFKCIASTYYRGAQAIIIVFHLIN DVASLEHTKQWLADALKDPSSVLLFLVGSKKDLSTPAQYALM EKDALQVAQEMKAEYMAVSSLTGENVRRFFFRVAALTEANVLA ELEKSGARRIGDVVRINSDDSNLYLTASKKKPTCCP 6319 88 717 AATMRLNQNTTLLGKKVVLVPYTSEHVPSRYHEWMKSEELQRLT ASEPLTLEQEYAMQCSWQEDADKCTFIVLDAEKWQAQPGATEES CMVGDVNLFTIDLEDLTLGEIEVMIAEPSSCRKGLGTBAVLAML	j j			VEVI.SAFGGATMUDVTIDII EIVI VII DII GEL GGUTTEGGATMUDVTIDII EIVI VII DII GEL GGUTTEGGATMUDVTIDII EIVI VII DII GEL GGUTTEGGATMUDVTIDII EIVI VII DII GEL GGUTTEGGATMUDVTIDII EIVI VII DII GEL GGUTTEGGATMUDVTIDII EIVI VII DII GEL GGUTTEGGATMUDVTIDII EIVI VII VII DII GEL GGUTTEGGATMUDVTIDII EIVI VII VII VII VII VII VII VII VII
VFEKHPCLYILMFGCVFAKVSQKLVVAHMTKSELYLQDTVFLGP GLLFLDQYFNNFIDEYVVLWMAMVISSFDMVIVFSALCLQISRH LHLNIFKTACHQAPEQVQVLSKSKQNNMD 792 VSAGAGTGIMGGTTSTREVTFEADENERITVVKGIRLSENVIDR MKESSPSGKSQRYSGAYGASVSDEBLKRRVAEBLALEQAKKES EDQKRLKQAKELDRERAAANEQLITRAILRERICSEEERAKAKHL ARQLEEKDRVLKKQDAFYKEQLARLEERSSEFYRVTTEQYQKAA EEVEAKFKRYESHPVCADLQAKILQCYRENTHOTLKCSALATQY MHCVNHAKQSMLEKGG 6317 102 839 PEAQTSAVLAREKGHLPTMRHEAPMOMASAQDARYGQKDSSDQN FDYMFKLLIIGNSSVGKTSFLFRYADDSFTSAFVSTVGIDFKVK TVFKNEKRIKLQIWDTAGQERYRTITTAYYRGAMGFILMYDITN EESFNAVQDWSTQIKTYSWDNAQVILVGNKCDMEDERVISTERG OHLGEQLGFEFFETSAKDNINVKQTFERLVDIICDKMSESLETD PAITAAKQNTRLKETPPPPQNCAC 6318 1765 733 PWHPLRTLPLHHPPPRPPRAEGREGADSMSHLPGLELRREAPPL LGPLLSPFPLPAGSWHRQMLRSSLRFPITNSAGAPCKAAGRMNI LAPVRRDRVLAELPQCLRKEAALHGHKDFHPRVTCACQEHRTGT VGFKISKVIVVGDLSVGKTCLINRFCKDTFDKNYKATIGVDFEM ERFEVLGIPFSLQLWDTAGQERFKCIASTYYRGAQAIIIVPNLN DVASLEHTKQNILADALKENDPSSVLLFLVGSKKDLSTPAQYALM EKDALQVAQEMKAEYMAVSSLTGENVREFFFRVAALTFEANVLA ELEKSGARR IGDVVR INSDBNLYLTASKKKPTCCP AATMRLNQNTLLLGKKVULVYYTSEHVPSXYHEMMKSEELQRLT ASEPLILEQEYAMQCSWQEDADKCTFIVLDAEKWQAQPGATEES CMVGDVNLFLTDLEDLTLGEIEVMLAEKWQAQPGATEES	1			HVILHGGVGKNGGTIDGTGVI.GDGI UTGI TITI ATMIYYYYA TO
GLLFLDQYFNNFIDEYVLWMAMVISSFDMVIYFSALCLQISRH LHLNIFKTACHQAPEQVQVLSSKSHQNNMD VSAGAGTGTMGGTTSTRRVTFFADENITVVKGIRLSENVIDR MKESSPSGSKSQRYSGAYGASVSDEELKRRVAEBLALEQAKKES EDQKRLKQAKELDRERAAANEQLTRAILRERICSEEERAKAKHL ARQLEEKDRVLKKQDAFYKEQLARLEERSSEFYRVTTEQYQKAA EEVEAKFKRYSESHPVCADLQAKILQCYRENTHQTLKCSALATQY MHCVNHAKQSMLEKGG 6317 102 839 PEAQTSAVLAREKGHLPTMRHEAPMQMASAQDARYGQXDSSDQN FDYMFKLLIIGNSSVGKTSFLFRYADDSFTSAFVSTVGIDFKVK TVFKNEKRIKLQIWDTAGQERYRTITTAYYRGAMGFILMYDITN EESFNAVQDWSTQIKTYSWDNAQVILVGNKCDMEDERVISTERG QHLGEQLGFEFFETSAKDNINVKQTFERLVDIICDKMSESLETD PAITAAKQNTRLKETPPPPQPNCAC 6318 1765 733 PWHPLRTLPLHHPHPRPPRPREGREGADSMSHLPGLELRREAPPL LGPLLSPFPLPAGSWHRQMLRSSLRFPITMSAGAPCKAAGRMNI LAPVRRDRVLAELPQCLRKEAALHGHKDFHPRVTCACQEHRTGT VGFKISKVIVVGDLSVGKTCLINRFCKDTPDKNYKATIGVDFEM ERFEVLGIPFSLQLWDTAGQERFKCIASTYYRGAQAIIVVRIN DVASLEHTKQWLADALKENDPSSVLLFLVGSKKDLSTPAQYALM EKDALQVAQEMKAEYWAVSSLTGENVRBFFFRVAALTFEANVLA ELEKSGARRIGDVVRINSDDSNLYLTASKKKPTCCP 6319 88 717 AATMRLNONTLLIGKVVUVPTTSEHVPSRYHEMMKSEELQRLT ASEPLTLEQEYAMQCSWQEDADKCTFIVLDAEKWQAQPGATEES CMVGDVNLFLTDLEDLTLGEISVMIABFSSCRGKGLGTEAVLAML				VERKHPCLYIIMEGCVEAKVSOKTAVAHMTYSELVIODTUBLOD
LHLNIFKTACHQAPEQVQVLSSKSHQNNMD VSAGAGTGIMGGTTSTRVTFEADENENITVVKGIRLSENVIDR MKESSPSGSKSQRYSGAYGASVSDELKRRVAEBLALEQAKKES EDQKRLKQAKELDRERAAANEQLTRAILERICSEEERAKAKHL ARQLEEKDRVLKKQDAFYKEQLARLEERSSEFYRVTTEQYQKAA EEVEAKFKRYESHPVCADLQAKILQCYRENTHQTLKCSALATQY MHCVNHAKQSMLEKGG 6317 102 839 PEAQTSAVLAREKGHLPTMRHEAPMQMASAQDARYGQXDSSDQN FDYMFKLLIIGNSSVGKTSFLFRYADDSFTSAFVSTYGIDFKVK TVFKNEKRIKLQIWDTAGQERYRTITTAYYRGAMGFILMYDITN EESFNAVQDWSTQIKTYSWDDAQVILVGNKCDMEDERVISTERG QHLGEQLGFEFFETSAKDNINVKQTFERLVDIICDKMSESLETD PAITAAKQNTRLKETPPPPPPPNCAC 6318 1765 733 PWHPLRTTPLHHEHPRPPRAEGREGADSMSHLPGLELRREAPPL LGPLLSPFPLPAGSWHRQMLRSSLRFPITNSAGAPCKAAGRMNI LAPVRRDRVLAELPQCLRKEAALHGHKDFHPRVTCACQEHRTGT VGFKISKVIVVGDLSVGKTCLINRFCKDTFDKNYKATIGVDFEM ERFEVLGIPFSLQLWDTAGQERFKCIASTYYRGAQAIIIVFNLN DVASLEHTKQWLADALKENDPSSVLLFLVGSKKOLSTPAQVALM EKDALQVAQEMKAEYNAVSSLTGENVRBFFFRVAALTFEANVLA ELEKSGARRIGDVVRINSDDSNLYLTASKKKPTCCP ASTMRLUNTLLLIGKVVLVPYTSEHVPSRYHEMMKSEELQRLT ASEPLTLEQEYAMQCSWQEDADKCTFIVLDAEKWQAQPGATEES CMVGDVNLFLTDLEDLTLGEISVMIABFSCRGKGLGTEAVLAML	1			GLLFLDOYFNNFIDEVVVIWMAMVISSEDMVIVESALGIOTORU
792 VSAGAGTGIMGGTTSTRRVTFEADENEITTVKGIRLSENVIDR MKESSPSGSKSQRYSGAYGASVSDEELKRRVABELALEQAKKES EDQKRLKQAKELDRERAAANEQLTRAILRERICSEEERAKAKHL ARQLEEKDRVLKKQDAFYKEQLARLEERSSEFYRVTTEQYQKAA EEVEAKFKRYESHPVCADLQAKILQCYRENTHQTLKCSALATQY MHCVNHAKQSMLEKGG 6317 102 839 PEAQTSAVLAREKGHLPTMRHEAPMQMASAQDARYGQKDSSDQN FDYMPKLLIIGNSSVGKTSFLFRYADDSFTSAFVSTVGIDPKVK TVFKNEKRIKLJUNDTAGQERYRTITTAYYRGAMGFILMYDITN EESFNAVQDWSTQIKTYSWDDAQVILVGNKCDMEDERVISTERG QHLGEQLGFEFFFETSAKDNINVKQTFERLVDIICDKMSESLETD PAITAAKQNTRLKETPPPPQPNCAC 6318 1765 733 PWHPLRTLPLHHPHPPRPPRAEGREGADSMSHLPGLELRREAPPL LGPLLSPFPLPAGSWHRQMLRSSLRFFITNSAGAPCKAAGRMNI LAPVRRDRVLAELPQCLRKEBAALHGHKDFHPRVTCACQEHRTGT VGFKISKVIVVGDLSVGKTCLINRFCKDTFDKNYKATIGVDFEM ERFEVLGIPFSLQLWDTAGQERFKCLASTYYRGAQAIIIVFNLN DVASLEHTKQWLADALKENDPSSVLLFLVGSKKDLSTPAQYALM EKDALQVAQEMKAEYWAVSSLTGENVREFFFRVAALTFEANVLA ELEKSGARRIGDVVRINSDDSNLYLTASKKKPTCCP AATMRLNQNTLLIGKKVVLVPYTSEHVPSRYHEWMKSEELQRLT ASSEPLTLEGEYAMQCSWQEDADKCTFIVLDAEKWQAQPGATEES CMVGDVNLFLTDLEDLTLGEIEVMLAEPSCRKGLGGTEAVLAML				LHLNIFKTACHOAPEOVOVISSKSHONNND
MKESSPSGSKSQRYSGAYGASVSDEBLKRRVABBLALEQAKKES EDQKRLKQAKELDRERAAANEQLTRAILRERICGEEERAKAKHL ARQLEBKDRVLKKQDAFYKEQLARLEERSSEFYNTTEQYQKAA EEVEAKFKYESHPVCADLQAKILQCYRENTHOTLKCSALATQY MHCVNHAKQSMLEKGG 6317 102 839 PEAQTSAVLAREKGHLPTMRHEAPMQMASAQDARYGQKDSSDQN FDYMFKLLIIGNSSVGKTSFLFRYADDSFTSAFVSTVGIDFKVK TVFKNEKRIKLQIWDTAGQERYRTITTAYYRGAMGFILMYDITN EESFNAVQDWSTQIKTYSWDNAQVILVGNKCDMEDERVISTERG QHLGEQLGFEFFETSAKDNINVKQTFERLVDIICDKMSESLETD PAITAAKQNTRLKETPPPPQPNCAC 6318 1765 733 PWHPLRTLPLHHPHPRPPRAEGREGADSMSHLPGLELRREAPPL LGPLLSPFPLPAGSWHRQMLRSSLRFPITNSAGAPCKAAGRMNI LAPVRRDRVLAELPQCLRKEAALHGHKDFHPRVTCACQEHRTGT VGFKISKVIVVGDLSVGKTCLINRFCKDTFDKNYKATIGVDFEM ERFEVLGIPFSLQLWDTAGQERFKCIASTYYRGAQAIIIVFNLN DVASLEHTKQWLADALKENDPSSVLLFLVGSKKDLSTPAQYALM EKDALQVAQEMKAEYWAVSSLTGENVREFFFRVAALTFEANVLA ELEKSGARRIGDVVRINSDDSNLYLTASKKKPTCCP AATMRLNQNTLLLGKKVVLVPYTSEHVPSRYHEWMKSEELQRLT ASEPLTILEGEYAMQCSWQEDADKCTFIVLDAEKWQAQPGATEES CMVGDVNLFLTDLEDLTLGEIEVMIAEFSCRGKGLGTEAVLAML	6316	1503	792	VSAGAGTGIMGGTTSTRRVTFEADENENTTVVVCTDLCENTITOD
EDQKRLKQAKELDRERAAANEQLTRAILRERICSEEERAKAKHL ARQLEEKDRVLKKQDAFYKEQLARLEERSSEFYRVTTEQYQKAA EEVEAKFKRYESHPVCADLQAKILQCYRENTHQTLKCSALATQY MHCVNHAKQSMLEKGG 6317 102 839 PERQTSAVLAREKGHLPTMRHEAPMQMASAQDARYGQKDSSDQN FDYMPKLLIIGNSSVGKTSFLFRYADDSFTSAFVSTVGIDFKVK TVFKNEKRIKLQIWDTAGQERYRTITTAYYRGAMGFILMYDITN EESFNAVQDWSTQIKTYSWDNAQVILVGNKCDMEDERVISTERG QHLGEQLGFEFFETSAKDNINVKQTFERLVDIICDKMSESLETD PAITAAKQNTRLKETPPPPQPNCAC 6318 1765 733 PWHPLRTLPLHHPPRPPRAEGREGADSMSHLPGLELRREAPPL LGPLLSPFPLPAGSWHRQMLRSSLRFPITNSAGAPCKAAGRMNI LAPVRRDRVLAELPQCLRKEAALHGHKDFHPRVTCACQEHRTGT VGFKISKVIVVGDLSVGKTCLINRFCKDTFDKNYKATIGVDFEM ERFEVLGIPFSLQLWDTAGQERFKCIASTYYRGAQAIIIVFNLN DVASLEHTKQWLADALKENDPSSVLLFLVGSKKDLSTPAQYALM EKDALQVAQEMKAETWAVSSLTGENVREFFFRVAALTFEANVLA ELEKSGARRIGDVVRINSDDSNLYLTASKKKPTCCP AATMRLNQNTLLGKKVVLVPYTSEHVPSRYHEWMKSEELQRLT ASEPLTILGGYAMQCSWQEDADKCTFIVLDAEKWQAQPGATEES CMVGDVNLFLTDLEDLTLGEIEVMIAEFSCRGKGLGTBAVLAML				MKESSPSGSKSORYSGAYGASVSDERLKRRVAERLALROAKKEG
ARQLEEKDRVLKKQDAFYKEQLARLEERSSEFYRVTTEQYQKAA EEVEAKFKRYESHPVCADLQAKILQCYRENTHQTLKCSALATQY MHCVNHAKQSMLEKGG PEAGTSAVLAREKGHLPTMRHEAPMQMASAQDARYGQKDSSDQN FDYMFKLLIIGNSSVGKTSFLFRYADDSFTSAFVSTVGIDFKVK TVFKNEKRIKLQIWDTAGQERYRTITTAYYRGAMGFILMYDITN EESFNAVQDWSTQIKTYSWDNAQVILVGNKCDMEDERVISTERG QHLGEQLGFEFFETSAKDNINVKQTFERLVDIICDKMSESLETD PAITAAKQNTRIKETPPPPQPNCAC 6318 1765 733 PWHPLRTLPLHHPPRPPRAGGREGADSMSHLPGLELRREAPPL LAPVRRDRVLAELPQCLRKEAALHGHKDFHPRVTCACQEHRTGT VGFKISKVIVVGDLSVGKTCLINRFCKDTFPKNYKATIGVDFEM ERFEVLGIPFSLQLWDTAGQERFKCIASTYYRGAQAIIIVFNLN DVASLEHTKQWLADALKENDPSSVLLFLVGSKKDLSTPAQYALM EKDALQVAQEMKAETWAVSSLTGENVREFFFRVAALTFEANVLA ELEKSGARRIGDVRINSDDSNLYLTASKKKPTCCP AATMRLNQNTLLGKKVVLVPYTSEHVPSRYHEWMKSEELQRLT ASEPLTILEQEYAMQCSWQEDADKCTFIVLDAEKWQAQPGATEES CMVGDVNLFLTDLEDLTLGEIEVMIAEFSCRGKGLGTBAVLAML				EDQKRLKQAKELDRERAAANEOLTRAILRERICSEEERAKAKHI.
EEVEAKFKRYESHPVCADLQAKILQCYRENTHQTLKCSALATQY MHCVNHAKQSMLEKGG PEAQTSAVLAREKGHLPTMRHEAPMQMASAQDARYGQKDSSDQN FDYMPKLLIIGNSSVGKTSFLFRYADDSFTSAFVSTVGIDPKVK TVFKNEKRIKLQIWDTAGQERYRTITTAYYRGAMGFILMYDITN EESFNAVQDWSTQIKTYSWDNAQVILVGNKCDMEDERVISTERG QHLGEQLGFEFFETSAKDNINVKQTFERLVDIICDKMSESLETD PAITAAKQNTRIKETPPPPQPNCAC 6318 1765 733 PWHPLRTLPLHHPPRFPRAGGEGADSMSHLPGLELRREAPPL LGPLLSPFPLPAGSWHRQMLRSSLRFPITNSAGAPCKAAGRMNI LAPVRRDRAVLAELPQCLRKEAALHGHKDFHPRVTCACQEHRTGT VGFKISKVIVVGDLSVGKTCLINRFCKDTFPKNYKATIGVDFEM ERFEVLGIPFSLQLWDTAGQERFKCIASTYYRGAQAIIIVFNLN DVASLEHTKQWLADALKBNDPSSVLLFLVGSKKDLSTPAQYALM EKDALQVAQEMKAEYMAVSSLTGENVREFFFRVAALTFEANVLA ELEKSGARRIGDVRINSDDSNLYLTASKKKPTCCP AATMRLNQNTLLLGKKVVLVPYTSEHVPSRYHEWMKSEELQRLT ASEPLTILEQEYAMQCSWQEDADKCTFIVLDAEKWQAQPGATEES CMVGDVNLFLTDLEDLTLGEIEVMIAEPSCRGKGLGTBAVLAML		}		ARQLEEKDRVLKKODAFYKEOLARLEERSSEFYRVTTEOYOKAA
6317 102 839 PEAQTSAVLAREKGHLPTMRHEAPMQMASAQDARYGQKDSSDQN FDYMPKLLIIGNSSVGKTSFLFRYADDSFTSAFVSTVGIDPKVK TVPKNEKRIKLQIWDTAGQERYRTITTAYYRGAMGFILMYDITN EESFNAVQDWSTQIKTYSWDNAQVILVGNKCDMEDERVISTERG QHLGEQLGPEFFETSAKDNINVKQTFERLVDIICDKMSESLETD PAITAAKQNTRLKETPPPPQPNCAC 6318 1765 733 PWHPLRTLPLHHPPHPPPRAGGREGADSMSHLPGLELRREAPPL LGPLLSPFPLPAGSWHRQMLRSSLRFPITMSAGAPCKAAGRMNI LAPVRRDRVLAELPQCLRKEAALHGHKDFHPRVTCACQEHRTGT VGFKISKVIVVGDLSVGKTCLINRFCKDTFDKNYKATIGVDPEM ERFEVLGIPFSLQLWDTAGQERFKCIASTTYRGAQAIIIVFNLN DVASLEHTKQWLADALKENDPSSVLLFLVGSKKDLSTPAQYALM EKDALQVAQEMKAETWAVSSLTGENVREFFFRVAALTFEANVLA ELEKSGARRIGDVRINSDDSNLYLTASKKKPTCCP AATMRLNQNTLLLGKKVVLVPYTSEHVPSRYHEWMKSEELQRLT ASEPLTILEQEYAMQCSWQEDADKCTFIVLDAEKWQAQPGATEES CMVGDVNLFLTDLEDLTLGEIEVMIAEPSCRGKGLGTEAVLAML	1			EEVEAKFKRYESHPVCADLOAKILOCYRENTHOTLKCSALATOY
FDYMPKLLIIGNSSVGKTSFLFRYADDSFTSAFVSTVGIDFKVK TVFKNEKRIKLQIWDTAGQERYRTITTAYYRGAMGFILMYDITN EESFNAVQDWSTQIKTYSWDNAQVILVGNKCDMEDERVISTERG QHLGEQLGFEFFETSAKDNINVKQTFERLVDIICDKMSESLETD PAITAAKQNTRIKETPPPPQPNCAC 6318 1765 733 PWHPLRTLPLHHPPRPPRAEGREGADSMSHLPGLELRREAPPL LGPLLSPFPLPAGSWHRQMLRSSLRFPITNSAGAPCKAAGRMNI LAPVRRDRVLAELPQCLRKEAALHGHKDFHPRVTCACQEHRTGT VGFKISKVIVVGDLSVGKTCLINRFCKDTFPKNYKATIGVDFEM ERFEVLGIPFSLQLWDTAGQERFKCIASTYYRGAQAIIIVFNLN DVASLEHTKQWLADALKBNDPSSVLLFLVGSKKDLSTPAQYALM EKDALQVAQEMKAETWAVSSLTGENVRBFFFRVAALTFEANVLA ELEKSGARRIGDVRINSDDSNLYLTASKKKPTCCP ASTMRLNQNTLLIGKKVVLVPYTSEHVPSRYHEWMKSEELQRLT ASEPLTILEQEYAMQCSWQEDADKCTFIVLDAEKWQAQPGATEES CMVGDVNLFLTDLEDLTLGEIEVMIAEPSCRGKGLGTBAVLAML				MHCVNHAKQSMLEKGG
FPYMPKLLIIGNSSVGKTSFLFRYADDSFTSAFVSTVGIDPKVK TVFKNEKRIKLQIWDTAGQERYRTITTAYYRGAMGFILMYDITN EESFNAVQDWSTQIKTYSWDNAQVILVGNKCDMEDERVISTERG OHLGGQLGFEFFETSAKDNINVKQTFERLVDIICDKMSESLETD PAITAAKQNTRLKETPPPPQPNCAC 6318 1765 733 PWHPLRTLPLHHPHPRPPRAEGREGADSMSHLPGLELRREAPPL LGPLLSPFPLPAGSWHRQMLRSSLRFPITNSAGAPCKAAGRMNI LAPVRRDRVLAELPQCLRKEAALHGHKDFHPRVTCACQEHRTGT VGFKISKVIVVGDLSVGKTCLINRFCKDTFDKNYKATIGVDFEM ERFEVLGIPFSLQLWDTAGQERFKCIASTYYRGAQAIIIVFNLN DVASLEHTKQWLADALKENDPSSVLLFLVGSKKDLSTPAQYALM EKDALQVAQEMKAEYWAVSSLTGENVREFFFRVAALTFEANVLA ELEKSGARRIGDVVRINSDDSNLYLTASKKKPTCCP AATMRLNQNTLLLGKKVVLVPYTSEHVPSRYHEMMKSEELQRLT AGSEPLTLEGEYAMQCSWQEDADKCTFIVLDAEKWQAQPGATEES CMVGDVNLFLTDLEDLTLGEIEVMIAEPSCRGKGLGTEAVLAML	6317	102	839	PEAQTSAVLAREKGHLPTMRHEAPMQMASAQDARYGOKDSSDON
TVFKNEKRIKLQIWDTAGQERYRTITTAYYRGAMGFILMYDITN EESFNAVQDWSTQIKTYSWDNAQVILVGNKCDMEDERVISTERG QHLGELGFEFFETSAKONINVKQTFERLVDIICDKMSESLETD PAITAAKQNTRLKETPPPPQPNCAC 6318 1765 733 PWHPLRTLPLHHPHPRPPRAEGREGADSMSHLPGLELRREAPPL LGPLLSPFPLPAGSWHRQMLRSSLRFPITNSAGAPCKAAGRMNI LAPVRRDRVLAELPQCLRKEAALHGHKDFHPRVTCACQEHRTGT VGFKISKVIVVGDLSVGKTCLINRFCKDTFDKNYKATIGVDFEM ERFEVLGIPFSLQLWDTAGQERFKCIASTYYRGAQAIIIVFNLN DVASLEHTKQWLADALKENDPSSVLLFLVGSKKDLSTPAQYALM EKDALQVAQEMKAEYWAVSSLTGENVREFFFRVAALTFEANVLA ELEKSGARRIGDVVRINSDDSNLYLTASKKKPTCCP AATMRLNQNTLLLGKKVVLVPYTSEHVPSRYHEWMKSEELQRLT ASEPLTILEQEYAMQCSWQEDADKCTFIVLDAEKWQAQPGATEES CMVGDVNLFLTDLEDLTLGEIEVMIAEPSCRGKGLGTBAVLAML	1 1		ĺ	FDYMFKLLIIGNSSVGKTSFLFRYADDSFTSAFVSTVGIDFKVK
EESFNAVQDWSTQIKTYSWDNAQVILVGNKCDMEDERVISTERG QHLGEQLGFEFFETSAKDNINVKQTFERLVDIICDKMSESLETD PAITAAKQNTRLKETPPPPQPNCAC 6318 1765 733 PWHPLRTLPLHHPPRPPRAEGREGADSMSHLPGLELRREAPPL LGPLLSPPLPAGSWHRQMLRSSLRFPITNSAGAPCKAAGRMNI LAPVRRDRVLAELPQCLRKEAALHGHKDFHPRVTCACQEHRTGT VGFKISKVIVVGDLSVGKTCLINRFCKDTFDKNYKATIGVDFEM ERFEVLGIPFSLQLWDTAGQERFKCIASTYYRGAQAIIIVFNLN DVASLEHTKQWLADALKENDPSSVLLFLVGSKKDLSTPAQYALM EKDALQVAQEMKAEYWAVSSLTGENVREFFFRVAALTFEANVLA ELEKSGARRIGDVVRINSDDSNLYLTASKKKPTCCP AATMRLNQNTLLGKKVVLVPYTSEHVPSRYHEWMKSEELQRLT ASEPLTILEQEYAMQCSWQEDADKCTFIVLDAEKWQAQPGATEES CMVGDVNLFLTDLEDLTLGEIEVMIAEFSCRGKGLGTEAVLAML	1 1	1	ļ	TVFKNEKRIKLQIWDTAGQERYRTITTAYYRGAMGFILMYDITN
OHLGEQLGFEFFETSAKDNINVKQTFERLVDIICDKMSESLETD PAITAAKQNTRLKETPPPPQPNCAC 6318 1765 733 PWHPLRTLPLHHPPRPPRAEGREGADSMSHLPGLELRREAPPL LGPLLSPFPLPAGSWHRQMLRSSLRFPITNSAGAPCKAAGRMNI LAPVRRDRVLAELPQCLRKEAALHGHKDFHPRVTCACQEHRTGT VGFKISKVIVVGDLSVGKTCLINRFCKDTFPKNYKATIGVDFEM ERFEVLGIPFSLQLWDTAGQERFKCIASTYYRGAQAIIIVFNLN DVASLEHTKQWLADALKENDPSSVLLFLVGSKKDLSTPAQYALM EKDALQVAQEMKAETWAVSSLTGENVRBFFFRVAALTFEANVLA ELEKSGARRIGDVVRINSDDSNLYLTASKKKPTCCP AATMRLNQNTLLGKKVVLVPYTSEHVPSRYHEWMKSEELQRLT ASEPLTILEQEYAMQCSWQEDADKCTFIVLDAEKWQAQPGATEES CMVGDVNLFLTDLEDLTLGEIEVMIAEPSCRGKGLGTBAVLAML	1 1		Į	EESFNAVQDWSTQIKTYSWDNAQVILVGNKCDMEDERVISTERG
FAITAAKQNTRLKETPPPPQPNCAC FAITAAKQNTRLKETPPPPQPNCAC PWHPLRTLPLHHPPHPPPRAGGREGADSMSHLPGLELRREAPPL LGPLLSPFPLPPAGSWHRQMLRSSLRFPITMSAGAPCKAAGRMNI LAPVRRDRVLAELPQCLRKEAALHGHKDFHPRVTCACQEHRTGT VGFKISKVIVVGDLSVGKTCLINRFCKDTFDKNYKATIGVDPEM ERFEVLGIPFSLQLWDTAGQERFKCIASTTYRGAQAIIIVFNLN DVASLEHTKQWLADALKENDPSSVLLFLVGSKKDLSTPAQYALM EKDALQVAQEMKAEYMAVSSLTGENVREFFFRVAALTFEANVLA ELEKSGARRIGDVVRINSDDSNLYLTASKKKPTCCP AATMRLNQNTLLLGKKVVLVPYTSEHVPSRYHEWMKSEELQRLT ASEPLTILEQEYAMQCSWQEDADKCTFIVLDAEKWQAQPGATEES CMVGDVNLFLTDLEDLTLGEIEVMIAEPSCRGKGLGTEAVJAML				QHLGEQLGFEFFETSAKDNINVKQTFERLVDIICDKMSESLETD
LGPLLSPFPLPAGSMHRQMLRSSLRFPITNSAGAPCKAAGRMNI LAPVRRDRVLAELPQCLRKEAALHGHKDFHPRVTCACQEHRTGT VGFKISKVIVVGDLSVGKTCLINRFCKDTFDKNYKATIGVDFEM ERFEVLGIPFSLQLWDTAGQERFKCIASTYYRGAQAIIIVFNLN DVASLEHTKQWLADALKENDPSSVLLFLVGSKKDLSTPAQYALM EKDALQVAQEMKAETWAVSSLTGENVRBFFFRVAALTFEANVLA ELEKSGARRIGDVVRINSDDSNLYLTASKKKPTCCP AATMRLNQNTLLLGKKVVLVPYTSEHVPSRYHEWMKSEELQRLT ASEPLTILEQEYAMQCSWQEDADKCTFIVLDAEKWQAQPGATEES CMVGDVNLFLTDLEDLTLGGEIEVMIAEPSCRGKGLGTEAVLAML	J-23.0			PAITAAKQNTRLKETPPPPQPNCAC
LGPLLSPFPLPAGSWHRQMLRSSLRFPITNSAGAPCKAAGRMNI LAPVRRDRVLAELPQCLRKEAALHGHKDFHPRVTCACQEHRTGT VGFKISKVIVVGDLSVGKTCLINRFCKDTFDKNYKATIGVDFEM ERFEVLGIPFSLQLWDTAGQERFKCIASTYYRGAQAIIIVFNLN DVASLEHTKQWLADALKENDPSSVLLFLVGSKKDLSTPAQYALM EKDALQVAQEMKAEYWAVSSLTGENVRBFFFRVAALTFEANVLA ELEKSGARRIGDVVRINSDDSNLYLTASKKKPTCCP 6319 88 717 AATMRLNQNTLLLGKVVLVPYTSEHVPSRYHEWMKSEELQRLT ASEPLTLEQEYAMQCSWQEDADKCTFIVLDAEKWQAQPGATEES CMVGDVNLFLTDLEDLTLGEIEVMIAEPSCRGKGLGTEAVLAML	0319	1762	733	PWHPLRTLPLHHPHPRPPRAEGREGADSMSHLPGLELRREAPPL
VGFKISKVIVVGDLSVGKTCLINRFCKDTFDKNYKATIGVDFEM ERFEVLGIPFSLQLWDTAGQERFKCIASTYYRGAQAIIIVFNLN DVASLEHTKQWLADALKENDPSSVLLFLVGSKKDLSTPAQYALM EKDALQVAQEMKAEYWAVSSLTGENVRBFFFRVAALTFEANVLA ELEKSGARRIGDVVRINSDDSNLYLTASKKKPTCCP AATMRLNONTLLLGKKVVLVPYTSEHVPSRYHEWMKSEELQRLT ASEPLTLEQEYAMQCSWQEDADKCTFIVLDAEKWQAQPGATEES CMVGDVNLFLTDLEDLTLGEIEVMIAEPSCRGKGLGTEAVLAML	1 1		ļ	LGPLLSPFPLPAGSWHRQMLRSSLRFPITNSAGAPCKAAGRMNI
ERFEVLGIPFSLQLWDTAGQERFKCIASTYYRGAQAIIIVFNLN DVASLEHTKQWLADALKENDPSSVLLFLVGSKKDLSTPAQYALM EKDALQVAQEMKAEYWAVSSLTGENVREFFFRVAALTFEANVLA ELEKSGARRIGDVVRINSDDSNLYLTASKKKPTCCP AATMRLNQNTLLLGKKVVLVPYTSEHVPSRYHEWMKSEELQRLT ASEPLTILEQEYAMQCSWQEDADKCTFIVLDAEKWQAQPGATEES CMVGDVNLFLTDLEDLTLGEIEVMIAEPSCRGKGLGTEAVLAML				LAPVRRDRVLAELPQCLRKEAALHGHKDFHPRVTCACQEHRTGT
DVASLEHTKQWLADALKENDPSSVLLFLVGSKKDLSTPAQYALM EKDALQVAQEMKAETWAVSSLTGENVRBFFFRVAALTFEANVLA ELEKSGARRIGDVVRINSDDSNLYLTASKKKPTCCP 6319 88 717 AATMRLNQNTLLLGKKVVLVPYTSEHVPSRYHEWMKSEELQRLT ASEPLTILEQEYAMQCSWQEDADKCTFIVLDAEKWQAQPGATEES CMVGDVNLFLTDLEDLTLGEIEVMIAEPSCRGKGLGTEAVIAML			1	VGFKISKVIVVGDLSVGKTCLINRFCKDTFDKNYKATIGVDFEM
EKDALQVAQEMKAEYMAVSSLTGENVREFFFRVAALTFEANVLA ELEKSGARRIGDVVRINSDDSNLYLTASKKKPTCCP AATMRLNQNTLLLGKKVVLVPYTSEHVFSRYHEWMKSEELQRLT ASEPLTILGEYAMQCSWQEDADKCTFIVLDAEKWQAQPGATEES CMVGDVNLFLTDLEDLTLGEIEVMIAEPSCRGKGLGTEAVLAML	}	1.	1	ERFEVLGIPFSLQLWDTAGQERFKCIASTYYRGAQAIIIVFNLN
ELEKSGARRIGDVVRINSDDSNLYLTASKKKPTCCP 6319 88 717 AATMRLNQNTLLLGKKVVLVPYTSEHVFSRYHEWMKSEELQRLT ASEPLTLEQEYAMQCSWQEDADKCTFIVLDAEKWQAQPGATEES CMVGDVNLFLTDLEDLTLGEIEVMIAEPSCRGKGLGTEAVLAML		ļ	1	DVASLEHTKQWLADALKENDPSSVLLFLVGSKKDLSTPAQYALM
AATMRLNONTLLLGKKVVLVPYTSEHVFSRYHEWMKSEELQRLT ASEPLTLEQEYAMQCSWQEDADKCTFIVLDAEKWQAQPGATEES CMVGDVNLFLTDLEDLTLGEIEVMIAEPSCRGKGLGTEAVLAML			İ	EKDALQVAQEMKAEYWAVSSLTGENVREFFFRVAALTFEANVLA
AATHALMQNIELLGARVVLOPITSEHVPSRYHEWMKSEELQRLT ASEPLTLEQEYAMQCSWQEDADKCTFIVLDAEKWQAQPGATEES CMVGDVNLFLTDLEDLTLGEIEVMIAEPSCRGKGLGTEAVLAML	6370-	- 00		ELEKSGARRIGDVVRINSDDSNLYLTASKKKPTCCP
CMVGDVNLFLTDLEDLTLGEIEVMIAEPSCRGKGLGTEAVLAML	0313	00	717	AATMRLNQNTLLLGKKVVLVPYTSEHVPSRYHEWMKSEELQRLT
CMVGDVNLFLTDLEDLTLGEIEVMIAEPSCRGKGLGTEAVLAML SYGVTTIGITEFERIGOGNEDETENERAL DEFOURMENT				ASEPLILEQEYAMQCSWQEDADKCTFIVLDAEKWQAQPGATEES
SYGVETEGETATION STATE ST	i i		ſ	CMVGUVNLFLTDLEDLTLGEIEVMIAEPSCRGKGLGTEAVLAML
VIQUE CENTED AND A CONTROL OF THE CO	<u> </u>	<u>-</u>	<u>_</u>	SYGVTTLGLTKFEAKIGQGNBPSIRMFQKLHFEQVATSSVFQEV

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ŀ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
}	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ŀ	amino acid	sequence	Codon, /=possible nucleotide deletion,
i	sequence		\=possible nucleotide insertion)
			TLRLTVSESEHQWLLEQTSHVEEKPYRDGSAEPC
6320	90	1111	RPRTGREKVAMAAVDSFYLLYREIARSCNCYMEALALVGAWYTA
]			RKSITVICDFYSLIRLHFIPRLGSRADLIKQYGRWAVVSGATDG
		1	IGKAYABELASRGLNIILISRNEEKLQVVAKDIADTYKVETDII
i		ŀ	VADFSSGREIYLPIREALKDKDVGILVNNVGVFYPYPQYFTQLS
			EDKLWDI INVNIAAASLMVHVVLPGMVERKKGAIVTISSGSCCK
			PTPQLAAFSASKAYLDHFSRALQYEYASKGIFVQSLIPFYVATS
ı	1		MTAPSNFLHRCSWLVPSPKVYAHHAVSTLGISKRTTGYWSHSIQ
1			FLFAQYMPEWLWVWGANILNRSLRKEALSCTA
6321	1418	341	HRKAALGALMAGRLLGKALAAVSLSLALASVTIRSSRCRGIQAF
			RNSFSSSWFHLNTNVMSGSNGSKENSHNKARTSPYPGSKVERSQ
	1		VPNEKVGWLVEWQDYKPVEYTAVSVLAGPRWADPQISESNP9PK
	1		FNEKDGHVERKSKNGLYEIENGRPRNPAGRTGLVGRGLLGRWGP
}	1		NHAADPIITRWKRDSSGNKIMHPVSGKHILQFVAIKRKDCGEWA
1			IPGGMVDPGEKISATLKREFGEBALNSLQKTSAEKREIEEKLHK
1			LFSQDHLVIYKGYVDDPRNTDNAWMETEAVNYHDETGEIMDNLM
1		•	LEAGDDAGKVKWVDINDKLKLYASHSQFIKLVAEKRDAHWSEDS
j	l .		EADCHAL
6322	2047	1083	NQEILKNVESSRTVQPHFLEFLLSLGWSVDVGRHPGWTGHVSTS
1			WSINCCDDGEGSQQEEVISSEDIGASIFNGQKKVLYYADALTEI
1			AFVVPSPVESLTDSLESNISDQDSDSNMDLMPGILKQPSLTLEL
1			FPNHTDNLNSSQRLSPSSRMRKLPQGRPVPPLGPETRVSVVWVB
İ			RYDDIENFPLSELMTEISTGVETTANSSTSLRSTTLEKEVPVIF
1	i i		IHPLNTGLFRIKIQGATGKFNMVIPLVDGMIVSRRALGFLVRQT
1			VINICRRKRLESDSYSPPHVRRKQKITDIVNKYRNKQLEPEFYT
			SLFQEVGLKNCSS
6323	1	656	PASTTDGAQEARVPLDGAFWIPRPPAGSPKGCFACVSKPPALQA
1			PAAPAPEPSASPPMAPTLFPMESKSSKTDSVRAAGAPPACKHLA
			EKKTMTNPTTVIEVYPDTTEVNDYYLWSIFNFVYLNFCCLGFIA
			LAYSLKVRDKKLLNDLNGAVEDAKTDRLINITRSGLAASCIMLW
			MALSVIATHRGLRSSASILVAEPHDWNTERPQVTFRERCPAL
6324	1	2061	EGAGMRRCPCRGSLNEAEAGALPAAARMGLEAPRGGRRRQPGQQ
			RPGPGAGAPAGRPEGGGPWARTEGSSLHSEPERAGLGPAPGTES
1			PQAEFWTDGQTEPAAAGLGVETERPKQKTEPDRSSLRTHLEWSW
			SELGTTCLWTETGTDGLWTDPHRSDLQFQPEBASPWTQPGVHGP
			WTELETHGSQTQPERVKSWADNLWTHQNSSSLQTHPEGACPSKE
1 ,			PSADGSWKELYTDGSRTQQDIEGPWTEPYTDGSQKKQDTEAARK
			QPGTGGFQIQQDTDGSWTQPSTDGSQTAPGTDCLLGEPEDGPLE
	 		EPEPGELLTHLYSHLKCSPLCPVPRLIITPETPEPEAQPVGPPS
			RVEGGSGGFSSASSFDESEDDVVAGGGGASDPEDRSGSKPWKKL
			KTVLKYSPFVVSFRKHYPWVQLSGHAGNFQAGEDGRILKRFCOC
			EQRSLEQLMKDPLRPFVPAYYGMVLQDGQTFNQMEDLLADFEGP
	J		SIMDCKMGSRTYLEEELVKARERPRPRKDMYEKMVAVDPGAPTP
] }			EEHAQGAVTKPRYMQWRETMSSTSTLGFRIEGIKKADGTCNTNF
[[1		KKTQALEQVTKVLEDFVDGDHVILQKYVACLEELREALEISPFF
1 1	ł		KTHEVVGSSLLFVHDHTGLAKVWMIDFGKTVALPDHQTLSHRLP
<u> </u>			WAEGNREDGYLWGLDNMICLLQGLAQS
6325	165	944	GLRDPFRRKRRLKPQVKMSNYVNDMWPGSPQEKDSPSTSRSGGS
	į		SRLSSRSRSRSFSRSSRSHSRVSSRFSSRSRRSKSRSRSRRRHO
	1		RKYRRYSRSYSRSRSRSRSRRYRERRYGFTRRYYRSPSRYRSRS
	ļ	•	RSRSRSRGRSYCGRAYAIARGQRYYGFGRTVYPBEHSRWRDRSR
			TRSRSRTPFRLSEKDRMELLEIAKTNAAKALGTTNIDLPASLRT
			VPSAKETSRGIGVSSNGAKPEVSILGLSEQNFQKANCQI
6326	538	680	GEPSPATQQKPSATGAGVLHQHFSSGHIYVLMGLLPPPWTISFT
			VQTTLQPPGGLPAAPVSGRMAFEPVGRDLARRMVPRAGKRTQTL
			GARRVAAQGARPLPEDRRPKSGERLHVTVAPCWEFVLPSVSLTA

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ŀ	amino acid	sequence	Godon / manifel manife
1	sequence	padrence	Codon, /=possible nucleotide deletion,
ļ	sequence		\=possible nucleotide insertion)
			QAWGGVGQEASSGVP
6327	1	1337	SLARLAPAGGSVVMPTQQPAAPSTRAPKPSRSLSGSLCALFSDA
		<u> </u>	DSGSGMKAELPPGPGAVGREMTKEEKLQLRKEKKQQKKKRKEEK
		·	GAEPETGSAVSAAQCQGPTRELPESGIQLGTPREKVPAGRSKAE
			LRAERRAKQEAERALKQARKGEQGGPPPKASPSTAGETPSGVKR
1			LPEYPQVDDLLLRRLVKKPERQQVPTRKDYGSKVSLFSHLPQYS
1			RQNSLTQFMSIPSSVIHPAMVRLGLQYSQGLVRGSNARCIALLR
1			ALQQVIQDYTTPPNEELSRDLVNKLKPYMSFLTQCRPLSASMHN
1			AIKFLNKEITSVGSSKREEEAKSELRAAIDRYVQEKIVLAAQAI
			SRFAYQKISNGDVILVYGCSSLVSRILQEAWTEGRRFRVVVVDS
1	1		RPWLEGRHTLRSLVHAGVPASYLLIPAASYVLPEVSTEEKDSKV
		!	GGEKV
6328	1030	276	HASAEVTTAAARGLGAMEBEMHTDAKIRAENGTGSSPRGPGCSL
			RHFACEQNLLSRPDGSASFLQGDTSVLAGVYGPABVKVSKEIFN
1	i	•	KATLEVILRPKIGLPGVAEKSRERLIRNTCEAVVLGTLHPRTSI
ľ			TVVLQVVSDAGSLLACCLNAACMALVDAGVPMRALFCGVACALD
	·		SDGTLVLDPTSKQEKEARAVLTFALDSVERKLLMSSTKGLYSDT
			ELQQCLAAAQAASQHVFRFYRESLORRYSKS
6329	3	2016	SSEVAAGGGTRSAMAEGSGEVVTVSATGAANGLNNGAGGTSATT
-	1 -	2010	CNDL CRYLLING DESCRIPTION DATE OF THE CONTROL OF TH
			SNPLSRKLHKILETRLDNDKEMLEALKALSTFFVENSLRTRRNL
			RGDIERKSLAINEEFVSIFKEVKEELESISEDVQAMSNCCQDMT
1			SRLQAAKEQTQDLIVKTTKLQSESQKLEIRAQVADAFLSKFQLT
1			SDEMSLLRGTREGPITEDFFKALGRVKQIHNDVKVLLRTNQQTA
1			GLEIMEQMALLQETAYERLYRWAQSECRTLTQESCDVSPVLTQA
			MEALQDRPVLYKYTLDEFGTARRSTVVRGFIDALTRGGPGGTPR
			PIEMHSHDPLRYVGDMLAWLHQATASEKEHLEALLKHVTTQGVE
1	[ENIQEVVGHITEGVCRPLKVRIEQVIVAEPGAVLLYKISNLLKF
			YHHTISGIVGNSATALLTTIEEMHLLSKKIFFNSLSLHASKLMD
}			KVELPPPDLGPSSALNQTLMLLREVLASHDSSVVPLDARQADFV
!			QVLSCVLDPLLQMCTVSASNLGTADMATFMVNSLYMMKTTLALF
			EFTDRRLEMLQFQIEAHLDTLINEQASYVLTRVGLSYIYNTVQQ
1			HKPEQGSLANMPNLDSVTLKAAMVQFDRYLSAPDNLLIPQLNFL
			LSATVKEQIVKQSTELVCRAYGEVYAAVMNPINEYKDPENILHR
			SPQQVQTLLS
6330	1151	333	FFYYTFYENKTFSRKMVAEKETLSLNKCPDKMPKRTKLLAQQPL
į			PVHQPHSLVSEGFTVKAMMKNSVVRGPPAAGAFKERPTKPTAFR
, ,			KFYERGDFPIALEHDSKGNKIAWKVEIBKLDYHHYLPLFFDGLC
1 1			EMTFPYEFFARQGIHDMLEHGGNKILPVLPQLIIPIKNALNLRN
]			RQVICVTLKVLQHLVVSAEMVGKALVPYYRQILPVLNIFKNMNV
j j			NSGDGIDYSQQKRENIGDLIQETLEAFERYGGENAFINIKYVVP
Į į			TYESCLIN
6331	3	495	QQQQRVRTRGRRACASATPLEGCVDLSYPRTHAALLKVAQMVTL
	l	· - -	LIAFICVRSSLWTNYSAYSYFEVVTICDLIMILAFYLVHLFRFY
	İ	.	RVLTCISWPLSELLHYLIGTLLLLIASIVAASKSYNQSGLVAGA
		1	IFGFMATFLCMASIWLSYKISCVTQSTDAAV
6332	1	878	VTESNKFDLVSFIPLLRERIYSNNQYARQFIISWILVLESVPDI
	- 1	3,0	
	1	ŀ	NLLDYLPEILDGLFQILGDNGKEIRKMCEVVLGEFLKEIKKNPS
!	i		SVKFAEMANILVIHCQTTDDLIQLTAMCWMREFIQLAGRVMLPY
[SSGILTAVLPCLAYDDRKKSIKEVANVCNQSLMKLVTPEDDELD
[ł		ELRPGOROAEPTPDDALPKQEGTASGEWTPSLHLTSCRGPREPD
			VIGVALGPHLSNQDYFMYVTHTIVAATQRSGSSGSPPFCRQDTG
6333			KLSTMATHSQLVKTGTGLEPRQAVSSSH
6333	3	1467	TRTPSEAEAGGESPOSCVSAAHSDWTAGKPVSLLAPLIPPRSAG
	ľ		QPLTFSPSGRQPLRSLLVGMCSGSGRRRSSLSPTMRPGTGAERG
		ł	GLMMGHPGMHYAPMGMHPMGQRANMPPVPHGMMPQMMPPMGGPP
L1			MGQMPGMMSSVMPGMMMSHMSQASMQPALPPGVNSMDVAAGTAS

Deginning nucleotide location cortesponding cortion cortesponding cofirst amino acid amino acid residue of amino acid amino	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
No:	ID	beginning		(A=Alanine, C=Cvateine, D=Aspertic Acid' P.
corresponding to first anino acid residue of sanno acid anino acid residue of sanno acid anno acid sequence (anno acid sequence) anino acid sequence (anno acid sequence) sequence (anno acid sequence) sequence (anno acid sequence) sequence (anno acid sequence) (NO:	nucleotide		Glutamic Acid. Paphenylalanine G-Glycine
to first amino acid residue of residue of residue of amino acid sequence se		location	corresponding	H-Histidine. In Isoleucine K-Lycine
amino acid residue of amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid sequence of secries, T-Threanine, V-Valine, M-Tryptophan, Y-Tyrosine, X-Unknown, *-stop Codon, /-possible nucleotide deletion)		corresponding	to first	L=Leucine, M=Methionine, N=Asparagine
amino acid sequence s	1		amino acid	P=Proline, Q=Glutamine, R=Arginine
mino acid sequence Metryptophan, Yefyrosine, Xeduknown, *stop Coden, /eposabile nucleotide deletide	İ	amino acid	residue of	S=Serine, T=Threonine, V=Valine
sequence seq	1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Ston
Apposable nucleotide insertion		amino acid	sequence	Codon, /=possible nucleotide deletion
GARSHWITEHKSPOGRTYYNTETKOSTWEKPDLIKTPARCILLS CPWEXYSBOSKOVYNTSOTICES RAMAPKELBLIGE GYNTTURAL SLITKSNILMANI KARESS SKORECTTISTA PUPTET I PTTWINNED ARRAAAVANAAAAAAAAAAANANINSTSSINTYOSTVPVYDER EVTS I VATVUDNENTYTI STERGAGLISTPALOGOSVEVISNITO BETS KORTVADPETKEREES OPAKKITYMINKERAKOAFRUIK KERRVESNASHEQAMKNI INDPRISALAKUSKKAAPRAYKVOLT EKK GASVARSTOTHIVKLOPA POKNINTORITATION ON THE CONTROLLER OF THE CONTROLLER ON THE CONTROLLER OF THE CONTROLLER O		sequence	1	\=possible nucleotide insertion)
CPMKZYKSDGKPYYTNSOTKESRMARYKELBILEGYGNTTYMAN SALTASANLAMIKAESSKOBECTTSTAPPYTTEI PITTMINA AREADAAVAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA				GAKSMWTEHKSPDGRTYYYNTETKOSTWEKPDDLKTPAFOLLSK
SLITKSNIHMIKABESSKOEKCTITISTAPVPTTE PTTMSTMA AARAAAANAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	J			CPWKEYKSDSGKPYYYNSOTKESRWAKPKELEDLEGYONTTVAG
AREADAWVAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA				SLITKSNLHAMIKAEESSKOEECTTTSTAPVPTTEIPTTMSTMA
EVTS LYATVUNENTUTI STEEQAQLISTPAIQOOG VERS SINTO BETS KQETVADPTPKKEEEESQAPAKTYTIWIKEBAKQAPKELL KERRVESKASKEQAMKMI INDPRYSALAKLSEKKQAPRAYKVQT EKK GASVAS GARVESTAGTHVALUPGAPOKRVYTYPKTTYDQMYNDLLAKKK ELYTONGILMMLDRIKKI KRAPER KQOKCODEJAKKX GEVSVRSTGTHVALUPGAPOKRVYTYPKTTYDQMYNDLLAKKK ELYTONGILMMLDRIKKI KRAPER KQOKCODEJALIKCEEXVYD QVVEDLINSRQGTCQPVHVNNVDIQDNIBEATLGAPLICELCQC IQHTEDMENI BIDELLQPEEKEKSGRTFLHTVCT QVVEDLINSRQGTCQPVHVNNVDIQDNIBEATLGAPLICELCQC IQHTEDMENI BIDELLQPEEKEKSGRTFLHTVCT GARVAGOSHLS 82 529 AARARFOVLCCELGAALGOGSRVEMSY 1FGQFYTAVVGRUH KLAQGENLILIFSI IGGIDDOBON PS SEDATUKGI YVTRVSEG GPAELAGLQIGOKINOVNGKODHTWATHOQARKRLIKRSEEVVRL LVYROSLOKAVOGSHLS AARARFOVLCCELLGAALGOGSRVEMSY 1FGQFYTAVVGRUH ALDOLVPHERI EAPWARVOGSHLS ADFULTENDLI PKLEQVLAPRKROCTGGYTEMICQI INNSDLRAK AAVISYKONLEPPIPLERRISHLIDIGALGGIROPESRIHLLRN LLINGLYRHERI EAPWARVODEMGYAEKLIDIGALGGIROPESRIHLLRN ALLINGLYRHERI EAPWARVODEMGYAEKLIDIGALGGIROPESRAMMA ADFULTENDLI PKLEQVLAPRKROCTGGYTEMICQI INNSDLRAK MAVISYKONLEPPIPLERRISHLITLINGLAGGROOLEGGEAS HISSHTAQTFEG ACCCRAGEWGSTLYTKAMI LICKRPYLELEFOYTONCAACSKLI PAPRWWRAKDNYYHLDCACCLCNQRFCVGDKFFLKINMILCQ TOVERGLIMKSGYAPOVR ACCCRAGEWGSTLYTKAMI LICKRPYLELEFOYTINNANNY KNYKKEVLALLYHEPPEDDKASQRQPEMEELI LELAQVILED KGVGGGLVDSEKDAAVAKKIGLITUSVYKKGDEVIEXDGEFS ADTIVELLIDVLEPPEDDKASQRQPEMEELI LELAQVILED KGVGGLVDSEKDAAVAKKIGLITUSVYKYKGDEVIEXDGEFS ADTIVELLIDVLEPPEDDKASQRQPEMEELI LELAQVILED KGVGGLVDSEKDAAVAKKIGLITUSVERIKRSTRAKHENDEFS ADTIVELLIDVLEPPENTENTEDDODDDD KGSHKKAFBIDAAEERHPYIPFFATPISKGAKKLTIKLMEIDFYE AFMEDVTI FDKYRSTEETIVFKTSTERLARPGIGVANVTHDESFS ADTIVELLIDVLEPPENTENTEDDDDDDDD FRAMBELEBRENDEDVEEGSINTEDDDDDDDD FRAMBELEBRENDEDVEEGSINTEDDDDDDDD FRAMBELEBRENDEDVEEGSINTEDDDDDDDD FRAMBELEBRENDEDVEEGSINTEDDDDDDDD FRAMBELEBRENDEDVEEGSINTEDDDDDDDD FRAMBELEBRENDEDVEEGSINTEDDDDDDDD FRAMBELEBRENDEDVEEGSINTEDDDDDDDD FRAMBELEBRENDERTSTERRENTI VODDGTTKEATSTGKINGDENTYTHMEGGGROOMICGLEFT KRQULLANTINTHANCGGROOMICGLEFT KRQULLANTINTHANCGGROOMICGLEFT KRQULLANTINTHANCGGROOMICGLEFT KRQULLANTINTHANCGGROOMICGLEFT KRQULSANGERSTYVKMEA			;	AAEAAAAVVAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
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GURLALLILLGLGTPKSGYQGQEGLDFPEYGGVDRYINNMAKNY KNVPKKYEVLALLYHEPPEDDKASQRQFEMEBLILELAAQVLED KGYGFGLVDSSKDAAVAKKLGLTEVDSMYVPKGDEVIEYDGEFS ADTIVEFLDVLEDPVELIEGERELQAFENIEDEIKLIGYFKSK DSEHYKAFEDAAEBFHPYIPFFATPDSKGAKKLTLKINSIDFYE AFMEEPVTIPDKPNSEEEIVNFVEEHRRSTLRKLKPESMYETWE DDMDGIHIVAPAEEADPDGFETLETLKAVAQDNTENPDLSIIWI DPDDFPLLVPYWEKTPTDIDLSAPQIGVVNVTDADRLWMEMDDEE DLPSAEELEDWLEDVLEGEINTEDDDDDDDD NRCDRGGGGGARQAGCGCRTQGAGPGFGHSFFSQGAMKAFH TFCVVLLVFGSVSEAKFDDFEDEDIVSYDDNDFAEFEDVMEDS VTESPQRVIITEDDEDDTTVELEGQDENQEGDFEDADTQEGDTE SEPYDDEEFEGYEDKPDTSSSKNKDPITIVDVPAHLQNSWESYY LEILMVTGLLAYIMNYIIGKNKNSRLAQAWFNTHRELLESNFTL VGDDGTNKEATSTGKLNQENEHIYNLWCSGRVCCEGMIQLKFL KRQDLLNVLARMMRPVSDQVQIKVTMNDEDMDTVVFAVGTRKAL VRLQKEMQDLSEFCSDKPKSGAKYGLPDSLAILSEMGEVTDGMM DTKMVHFLTHYADKIESVHFSDQFSGPKIMQEGOPLKLPDTKR TLLLTFNVPGSGNTYPKDMEALLPLMNMVIYSIDKAKKFRLNREE GKQKADKNRARVSENFLKLTHVQRQEAAQSRREEKKRAEKERIM NEEDPEKQRLEEBAALRREQKKLEKKQMKMKQIKVKAM 6340 2 583 EACAHTLSCPAFFARLGRARREPWMSHRTSSTFRAERSFISSSSS SSSSTSSSASRALPAQDPDMEKALSMFSDDFSFRPHSBFLAF PARRGGGGIKTIGDAYEFAYDVRDFSPEDIIVTTSNNHIEVRA EKLAADGTVMNNFAHKCQLPEDVDFISVTSALREDGSLTIRARR HPHTEHVQQTFRTEIKI KMAVLSAPGLRGFRILGLRSSVGPAVQARGVHQSVATDGPSSTQ PALPKARAVAPKPSSRGEYVVAKLDDLVWWARRSSLMPMTGGLA	6338	66	13/19	
KOVFKKYEVIALLYHEPPEDDKASQRQFEMEBLILELAAQVLED KGVGFGLVDSEKDAAVAKKLGLTEVDSMYVFKGDEVIEYDGEFS ADTIVEFLLDVLEDPVELIEGERELQAFENIEDEIKLIGYFKSK DSEHYKAFEDAAEEPHPYIPPFATFDSKGAKKLTLKLMEIDFYE AFMEEPVTIPDKPNSEEEIVNFVEEHRRSTLRKLKPESMYETWE DDMDGIHIVAFAEEADPDGFFFLETLKAVAQONTENPDLSIIWI DPDDFPLLVPYWEKTPDIDLSAPQIGVVNVTDADRLWMEMDDEE DLPSAEELEDWLEDVLEGEINTEDDDDDDD 6339 246 1823 NRCDRGGGGAERQAGGGCRTOGAGPGFGFGHSFFSQGAMKAPH TFCVVLLVFGSVSAKFDDFEDEDIVEYDDNDFAEFEDVMEDS VTESPQRVIITEDDEDETTVELEGQDENGEGPEDADTOEGDTE SEPYDDEEFEGYEDKPDTSSSKNKDPITIVDVPAHLQNSWESYY LEILMYTGLLAYIMNYIIGKNKNSRLAQAWFNTHRELLESNFTL VGDDGTNKEATSTGKLNQENEHIYNLWCSGRVCCEGMLIQLRFL KRQDLLNVLARMMRPVSDQVQIKVTMNDEDMDTYVFAVGTRKAL VRLQKEMQDLSEFCSDKPKSGAKYGLPDSLAILSEMGEVTDGMM DTKMYHFLTHYADKIESVHFSDGFSGFKIMQEEGOPLKLPDTKR TLLLTFNVPGSGRTYPKOMBALLPLMMNVIYSIDKAKKFRLNRE GKQKADKNRAVEENFLKLTHVQRQEAAQSREEKKRAEKRIM NEEDPEKQRRLEBAALRREQKKLEKKQMKMKQIKVKAM 6340 2583 EACAHTLSCPAFARLGRARRRPWMSHRTSSTFRAERSFHSSSSS SSSTSSSASRALPAQDPPMEKALSMPSDDFGSFMRPHSBELAF PARPGGAGRIKTLGDAYEFAVDVRDFSPEDIIVTTSNNHIEVRA EKLAADGTVMNNFAHKCQLPBDVDPTSVTSALREDGSLTIRARR HPHTEHVQQTFRTEIKI VMAVLSAPGLRGFRILGLRSSVGPAVQARGVHQSVATDGPSSTQ PALPKARAVAPKPSSRGEYVVAKLDDLVNWARRSSLWPMTFGLA			1347	GLELALLILLICIGTEVECUCCOECI DEDENOCUEDIUTATIVA
KGYGFGLVDSEKDAAVAKKLGLTEVDSMYVFKGDEVIEYDGEFS ADTIVEFLLDVLEDPVELIEGERELQAFENIEDEIKLIGYFKSK DSEHYKAFEDAABEFHPYIPFFATFDSKGAKKLTLKLUKIDFYE AFMEEPVTIPDKPNSEEEIVMFVEEHRRSTLRKLKPESMYETWE DDMDGIHLVAFAEEADPDGFEFLETLKAVAQDNTENPDLSIIWI DPDDFPLLVPYWEKTETDIDLSAPQIGVVNVTDADRLWMEMDDEE DLPSAEELEDWLEDVLEGEINTEDDDDDDDD 6339 246 1823 NRCDRGGGGABRQAGGCCRTGGAGFGFGKSFFSGGMKAFH TFCVVLLVFGSVSEAKFDDFEDEEDIVEYDDNDFAEFEDVMEDS VTESPQRVIITEDDEEDIVEYDDNDFAEFEDVMEDS VTESPQRVIITEDDEEDIVEYDDNDFAEFEDVMEDS VTESPQRVIITEDDEEDITVELBGQDENGEGFEDADTQEGDTE SEPYDDEEFEGYEDKPSSKKNKDPITIVDVAHLQNSWEBYY VGDDGTNKEATSTGKLNQENEHIYNLWCSGRVCCEGMLIQLRFL KRQDLLNVLARMMRPVSDQVQIKVTMNDEDMDTYVFAVGTRKAL VRLQKEMQDLSEFCSDKPKSGAKYGLPDSLAILSENGEVTTGMM DTKMVHFLTHYADKIESVHFSDQFSGFKIMQEEGQPLKLPDTKR TLLLTFNVPGSGNTYPKOMBALLPLMNMVIYSIDKAKKFFLINRE GKQKADKNRARVEENFLKLTHVQRQEAAQSRREEKKRAEKERIM NEEDPEKQRRLEBAALRREQKKLEKKQMKMKQIKVKAM 6340 2 583 EACAHTLSCPAFARREPWMSHRTSSTFRAERSFHSSSS SSSSTSSSASRALPAQDPPMEKALSMFSDDFGSFMRPHSBPLAF PARPGGAGNIKTLGDAYEFAVDVRDFSPEDIIVTTSNNHLEVRA EKLAADGTVMNNFAHKCQLPBDVDPTSVTSALREDGSLTIRARR HPHTEHVQQTFRTEIKI KMAULSAPGLRGFRILGLRSSVGPAVQARGVHQSVATDGFSSTQ PALPKARAVAPKPSSRGEYVVAKLDDLVWWARRSSLWPMTFGLA	!			KNVEKKYEVI AT T. VHEDDEDDVA CODOREMENT TO BE A SOUTH
ADTIVEFILDVLEDPVELIEGERELQAFENIEDE IKLIGYFKSK DSEHYKAFEDAAEEFHPYIPFFATPDSKGAKKLTILKINEIDFYE AFMEEPVTIPDKPNSEEE IVNFVEEHRRSTLRKLKPESMYETWE DDMDGIHIVAFAEEADPDGFEFLETLKAVAQONTENPDLSIIWI DPDDFPLLVPYWEKTFOIDLSAPQIGVVNVTDADRLWMEMDDEE DLPSAEELEDWLEDVLEGEINTEDDDDDDDD RCDRGGGGQAERQAGGGCTTQGAGFGFGFGFSFSTSGGAMKAFH TFCVVLLVFGSVSEAKFDDFEDEEDIVEYDDNDFAEFEDVMEDS VTESPQRVIITEDDEDETTVELEGQDENQEGDPBDADTQEGDTE SEPYDDEEFEGYEDKPDTSSSKNKDPITTVDVPAHLQNSWESYY LEILMVTGLLAYIMNYIIGKNKNSRLAQAWFNTHRELLESNFTL VGDDGTNKEATSTGKLNQENEHIYNLWGSGRVCCGGMLIQLRFL KRQDLLNVLARMMRPVSDQVQIKVTMNDEDMDTYVFAVGTRKAL VRLQKEMQDLSEFCSDKPKSGAKYGLPDSLAILSEMGEVTDGMM DTKMVHFLTHYADKIESVHPSDQFSGPKIMQEEGOPLKLPDTKR TLLLTFNVPGGGNTYPKDMEALLPLMNNVIYSIDKAKKFRLNRE GKQKADKNRARVEENFLKLTHVQRQEAAQSRREEKKRAEKERIM NEEDPEKQRRLEBAALRREQKKLEKKOMMKQIKVKAM SSSSTSSASRALPAQDPPMEKALSMPSDDFGSFMRPHSEPLAF PARPGGAGNIKTLGDAYEFAVDVRDFSPEDIIVTTSNNHIEVRA EKLAADGTVMNNFAHKCQLPBDVDPTSVTSALREDGSLTIRARR HPHTEHVQQTFRIBIKI 6341 2 645 KMAVLSAPGLRGFRILGERSVGPAVQARGVHQSVATDGPSSTQ PALPKARAVAPKPSSRGEYVVAKLDDLVMWARRSSLWPMTFGLA	1 1			KGVGFGLVDSEKDAAVAKKI GI TEUDSMYUEVCDEUTEVDGEED
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AFMEEPVTIPDKPNSEEEIVMFVEEHRRSTLRKLKPESMYETWE DDMDGIHIVAFAEEADPDGFFLETLKAVAQDNTENPDLSIIWI DPDDFPLLVPYWEKTFDIDLSAPQIGVVNVTDADRLWMEMDDEE DLPSAEELEDWLEDVLEGEINTEDDDDDDDD DLPSAEELEDWLEDVLEGEINTEDDDDDDDD TFCVVLLVFGSVSEAKFDDFEDEEDIVEYDDNDFAEFEDVMEDS VTESPQRVIITEDDEDETTVELBGQDENQBGDFEDADTQEGDTE SEPYDDEEFEGYEDKPDTSSSKNKDPITIVDVPAHLQNSWBSYY LEILMVTGLLAYIMNYIIGKNKNSRLAQAWFNTHRELLESNFTL VGDDGTNKEATSTGKLNQENEHIYNLWCSGRVCCEGMLIQLRFL KRQDLLNVLARMMRPVSDQVQIKVTMNDEDMDTYVFAVGTRKAL VRLQKEMQDLSEFCSDKPKSGAKYGLPDSLAILSEMGEVTDGMM DTKMVHFLTHYADKIESVHFSDQFSGPKIMQEEGQPLKLPDTKR TLLLTFNVPGSGNTYPKDMEALLPLMNMVIYSIDKAKKFRINRE GKQKADKNRARVBENFFLKLTHVQRQEAAQSRREEKKRAEKKRIM NEEDPEKQRRLEBAALRREQKKLEKKQMKMKQIKVKAM NEEDPEKQRRLEBAALRREQKKLEKKQMKMKGIKVKAM SSSSTSSSASRALPAQDPPMEKALSMFSDDFGSFMRPHSEPLAF PARPGGAGNIKTLGDAYEFAVDVRDFSPEDIIVTTSNNHIEVRA EKLAADGTVMNNFAHKCQLPBDVDPTSVTSALREDGSLTIRARR HPHTEHVQQTFRTEIKI 6341 2 645 KMAVLSAPGLRGFRILGRSSVGPAVQARGVHQSVATDGPSSTQ PALPKARAVAPKPSSRGEYVVAKLDDLVNWARRSSLWPMTFGLA	1 1			DSEHYKAFEDAAERFHDVIDFFATEDSKGAKKLTLVINGIDEVE
DDMDGIHIVAFAEEADPDGFEFLETLKAVAQDNTENPDLSIIWI DPDDFPLLVPYWEKTFDIDLSAPQIGVVNVTDADRLWMEMDDEE DLPSAEELEDWLEDVLEGEINTEDDDDDDDD RCDRGGGOAERQAGGCRTQAGGFGFGGHSFFSQGAMKAFH TFCVVLLVFGSVSEAKFDDFEDEEDIVEYDDNDFAEFEDVMEDS VTESPQRVIITEDDEDETTVELEGQDENQEGDFEDADTQEGDTE SEPYDDEEFEGYEDKPDTSSSKNKDPITIVDVPAHLQNSWESYY LEILMVTGLLAYIMNYIIGKNKNSRLAQAWFNTHRELLESNFTL VGDDGTNKEATSTGKLNQENEHIYNLWCSGRVCCEGMLIQLRFL KRQDLLNVLARMMRPVSDQVQIKVTMNDEDMDTYVFAVGTRKAL VRLQKEMQDLSEFCSDKPKSGAKYGLPDSLAILSEMGEVTDGMM DTKMVHFLTHYADKIESVHFSDQFSGPKIMQEEGQPLKLPDTKR TLLLTFNVPGSGNTYPKDMBALLPLMNMVIYSIDKAKKFRLNRE GKQKADKNRARVEENFLKLTHVQRQEAAQSRREEKKRAEKRIM NEEDPEKQRRLEEBAALRREQKKLEKKQMKMKQIKVKAM NEEDPEKQRRLEEBAALRREQKKLEKKQMKMKQIKVKAM 6340 2 583 EACAHTLSCPAFARLGRARRRPWMSHRTSSTFRAEESFHSSSSS SSSSTSSSASRALPAQDPPMEKALSMFSDDFGSFMRPHSEPLAF PARPGGAGNIKTLGDAYEFAVDVRDFSPEDIIVTTSNNHIEVRA EKLAADGTVMNNFAHKCQLPEDVDTSVTSALREDGSLTIRARR HPHTEHVQQTFRTEIKI 6341 2 645 KMAVLSAPGLRGFRILGLRSSVGPAVQARGVHQSVATDGPSSTQ PALPKARAVAPKPSSRGEYVVAKLDDLVNWARRSSLWPMTFGLA	1 1			AFMEEPVTIPDKPNSEEEIVNFVEEHRRSTI.RKI.VDECMVETWR
DPDDFPLLVPYWEKTFDIDLSAPQIGVVNVTDADRLWMEMDDEE DLPSAEELEDWLEGEINTEDDDDDDDD 1813 NRCDRGGGQAERQAGGCRTQAGGFGFGHSFFSQGAMKAFH TFCVVLLVFGSVSEAKFDDFEDEEDIVEYDDNDFAEFEDVMEDS VTESPQRVIITEDDEDBTTVELEGQDENQEGDFBDADTQEGDTE SEPYDDEEFEGYEDKPDTSSSKNKDPITIVDVPAHLQNSWESYY LEILMVTGLLAYIUNYIIGKNKNSRLAQAWFNTHRELLESNFTL VGDDGTNKEATSTGKLNQENEHIYNLWCSGRVCCEGMIJQLRFL KRQDLLNVLARMMRPVSDQVQIKVTMNDEDMDTYVFAVGTRKAL VRLQKEMQDLSEFCSDKPKSGAKYGLPDSLAILSEMGEVTDGMM DTKMVHFLTHYADKIESVHPSDQFSGPKIMQEEGQPLKLPDTKR TLLLTFNVPGSGNTYPKDMBALLPLMNMVIYSIDKAKKFRLNRE GKQKADKNRARVBENFLKLTHVQRQEAAQSRREEKKRAEKERIM NEEDPEKQRRLEEBALRREQKKLEKKQMKMKQIKVKAM NEEDPEKQRRLEEBALRREQKKLEKKQMKMKQIKVKAM SSSSTSSSASRALPAQDPPMEKALSMFSDDFGSFMRPHSEPLAF PARPGGAGNIKTLGDAYEFAVDVRDFSPEDIIVTTSNNHIEVRA EKLAADGTVMNNFAHKCQLPBDVDPTSVTSALREDGSLTIRARR HPHTEHVQQTFRTEIKI 2 645 KMAVLSAPGLRGFRILGLRSSVGPAVQARGVHQSVATDGPSSTQ PALPKARAVAPHPSSRGEYVVAKLDDLVNWARRSSLWPMTFGLA	i l	İ		DDMDGIHIVAFAEEADPDGFEFLETIKAVAODNTENDDIGTINT
DLPSAEELEDWLEDVLEGEINTEDDDDDDDD 6339 246 1823 NRCDRGGGGQAERQAGCGCRTQGRGFGFGHSFFSQGAMKAFH TFCVVLLVFGSVSEAKFDDFEDEEDIVEYDDNDFAEFEDVMEDS VTESPQRVIITEDDEDBTTVELEGQDENQEGDFBDADTQEGDTE SEPYDDEEFEGYEDKPDTSSSKNKDPITIVDVPAHLQNSWESYY LEILMVTGLLAYIMNYIIGKNKNSRLAQAWFNTHRELLESNFTL VGDDGTNKEATSTGKLNQENEHIYNLWCSGRVCCEGMLIQLRFL KRQDLLNVLARMMRPVSDQVQIKVTMNDEDMDTYVFAVGTRKAL VRLQKEMQDLSEFCSDKPKSGAKYGLPDSLAILSEMGEVTDGMM DTKMVHFLTHYADKIESVHFSDQFSGFKIMQEEGQPLKLPDTKR TLLLTFRVYGSGNTYPKDMEALLPLMNMVIYSIDKAKKFRLNRE GKQKADKNRARVEENFLKLTHVQRQEAAQSRREEKKRAEKERIM NEEDPEKQRRLEBAALRREQKKLEKKQMKMKQIKVKAM 6340 2 583 EACAHTLSCPAFARLGRARRRPWMSHRTSSTFRAERSFHSSSS SSSSTSSSASRALPAQDPPMEKALSMFSDDFGSFMRPHSEPLAF PARPGGAGNIKTLGDAYEFAVDVRDFSPEDIIVTTSNNHIEVRA EKLAADGTVMNTAHKCQLPBDVDTSVTSALREDGSLTIRARR HPHTEHVQQTFRTEIKI 6341 2 645 KMAVLSAPGLRGFRILGLRSSVGPAVQARGVHQSVATDGPSSTQ PALPKARAVAPKPSSRGEYVVAKLDDLVNWARRSSLWPMTFGLA	l i			DPDDFPLLVPYWEKTFDIDLSAPOIGVVNVTDADRIWMENDDEE
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Seg	SEQ	Predicted	Predicted end	Daine
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location corresponding to first amino acid acid sequence amino acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequence acid sequen				(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
corresponding to first amino acid residue of amino acid residue of amino acid sequence acid sequence acid se			1	Grutamic Acid, Fernenylalanine, GeGlycine,
to first amino acid residue of amino acid anino acid sequence Percoline, Q-Glutamine, Newprinine, Martyptophan, Y-Tyrosia, Kuchknown, *-Stop Codon, /-possible nuclectide deletion, Apposible nuclectide insertively Palakwylopmesprvyvsyssolanoscopy Tyrosysovaccopy Tyrosysovaccopy Palakwylopmesprvyvsyssolanoscopy Tyrosysovaccopy Tyrosysova	1			Hanistidine, Ialsoleucine, Kalysine,
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residue of amino acid sequence M=Tryptophan, Y=Tyrcoine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,				P=Proline, Q=Glutamine, R=Arginine,
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YMNFMNIP HAQKQNILIDACVLDSDSGLLQACDITGGLYLKV POMPSLLQYLLWWTPDDQDRSQLILPPYHVDYRAACPCHRNL 18IGYVCSVCLSIFCNFSPICTTCETAFKISLPPVLKAKKKKLK VSA 147 TMPTATLGNLRGYGMAS PGLAAPSLTPPQLATPNLQQFFPQATR QSLLGPPPVQVPMNFSQFNLGGRNPQKQARTSSSTTPNRKDSSS QTMPVEDKSDPPBGSEBAAEPRMDTFEDQDLPCPEDLAKKKT PAPPPBECEASELPAKRLRSSEEPTKEPPGLQVKAQPQOARMT VPKGTQTPDLLPEALEAQVLPRFQPRVLQVQAQVGSOTQPRIPS TDTQVQPKLQKQAQPTGTPBERLUCQVQVQQVQQDQAAEPQKQVQ POVQPQAHSQGPRQVQLQQEAEPLKQVQVQVQQAASQPPRQVQ LOLGKQVQTQTYPQVHTQAQDSVQPQEHPPAQVSVQPPEQTHBQ PHTQPQVSLLAPEGTPVVVHVCGLEVGHPAQVSVQPPEQTHBQ PHTQPQVSLLAPEGTPVVVHVCGLEVGHPAQVSVQPDEGTHBQ PHTQPQVSLLAPEGTPVVVHVGLADLESLLPVPR DVLETEDEEPPRRRCNTCQLYYMGDLIGHRTQDHKIAKQSLR PFCTVCNRYKTPRFKYPEVHXSGALGEIGHMSQACLISLLPVPR DVLETEDEEPPPRRRCNTCQLYYMGDLIGHRTQDHKIAKQSLR PFCTVCNRYKTPRFKYPEVHXSGALGEICHMSQACLISLLPVPR DVLETEDEEPPPRRRCNTCQLYYMGDLIGHRTQDHKIAKQSLR PFCTVCNRYKTPRFKYPEVHXSGALCEICHMSQACLISLLPVPR DVLETEDEEPPRRRVCNTCQLYYMGDLIGHRTQDHKIAKQSLR PFCTVCNRYKTPRFKYPEVHXSGALCEICHMSQACLISLLPVPR DVLETEDEEPPRRRVCNTCLYYMGDLIGHRTQDHKIAKQSLR PFCTVCNRYKTPRFKYPEVHXSGALCEICHMSQACLISLLPVPR DVLETEDEEPPRRNTCNTCQLYYMGYLCTCHKFYHISNGSQL SHCKSLGHFEBLQKYKAAKNPSTTPTPVSRRCAINARNALTALF TSSGRPPSGPNTONKTPSKVTARPSQPPLPRRSTRLKT TSSGRPPSGPNTONKTPSKVTARPSQPPLPRRSTRLKT TSSGRPPSGPNTONKTPSKVTARPSQPPLPRRSTRLKT TSSGRPPSGPNTONKTPSKVTARPSQPPLPRRSTRLKT EQQATDQRSNIRDNVEMIKLHQULVEKSNALSAMEGKFIQLOEKV ANENAGLGECPRKSIKFQDADVETPHMFTKYGNSLLEEARGE IRLEUVTJOSGRGIEELHELLAEILKTQLRRKENEILELLLQLR EQQATDQRSNIRDNVEMIKLHQULVEKSNALSAMEGKFIQLOEKV QRTILSLSHDALMANGDELMNQLKEGRLKCCLEKQLHKMKFSER RIEELQDRINDLEKERELLKENPUKLYSASAAALAGKE QQKIGOLSFLVKVDSSINKDLERSMELQATHATVQELSKTRNM LIMQHKINKDYOMEVERAVTRKMENLOQDYELKVEGVYHLLDIRA ARIHKLERQLKDIAYGTKQYKFPEIMPDDSVDEFDETILLERG ENLFSIHINKVTFSSEVLQASGDKEPVTFCTYAFYDFELQTTPV VRGLHFBETHFSSEVLQASGDKEPVTFCTYAFYDFELQTTPV VRGLHFBETHFSSEVLQASGDKEPVTFCTYAFYDFELQTTPV VRGLHFBETHFSSEVLQASGDKEPVTFCTYAFYDFELQTTPV VRGLHFBETHFSSEVLQASGDKEPVTFCTYAFYDFELQTTPV VRGLHFBETHFSSEVLQASGDKEPVTFCTYAFYDFELGTTPF TTAACQLKFHEILEKSERTPCTASLITKGIPGDIFBTEWTHFFFA BVMDQAIRLYRERAKALGYITSNFKGFERMGL				GNPPEFNPSGSKDGKYELLTSANEVIVEEIKDLMTKSDIKGQHT
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POMPSLLGYLLWVFLPEQDORSOLLLPPPVHYDVRAACFCHRNL 1B1GVCSVCLSIFCNFSPICTTCETAFKISLPPVLKAKKKKK VSA TMPTATLGNLRGYGMASPGLAAFSLTPPOLATPNLQQFFPQATR QSLLGPPPVGVPMNPSQFHLGGRPDCKQARTSSSTTNRKDSSS QTMPVEDKSDPPSGSEBAAEPRMDTPEDQDLPPCPEDLAKEKRT PAPPEPCEASELPAKRLRSSEPTEKKEPPGQLQVKAQPOGNRMT VPKQTQTPDLLPPALEAGQVLPRFQPRVLQVQAQVOSTQPRIPS TDTQVQPKLQKQAQTQTSPEHLVLQQKQVQPQLQQAEPGQKQVQ POVQPQAHSGGPRQVQLQQEAEPLKQVQPQVQDQASQPPBQVQ LQLQKQVGTQTYPQVETQAQPSVQPGEHPPAQVSVQPPEQTHEQ PHTQPQVSLLAPEQTPVVVHVCGLEMPAVEAGGGSKKVTI LQSSDSRAFSTVPLTPVPRPSDSVSSTPAATSTPSKQALQFPCY ICKASCSQQEFQDHMSEPGQAGGEICHMSQACLLSLLPVPR DVLETEDEBPPRRWCNTCQLYYMGDLIQHRYTQDHKIAKQSLR PFCTVCNRYKTPRKFVEHVXSQGHKXAKELKSLEKEIAGQDE BHITTDAVGCGEGEEEEBDEELECKQVRSRDIS REEWKGSETYSPNTAYGUPFLVPVBYSCALISLLPVPR SKCKSGFTYSPNTAYGUPFLVPVRSCALISLLFYHSNGAQL SKCKSLGHFENLQKYKAAARDPSPTTRVSVRCAINARNALITALF TSSGRPPSQPNTQDKTPSKVTXARSQFPLPRRETRLKT TSSGRPPSQPNTQDKTPSKVTXARSQFPLPRRETRLKT TSSGRPPSQPNTQDKTPSKVTXARSQFPLPRREMEMETGLGEK ANENAGLQECPRKGIKPQDAVAETPHPMFTKYGNSLLEEARGE IRNLENVIQSGRGIEEBHLABILKTQLREKENEIELSLLQLR GQATDQRSNIRDNVEMIKHKQLVEKSNALSAMGKFFQLGKK QRTLKISHDALMANGDELHMQLKEQRLKCSLEKQLHSMKFFER RIEELQDRINDLEKRELLKENDYKLYDSAFSAAHEEQWKLKEQ QLXVQLAQLETALKSDLTDKTEILDRLKTERDONEKLVQENSEL QQXTDQRSNIRDMYSEINKDLESSARSLQATAASTVQELEKTRNM LIMQHKINKDYMSVEAVTRKMENLQQDYELKVEQVYHLLDIRA ARIHKLEAQLKDIAYGTKQWKFKPEIMPDSUDEFDETILLERG ENLFFIHINKUTFSSEVLQASGRKEPVTFCTYAFYDFELQTTPV VRGLHPEYNFTSQXLVWNDLFLQYIQKNTTLEVHQAYSTEYE TLAACQLKFHBILEKSGRIFCTASIGTKGDIPNFGVEYWFRL RVPMDQAIRLYRERAKALGYITSNFKGPEHMGSLSQQAPKTAQL SSTDSTDONLMELHITIRCCMHLQSRASHLQPHPYVYVKFFDFA DHDTAIISSSNDPGDDDHMEDLBTLEKSSLSQCAPKTAQL SSTDSTDONLMELHITIRCCMHLQSRASHLQPHPYVYVKFFDFA DHDTAIISSSNDPGDDDHMERBLLGYKGPDDDNTLFFTVYFYFD	1			YMNFMNVIFAAQKQNILIDACVLDSDSGLLOOACDITGGLYLKV
1816YVCSVCLSIFCNFSPICTTCETAFKISLPPVLKAKKKKLK VSA 6344 2508 147 TMFTATLGNLRGYGMASPGLAAFSLTPPQLATPNLQQFFPQATR QSLLGPPPVGVPMNPSQFRLSGRNPQKQARTSSSTTPNRKDSSS QTMPVBCKSDPPBGSBRAABFBMTPFEDQLLPPCPEDIAKERT PAPEPEPCEASELPAKRLRSSEPTEKEPPGQLQVKAQPQARMI VPKQTQTPDLLPEALEAQVLPRFQPRUVQAQVGSCTIOPRIPS TDTQVQPKLQKQAQTGTSPEHLVLQQKQVQPQLQQEAEPQKQVQ PQVQPAHSGGPRQVQLQQEAEPLKQVQPQQPQAHSGPPRQVQ LQLQKQVQTQTYPQVTQAQPSQVPGEHPPAQVSVQPPEQTHEQ PHTQPQVSLLAPEQTPVVVHVCGLEMPPDAVEAGGGMEKTLPSP VGTQVSMEEIQNESACGLDVGECENRAREMGVWGAGGSLKVTI LQSSDSRAFSTVPTPVPRPSDSVSTPAATSTPSKQALQFFCY ICKASCSSQQEPQDHMSEPQHQQRLGEIQHMSQACLLSLLPVPR DVLETEDEBPPRRNCNTCQLYYMGDLJQHRTQDHKIRKQSLR PFCTVCNRTYKTPRKVPEHVXSQGHKDKAKELKSLKELIAQDE DHFITVDAVGCPEGDEBEBEDDEBEIEVEBELCKQVRSRDIS REEMKGSETYSPNTAYGVDFLVPVMSTICRICKFYHSMSGAQL SHCKSLGHFENLQKYKAAKNSPSPTTRPVSRCAINANNALTALF TSSGRPPSQPNTQDKTPSKVTARPSQPPLPRRSTRLKT TSSGRPPSQPNTQDKTPSKVTARPSQPPLPRRSTRLKT TSSGRPPSQPNTQDKTPSKVTARPSQPPLPRRSTRLKT TSSGRPPSQPNTQDKTPSKVTARPSQPPLPRRSTRLKT TSSGRPPSQPNTQDKTPSKVTARPSQPPLPRRSTRLKT TSSGRPPSQPNTQDKTPSKVTARPSQPPLPRRSTRLKT TSSGRPPSQPNTQDKTPSKVTARPSQPPLPRRSTRLKT TSSGRPPSQPNTQDKTPSKVTARPSQPPLPRRSTRLKT TSSGRPPSQPNTQDKTPSKVTARPSQPPLPRRSTRLKT TSSGRPPSQPNTQDKTPSKVTARPSQPPLPRRSTRLKT TSSGRPPSQPNTQDKTPSKVTARPSQPPLPRRSTRLKT TSSGRPPSQPNTQDKTPSKVTARPSQPPLPRRSTRLKT TSSGRPPSQPNTQDKTPSKVTARPSQPPLPRRSTRLKT TSSGRPPSQPNTQDKTPSKVTARPSQPPLPRRSTRLKT TSSGRPPSQPNTQDKTPSKVTARPSQPPLPRRSTRLKT TSSGRPPSQPNTQDKTPSKVTARPSQPPLPRRSTRLKT TSGRPPSQPNTQDKTPSKVTARPSQPPLPRRSTRLKT TSSGRPPSQPNTQDKTPSKVTARPSQPPLPRRSTRLKT TSGRPPSQPNTQDKTPSKVTARPSQPPLPRRSTRLKT TSSGRPPSQPNTQDKTPSKVTARPSQPPLPRRSTRLKT TCHCKSLGHEALLANDLARTCKTPSKVTARPSQPPLRRSTRLLCLQLCKV ANENAACLGECTALTSATQTTCTTAKTCCSLEKQLHSMKFSER REELQDRINGLEKRELLKENDYKLYUSAFSAAHEEMKLLCLA CQQATOGRSNIRDNVEMILKLKQLVEKSNALSAMEGKFIQLGEK QRKGILSFLVKVDSEINKDLERSMELLGATHAETVQELSKTRNM LIMQHKINNDYMSVEAVTRMENLQQDYELKVEQVVHLLDIRA ARIHKLEAQLKDIAJATKQYKFYFEDHPDDSVDEPDETIHLERG ENLFEIHINKVTFSSEVLQASGKEVPTTCTTAFVDFELQTTPV VRGLHPENNFTSQVLVMVNDLFLQYTQMTTTLEVHQAYSTEYE TTAACQLKFHEILERESGRFCTASLIGTKGDTPRGTVEYWFL RVMDQAIR				PQMPSLLQYLLWVFLPDQDQRSQLILPPPVHVDYRAACFCHRNI.
6344 2508 147 TMPTATLGNLRGYGMASPGLAAPSLTPPQLATPNLQQFFPQATR QSLLGPPPVGVPMNPSQFNLSGRNPQKQARTSSSTTNRKDSSS QTMPVERKSDPPSGSEBAAEPRMDTPEDQLPPCPEDLAKEKRT PAPPEPECRASELPAKRLRSSEEPTEKEPPGQLQVKAQPQARMT VPKQTQTPDLLPBALEAQVLPRFQPRVLQVQAQVQSTQPRIPS TDTQVQPKLQKQAQTQTSPEHLVLQQKQVQQQLQQAEPQKQVQ LQLQKQVCTQTYPQVHTQAQPSVQPQEHPPAQVSVQPPEQTHEQ PHYQPQVSLLAPEQTPVVVHVCGLEMPPDAVEAGGGGKKTLPPP VGTQVSMEEIQNESACGLDVGERARAEMEGVWGAGGSLKVTL LQSSDSRAFSTVPLTPVPRPSDSVSSTPAATSTPSKQALQFFCY ICKASCSSQQEFQDIMSPPQIQQLIGEIQMSQACLLSLLPVPR DVLETEDEEPPPRRMCNTQLYYMGDLIGHRTQDHKIAKGSLR PFCTVCNRYFKTPRKFVEHVXSQGHKKKAKELKSLEKELAQQDE DHFITVDAVGCPEGDEEEEDDEDEEEISVEEBLCKQVSRSDIS REBWKGSETYSNNTAYGVDFLVPVMGYICRICHKFYHSNSGAQL SHCKSLGHFENLQKYKAAKNPSPTTRPVSRCAINARNALTALF TSGGRPSQPNTQDATPSKVTARPSQPPLPRRSTRLKT TSGGRPSQPNTQDATPSKVTARPSQPPLPRRSTRLKT ANENNAGLØSCPRKGIKKQCGVEEEEMIEQLQEKV HELEKQNDTLKNRLISAKQQLQTGGYKGTPVNNVOSRINTGRKK ANENNAGLØSCPRKGIKKPQLKECSLEKQLHSMKPSER EQQATDQRSNIRDNVEMIKLHKQLVEKSNALSAMEGKFIOLQEK QRTLKISHDALMANDGLINMQLKCGCLKCGSLEKQLHSMKPSER RIBELQDRINDLEKERELLKENYDKLYDSAFSAAHEEQWKLKEQ QKNGLSPLVKVDSEINKDLERSMRELQATHAETVQELEKTRNM LIMQKIINDYGMSVEAVTRRMENLQQDYELKVEQYVHLDIRA ARIHKLEAQLKDIRJKKRIKLYNDENDINADELSEALLLIKAQKE QKNGDLSPLVKVDSEINKDLERSMRELQATHAETVQELEKTRNM LIMQKIINDYGMSVEAVTRRMENLQQDYEKVEQYVHLDIRA ARIHKLEAQLKDIRJKKYRKLYNDENDINADELSEALLLIKAQKE ENLFEIHINKVTFSSEVLQASGDKEPVTFCTYAFYDFELQTTPV VRGLHPENFTSGYLVMVNDLFLQYIQKNTTLLEPHQAYSTEYE TTAACQLKFHEILEKSGRIFCTASLIGTKGDIPNFGTVEYWFRL RVPMQAARLVRERAKALGYTTSNFKGPEHMQSLSQQAPKTAQL SYDDTOINMELHITIRCCNHLQSABSHLQPHPYVVYKFFDFA DHDTAIIPSSNDPQFDDHMKFPVPMMMDLDRYLKSESLSFYVFD	1 1			IBIGYVCSVCLSIFCNFSPICTTCETAFKISLPPVLKAKKKKLK
QSLLGPPPVQPMMPSQFNLSGRNPQKQARTSSTTPNRKDSSS QTMPVEDKSDPPEGSERABPRMDTPEQQLPPCPEDLAKEKRT PAPEPEPCASELPAKRLRSSEPTEKEPPGQLQVGAQVQSGTQRRIPS TDTQVQPKLQKQAQTOTSPEHLVLQQKQVQSQTQPRIPS TDTQVQPKLQKQAQTOTSPEHLVLQQKQVQPQAHSQPPRVQV PQVQPQAHSQSPRQVQLQGEAEPPAQVSVQPPEQTHEQ PHTQPQVSLLAPEQTPVVVHYCQLEMPPDAVEAGGGMEKTLPEP PHTQPQVSLLAPEQTPVVVHYCQLEMPPDAVEAGGGMEKTLPEP PHTQPQVSLLAPEQTPVVVHYQLEOHRPDAVEAGGGMEKTLPEP QGTQVSMEEIQNESACGLUGGECENRAEMPEGVWGAGGSLKVTI LQSSDSRAFSTVPLTPVPRPSDSVSSTPARTSTPSKQALQFFCY ICKASCSSQCEFQDHMSEPQHQQRLGEIQHMSQACLLSLLPVPR DVLETEDEEPPPRRKCNTCLYMGDLIQHRRTQDHKIAKQSLR PFCTVCRNYFKTPRKFVEHVKSQGHKDKAKELKSLEKEIAGQDE DHFITVDAVGCFEGGBEEBEDDEDEEEISVEEBLCKQVSRDIS REEMKGSETTSPNTAYGVDPLVPVMGYICRICHKFYHSNSGAQL SHCKSLGHFENLQKYKAAKNPSPTTRPVSRCAINARNALTALF TSSGRPPSQPNTQDKTPSKVTARPSQPPLPRRSTRLKT TSSGRPSQPNTQDKTPSKVTARPSQPPLPRRSTRLKT TSSGRPSQPNTQDKTPSKVTARPSQPPLPRRSTRLKT ANENAGLGECPRKGIKPQGDFKLGRUFMEMIEIGLQEKV HBLEKQNDTLKNRLISAKQQLQTQGYRQTPYNNVOSRINTGRKK ANENAGLGECPRKGIKPQDADVAETPHPMTKYGNSLLEEARGE IRNLENVIGSQRQIEELEHLAEILKTQLRRKENSIELSLLQLR EQQATDQRSNIRDNVBMIKHKQLVEKSNALSAMEGKFIQLGEK QRTLKISHDALMANGDELMMQLKEQRLKCCSLEKQLHSMKPSER RIBELQDRINDLEKERELLKERYDKLYDSAFSAAHEGWKLKEQ QKNGDLSFLVKVDSEINKDLERSMELQATHAETVQELEKTRNM LTMQHKINNDYGMEVEAVTRKMENLQQDYELKVEQYVWLLDIRA ARIHKLEAQLKDLAYGTKGYKFKPEIMPDGSVDEFDETIHLERG ENLFEIHINKVTFSSEVLQASGDKEPVTFCTYAFYDFELQTTPV VRGLHPEYNFTSQYLVHVNDLFLQYIGKNTTTLEVHQAYSTEYE TIAACQLKFHEITLEKSGRIFCTASLIGTKGDIPRGTVEYWFRL RVPMDQAIRLYRERAKALGYITSNFKGPEHMQSLSQQAPKTAQL SSTDSTDGNLEHLHITIRCSHLOGRKDLKSGLGQNAPKTAQL SSTDSTDGNLEHLHITIRCSHLOGRKDLYKSGSQAPKTAQL SSTDSTDGNLEHLHITIRCSHLOGRKDLYKSGSQAPKTAQL SSTDSTDGNLEHLHITIRCSHLOGRHONDRDLINGSGQAPKTAQL SSTDSTDGNLEHLHITIRCSHLOGRHONDRDLINGSGAPKTAQL SSTDSTDGNLEHLHITIRCSHLOGRHONDRDLINGSGAPKTAQL SSTDSTDGNLEHLHITIRCSHLOGRHONDRDLINGSGAPKTAQL SSTDSTDGNLEHLHITIRCSHLOGRHONDRDLINGSGAPKTAQL SSTDSTDGNLEHLHITIRCSHLOGRHONDRDLINGSGAPKTAGL STDSTDGNLEHLHITIRCSHLOGRHONDRDLINGSGAPKTAGL STDSTDGNLEHLHITIRCSHLOGRHONDRDLINGSGAPKTAGL STDSTDGNLEHLHITIRCSHLOGRHONDLINGSGAPKTAGL	L			VSA
QSLLGPPPVGVPMPSGFNLSGRNPQKQARTSSSTTPNRKDSSS QTMPVEDKSDPPGGSEAAEPRMTPEDQDLPPCPEDLAKEKRT PAPEPPCEASELPARKLRSSEEPTEKEPSGCLQVKAQPQARMT VPKQTQTPDLLPBALERQVLPRFQPRLQVQAQVQSQTQPRIPS TDTQVPKLQKQAQTOTSPEHLVLQQKQVQQPQAASQPPRKQVQ PQVQPAHSQGPRQVUQQEAEPLKUQQKQVQPQAASQPPRKQVQ LOLQKQVQTQTYPQVHTQAQPSVQPQEBPPAQVSVQPPEQTHEQ PHTQPQVSLLABEQTPVVVWLYCGLEMPPDAVEAGGMEKTLPEP VGTQVSMEEIQNESACGLDVGECENRAREMPGVWGAGGSLKVTI LQSSDSRAFSTVPLTTEVPRPSDSVSSTPAATSTPSKQALQFFCY ICKASCSSQGEfQDHMSEPGHQQRLGEIQHMSQACLLSILPVPR DVLETEDEEPPPRRWCNTCQLYYMGDLIGHRRTQDHKIAKQSLR PFCTVCNRYFKTPRKFVEHVKSQGHKDKAKELKSLEKEIAGQDE DHTITVDAVGCFGDBEEEBEDDEEEISVEBELCKQVRSRDIS REEMKGSETYSPNTAYGVDFLVPWGYICRICHKFYHSNSGAQL SHCKSLGHFENLQKYKAAKNBSPTTERPVSRCAINARNALTALF TSSGRPPSQBNTDQXTPSKYVTARPSQPPLPRSTRLKT TSSGRPPSQBNTDQXTPSKYVTARPSQPPLPRSTRLKT ANENNACIQECPRG IKPQDAVAETHPMFTKYGNSLLEEAAGE IRNLEWVIGSQRGQIEELHLABILKTQLRKENBEIELSLLQLR EQQATDQRSNIRDNVBMIKLHKQLUVEKSALSABMEKFIQLQEK QRTLKISHDALAMANGDELMMQLKEGRLKCSLEKQLHSMKYFSER RIBELQDRINDLEKKRILLDRLKTERDQNEKLVQENREL QLKVQIAQLETALKSDLTDKTEILDRLKTERDQNEKLVQENREL QLXQVIAQLETALKSDLTDKTEILDRLKTERDQNEKLVQENREL QLXQVIAQLETALKSDLTDKTEILDRLKTERDQNEKLVQENREL QLXQVIAQLETALKSDLTDKTRILDRLKTERDQNEKLVQENREL LUMQHKINKDYGMEVGAVTKNENLOQDYELKVSQYVHLDIRA ARIHKLEAQLKDIAYGTKGYKKYEPEIMPDSWDEEDETTHLERG ENLFEILINKVTFSSEVLQASGDKEPVTFCTYAFYDFELQTTPV VRGLHPEYNFTSQYLVHVNDLPLQYIGCNTITLEVHQAYSTEYE TTAACQLKFHSILEKSGRIFCTASLIGTKGDIPNGTVEYWFRL RVPMQAIRLYRERAKALGYITSNFKGPEHMQSLSQQAPKTAQL SSTDSTDGNLEELHITIRCCSHLOSRASHLQPHPYVVYKFFDFA BUDDTAIIPSSNDOLPGDPDTHMYPYPVNMDLDRLYKSSLSQAPKTAQL SSTDSTDGNLEELHITIRCCSHLOSRASHLQPHPYVVYKFFDFA BUDDTAIIPSSDDOPDDDHMYPYPVPNMDLDRLYKSSLSQAPKTAQL SSTDSTDGNLEELHITIRCCSHLOSRASHLQPHPYVVYKFFDFA	6344	2508	147	TMPTATLGNLRGYGMASPGLAAPSLTPPOLATPNLOOFFPOATR
QTMPVENKSDPPEGSERAREPRMDTPEDQDLPPCPEDIAKEKRT PAPEPECRASELPAKRIRSSEPTEKEPPGQLQVKAQPOARMT VPKQTQTPDLLPEALERQVLERFQPRULQVQAQVOSQTQPRIPS TDTQVQPKLQKQAQTOTSPEHLVLQQKQVQPQLQQEAEPQKQVQ PQVQPAHSQBPRQVQLQQEAEPLKQVQPQVQPAHSQPPRQVQ LQLQKQVQTQTYPQVHTQAQPSVQPQEHPPAQVSVQPPEQTHEQ PHTQPQVSLLAPEQTPVVVHVCGLEMPPDAVEAGGGMEKTLPEP VGTQVSMEEIQNESACGLDVGECENRAREMGGVWGAGGSLKVTI LQSSDSRAFSTVPLTPVFRPSDSVSSTFAATSTPSKQALKVTI LQSSDSRAFSTVPLTPVFRPSDSVSSTFAATSTPSKQALKVTI LQSSDSRAFSTVPLTPVFRPSDSVSSTFAATSTPSKQALKVTI LQSSDSRAFSTVPLTPVFRPSDSVSSTFAATSTPSKQALKVTI LQSSDSRAFSTVPLTPVFRPSDSVSSTFAATSTPSKQALKVTI LQSSDSRAFSTVPLTPVFRPSDSVSSTFAATSTPSKQALKVTI LQSSDSRAFSTVPLTPVFRPSDSVSSTFAATSTPSKQALKVTI LQSSDSRAFSTVPLTPVFRPSDSVSSTFAATSTPSKQALLFPR DVLETEDEEPPPRRWCNTCQLYMGDLLQHRRTCDHKLAKQSLR PFCTVCRRYFKTPKKFVEHVKSQGHKDGAKELKSLIKEFELEAGQE DHFITTVDAVGCFEGDBEEBEDDEDEEEIBVEEBLCKQVRSRDIS REEKKSSCHFENLQKYKRAKRYPSPTTRPVSRCAINARNALTALF TSSGRPSQENTQDKTPSKVTARPSQPPLPRRSTRLKT TSSGRPSQENTQDKTPSKVTARPSQPPLPRRSTRLKT TSSGRPSQENTQDKTPSKVTARPSQPPLPRRSTRLKT TSSGRPSQENTQDKTPSKVTARPSQPPLPRRSTRLKT SGRPSQENTQDKTRSKVTARPSQPPLPRRSTRLKT TSSGRPSQENTQDKTPSKVTARPSQPPLPRRSTRLKT SGRPSQENTQDKTRSKVTARPSQPPLPRRSTRLKT TSSGRPSQENTQDKTRSKVTARPSQPPLPRRSTRLKT TSGGRPSQCOTTARSTRAFTCTSLTGTKKGNSLEEEAGLEAGLEAGLEAGLEAGLEAGLEAGLEAGLEAGLE	Ì			QSLLGPPPVGVPMNPSOFNLSGRNPOKOARTSSSTTPNPKDSSS
PAPEPECEASELPAKRIRSSEPTEKEPPGGLQVKAQPOARMT VPKQTQTPDLDEALEAQVLPRFQPRVLQVQAQVQSQTQPRIPS TDTQVQPKLQKQAQTQTPSPHLVLQQKQVQPQLQGEAEPQKQVQ PQVQPQAHSQGPRQVQLQGEAEPLKQVQPQVQPQAHSQPPRQVQ LOLQKQVQTQTYPQVHTQAQPSVQPQEHPPAQVSVQPPEQTHEQ PHTQPQVSLLAPEQTPVVVHVCGLEMPPDAVEAGGMEKTLPEPP VGTQVSMEEIQNESACGLDVGECERRAREMPQVWGAGGSLKVTI LQSSDSRAFSTVPLTPVFRPSDSVSSTPAATSTPSKQALQFFCY ICKASCSSQGEFQHMMSEPQHQQRIGEIQHMSQACLLSLLPVPR DVLETEDEEPPPRRWCNTCQLYYMGDLIGHRRTODHKIAKQSLR PFCTVCNRYFKTPKFVEHVKSQGHKDKAKELKSLEKEIAGQDE DHFITVDAVGCPEGDEEEEBDDEDEELISVEEBLCKQVRSRDIS REEWKGSETYSPNTAYGVDFLVPVMGYICTICHKFYHSNSGAQL SHCKSLGHFENLQXYKAAKNPSPTTRPVSRRCAINARNALTALF TSSGRPPSQPNTQDKTPSKVTARPSQPPLPRRSTTLKT TSSGRPPSQPNTQDKTPSKVTARPSQPPLPRRSTTLKT TSSGRPPSQPNTQDKTPSKVTARPSQPPLPRRSTTLKT ANENAGLQECPRIGIKFQOADVAETPHPMFTKYGNSLLEEARGE IRNLENVIQSQGGJEELEHLAEILKTQLRRKEREIELSLLQLR EQQATDQRSNIRDNVEMIKLHKQLVEKSNALSAMEGKFIQLQEK QRTLKISHDALMANGDELHNQLKEGRLKCCSLEKQLHSMKFSER RIEELQDRINDLSKERELLKENYDKLYDSAFSAAHEEQWKLKEQ QLXYLEOKQQLDELKKRIKLJNQENDINADELSBALLIKAQKE QLXYLEOKQQLDELKKRIKLJNQENDINADELSBALLIKAQKE QKNGOLSFLVKVDSEINKQLBESMRELQATHAETVQELEKTRIM LIMQHKINNDYQMEVEAVTRKWENLQDYBLKVQYVHLLDIRA ARIHKLEAQLKDIAYGTKQYKFXPEIMPDDSVDEFDETIHLERG ENLFEIHINKVTFSSEVLQASGNKEPVTFCTYAFYDFELQTTPV VRGLHPEYNFTSQYLVHVNDLEILQYLQXNTITLEVHQAYSTEYE TIAACQLKFHEILEKSGRIFCTASLIGTKGDIPNGTVEYMFRL RVFMDQAIRLYRERAKALGYITSNFKGPEHMQSLSQQAPKTAQL SSTDSTDGNINELHTIRCCNHLQSRASHLQPHPYVYYKFFDFA DHDTAIISSNDPQFDDHWMYPPVPMMDDLDFLYKSSELSFVYFD	1 1			QTMPVEDKSDPPEGSEBAAEPRMDTPEDODLPPCPEDTAKEKPT
VPKOTOTPDLIPBALEAQVLPRFOPRVLQVQAQVGOTQPRIPS TDTQVQPKLQKQAQTQTSPEHLVVLQKQVQPQLQQEAEPQKQVQ PQVQPQAHSQGPRQVQLQQEAEPLKQVQPQVQPQAHSQPPRQVQ LOLOKQVQTQTYPQVHTQAQPSVQPQEMPPAQVSVQPPEQTHEQ PHTQPQVSLLAPEQTPVVVHVCGLEMPPDAVEAGGGMEKTLEPP PHTQPQVSLLAPEQTPVVVHVCGLEMPPDAVEAGGGMEKTLEPP VGTQVSMEEIQNESACGLDVGECENRAREMEGVWGAGGSLKVTI LQSSDSRAFSTYPLTPVPRPSDBVSTPAATSTPSKQALQFFCY ICKASCSSQDEFQDHMSEPQHQQRLGEIQHMSQACLLSLLPVPR DVLETEDEEPPPRRKONTCQLYYMGDLJOHRTAKQSLR PFCTVCNRYFKTPRKFVEHVKSQGHKDKAKELKSLEKEIAGQDE DHFITVDAVGCFEGDEEEEBDDEEEIBVEEBLCKQVRSRDIS REEMKGSSTYSPNTAYGVDFLVPVMGYICRICHKFYHSNSGAQL SHCKSLGHFENLQKYKAAKNPSPTTRPVSRRCAINARNALTALF TSSGRPSQPNTODKTPSKVTTARPSQPPLPRRSTRLKT TSSGRPSQPNTODKTPSKVTTARPSQPPLPRRSTRLKT TSSGRPSQPNTODKTPSKVTTARPSQPPLPRRSTRLKT TSSGRPSQPNTODKTPSKVTTARPSQPPLPRRSTRLKT ANENAGLQECPRKGIKFQDADVAETPHPMFTKYGNSLLEEARGE IRNLENVIQSQRGQIEELEHLAEILKTQLREKENEIELSLQLR EQQATDQRSNIRDNVEMMKLHKQLVEKSNALSAMEGKFICLQEK QRTLKISHDALMANGDELNMQLKEQRLKCCSLEKQLHSMKFSER RIEELQDRINDLEKERELLKENDKLYCENSELVGENREL QLQYLEQKQQLDBLKKRIKLYNQENDINADELSEALLLIKAQKE QKNGDLSFLVKVDSEINKDLERSMELQATHABTVQELSTRNM LLMQHKINKDYQMEVEANTRMENLQODVELKVEQYVHLLDIRA ARIHKLEAQLKDIAYGTKQYKFKPEIMPDDSVDEFDETIHLERG ENLFEIHINKVTFSSEVLQASGDKEPVTFCTTAFYDFELQTTPV VRGLHBEYNFTSQYLVHVNDLFLQYIQKNTITLEVHQAYSTEYE TTAACQLKFHEILEKSGRIFCTASLIGTKGDIPNFGTVEWFRIL RVFMDQAIRLYRERAKALGYITSNFKGPEHMQSLSQQAPKTAQL SSTDSTDGNLNELHITIRCCNHLQKSRSHLQPHPYVVYKFFDFA DHDTAIIPSSNDPQFDDHMYPVPYMMDLDRYLKSBSLSFYVFD	1			PAPEPEPCEASELPAKRLRSSEEPTEKEPPGOLOVKAOPOARMT
TDTOYOPKLOKOACTOTSPEHLULOCKCYOPOLOCEAEPOKOVO POVOPOAHSGOPROVOLOCEAEPLKOVOPOLOCEAEPOKOVO POVOPOAHSGOPROVOLOCEAEPLKOVOPOLOCEAEPOROVO LOLOKOVOTOTYPOVHTOAOPSVOPOEPHPAQVSVOPPEOTHEO PHTOPOVSLLAPEOTPUVUHVCGLEMPPDAVEAGGGMEKTLPEP VGTOVSMEELOMESACGLDUSGEENRAREMEGWGAGGSLKVTI LQSSDSRAFSTYPLTPVPPYPRSDSVSSTPAATSTPSKQALQFFCY ICKASCSSQQEFQDHMSEPQHQORLGEIQHMSQACLLSLLPVPR DVLETEDEEPPPRRKOTTOQLYYMGDLIQHRRTODHKIAKQSLR PFCTVCNRYFKTPRKFVEHVKSQGHKDKAKÉLKSLEKELAGQDE DHFITVDAVGCFEGDEEBEEDDEDEEEIBVEBELCKQVRSRDIS REEKKGSETYSPNTAYGVDFLUPVMGYICRICHKFYHSNSGAQL SHCKSLGHFENLQKYKAAKNPSPTTRPVSRRCAINARNALTALF TSSGRPPSQPNTONKTPSKVTARPSQPPLPRSETRLKT TSSGRPPSQPNTONKTPSKVTARPSQPPLPRSETRLKT TSSGRPPSQPNTONKTPSKVTARPSQPPLPRSETRLKT ANENAGLQECPRKGIKPQDADVAETPHPMFTKYGNSLLEEARGE IRNLENVIQSQRGGIESLEHLAEILKTQLRRKEMEISLSLLQLR EQQATDQRSNIRDNVEMIKLHKQLVEKSNALSAMEGKFIQLQEK QRTLKISHDALMANGDBLINMQLKEQRLKCCSLEKQLHSMKFSER RIBELQDRINDLEKERELLKENYDKLYDGAFSAAHEEQWKLKEQ QLKVQIAQLETALKSDLTDKTEILDRLKTERDONBKLVQENREL QLVYLEQKQQLDBLKKRIKLYNQENDINADELSEALLLIKAQKE QKNGDLSFLVKVDSEINKDLERSMRELQATHAETVQELEKTRNM LTMQHKINKDYOMEVEAVTRKMENLQODYELKVEQTVHLLDIRA ARIHKLEAQLKDIAYGTKQYKFKPEIMPDDSVDEFDETIHLERG ENLFEIHINKUTTSSEVLQASGDKEPVTFCTTAFYDFELGTTPV VRGLHPEYMFTSQYLVHVNDLPLQYIQKNTITLEVHQAYSTEYE TIAACQLKFHEILEKSGRIFCTASLIGTKGDIPNFGTVEEWFRL RVFMDQAIRLYRERAKALGYITSNFKGPEHMGSLSQQAPKTAQL SSTDSTDGNLNELHITIRCCUHLQSRSHLQPHPYVVYKFFDFA DHDTAIIPSSNDPQFDDHMKYPVPMMMDLDRYLKKSSSLSFVVFD DHDTAIIPSSNDPQFDDHMKYPVPMMMDLDRYLKKSSSLSFVVFD				VPKQTQTPDLLPEALEAQVLPRFQPRVLQVQAQVQSQTQPPT PS
POVOPOAHSGERQUQLQGEAPLKQVQPQVQPQAHSQPPRQVQ LOLOKQVQTOTYPQVHTQAPSVQPQEHPPAQVSVQPPEQTHEQ PHTQPQVSLLAPEQTPVVVIVCGLEMPPPAQVSVQPPEQTHEQ PHTQPQVSLLAPEQTPVVVIVCGLEMPPPAQVSVQPPEQTHEQ VGTQVSMEEIQMESACGLDVGECRNRAREMPGVWGAGGSLKVTI LQSSDSRAFSTVPLTPVPRPSDSVSSTPAATSTPSKQALQFFCY ICKASCGSQQEFQDHMSEPQHQQRLGEIQHMSQACLLSLLPVPR DVLETEDEEPPPRRWCNTCQLYYMGDLIQHRRTQDHKIAKQSLR PFCTVCNRYFKTPRKEVEHVKSQGHKDKAKELKSLEKEIAGQDE DHFITVDAVGCPEGDEEEBEDDEDEEEIEVEEELCKQVRSRDIS REEWKGSETYSPNTAYGVDFLVPVMGYICRICHKFYHSNSGAQL SHCKSLGHFENLQKYKAAKNPSPTTRPVSRCCAINARNALTALF TSSGRPPSQPNTQDKTPSKVTARPSQPPLPRRSTRLKT TSSGRPPSQPNTQDKTPSKVTARPSQPPLPRRSTRLKT TSSGRPPSQPNTQDKTPSKVTARPSQPPLPRRSTRLKT ANENAGLQECPRKGIKFQDADVAETPHHMFTKYGNSLLEEARGE IRNLENVIQSGRGGIEELBHLAEILKTQLRRKENEIELSLLQLR EQQATDQRSNIRDNVEMIKLHKQLVEKSNALSAMEGKFIQLQEK QRTLKISHDALMANGDELMMQLKEORLKCCSLEKQLHSMKFSER RIBELQDRINDLEKERELLKENYDKLYDSAFSAAHEEQWKLKEQ QLKVQIAQLETALKSDLTDKTEILDRLKTERDONEKLVQENREL QLXVQIAQLETALKSDLTDKTEILDRLKTERDONEKLVQENREL QLXVQIAQLETALKSDLTDKTEILDRLKTERDONEKLVQENREL QLXVQIAQLETALKSDLTDKTEILDRLKTERDONEKLVQENREL LIMQHKINKDYQMSVEAVTRKMENLQQDYELKVEQVHLLDIRA ARIHKLEAQLKDIAYGTKQYKFKPEIMPDDSVDEFDETIHLERG ENLFEIHINKVTFSSEVLQASGDKEPVTFCTYAFYDFELQTTPV VRGLHPBYNFTSQVLVHVNDLPIQYIQKNTITLEVHQAYSTEYE TIAACQLKFHEILEKSGRIFCTASLIGTKGDIPNGTVEYWFRL RVFMDQAIRLYRERAKALGYITSNFKGPEHMQSLSQQAPKTAQL SSTDSTDGNLNELHITIRCCNHLQSRSELLQPHPVVYKFFDFA DHDTAIIPSSNDPQFDDHMYPPVPMMNDLDRYLKSESLLSFVVFD	1 1			TDTOVOPKLOKOAOTOTSPEHLVLOOKOVOPOLOOFAEROVOVO
LOLOKQVOTOTYPQVHTQAGPSVQPQEHPPAQVSVQPPECTHEQ PHTQPQVSLLAPEQTPVVVHVCGLEMPPAVEAGGGIEKTI_PEP VGTQVSMEEIQNESA-GGLDVGEGENRAREMPGWGAGGSLKVTI LQSSDSRAFSTVPLTPVPRPSDSVSSTPAATSTPSKQALQFFCY ICKASCSSQQEFQDHMSEPQHQQRLGEIQHMSQACLLSLLPVPR DVLETEDEEPPPRRWCNTCQLYYMGDLIQHRRTQDHKIAKQSLR PFCTVCNRYFKTPRKFVEHVKSQGHKDKAKELKSLEKEIAGGDE DHFITVDAVGCPEGDEEEBEDDEDEEEIBVEEBLCKQVRSRDIS REEWKGSETYSPNTAYGVDPLVVWGYICRICHKFYHISNSGAQL SHCKSLGHFENLQKVKAAKNPSPTTRPVSRRCAINARNALTALF TSSGRPPSQPNTQDKTPSKVTARPSQPPLPRRSTRLKT TSSGRPPSQPNTQDKTPSKVTARPSQPPLPRRSTRLKT ANENAGLQECPRKGIKFQDADVAETPHPMFTKYGNSILIEEARGE IRNLENVIQSQRGQIEELEHLABILKTQLRRKENEIELSLLQLR EQQATDQRSNIRDNVEMIKLHKQLVEKSMALSAMEGKFIQLQEK QRTLKISHDALMANGDELNMQLKEQRLKCCSLEKQLHSMKFSER RIEELQDRINDLEKERELLKENYDKLYDSAFSAAHEEQWKLKEQ QLQYLEQKQQLDBLKKRIKLYNQENDLINABLISEALLLIKAQKE QLQYLEQKQQLDBLKKRIKLYNQENDLINABLISEALLLIKAQKE QLQYLEQKQQLDBLKKRIKLYNQENDLINABLISEALLLIKAQKE QLQYLEQKQQLDBLKKRIKLYNQENDLINABLISEALLLIKAQKE QLQYLEQKQQLDBLKKRIKLYNGENDLINABLISEALLLIKAQKE ENLFEIHINKVTFSSEVLQASGDKEPVTFCTYAFTDFELQTTPV VRGLHBEYNFTSQVLVADSGIKPCTTCTYAFTDFELQTTTPV VRGLHBEYNFTSQVLVADSGIKEPCTTAFLYFDFELQTTTPV VRGLHBEYNFTSQVLVADSGIKEPCTTAFLYFDFELQTTPV VRGLHBEYNFTSQVLVANDLFLQYIQKNTTLEVHQAYSTEYE TIAACQLKFHEILEKSGRIFCTASLIGTKGDIPNGTVEYWFRL RVFMDQAIRLYRERAKALGYITSNFKGPEHMQSLSQQAPKTAQL SSTDSTDGDILNELHITIRCCNHLQSRASHLQPHPYVYKFFDFA DHDTAIIPSSNDPQFDDHMYPPVPMMMDLDRLAGPHPYVYKFFDFA DHDTAIIPSSNDPQFDDHMYPPVPMMMDLDRLAGSBLSFVFD		** *		POVOPOAHSOGPROVOLOGEA EPT. KOVOPOVOPOAUSOPPROVO
PHTOPQVSILAPROTPVVVHVCGLEMPPDAVEAGGGMEKTLPEP VGTQVSMEBIQNESACGLDVGECENRAREMPGVWGAGGSLKVTI LQSSDSRAPSTVPLTPVPRPSDSVSSTPAATSTPSKQALQFFCY ICKASCSSQQEFQDHMSEPQHQQRLGEIQHMSQACLLSLLPVPR DVUETEDEEPPPRRWCNTCQLYMGDLIQHRTQDHKIAKQSLR PFCTVCNRYFKTPRKFVEHVKSQGHKDKAKELKSLEKEIAGQDE DHFITVDAVGCYEGDEEBEBDDDEEEIEVEBELCKQVRSRDIS REEWKGSETYSPNTAYGVDFLVPVMGYICRICHKFYHSNSGAQL SHCKSLGHFENLQKYKAAKNPSPTTRPVSRRCAINARNALTALF TSSGRPPSQPNTQDKTPSKVTARPSQPPLPRRSTRLKT TSSGRPPSQPNTQDKTPSKVTARPSQPPLPRRSTRLKT ANENAGLQECPRKGIKPQDADVAETPHPMFTKYGNSLLEEARGE IRNLENVIQSQRGQIEELBHLAEILKTQLRRKENEIELSLLQLR EQQATDQRSNIRDNVEMIKLHKQLVEKSNALSAMEGKFIQLQEK QRTLKISHDALMANGDELNMQLKECRLKCCSLEKQLHSMKFSER RIBELQDRINDLEKERELLKENYDKLYDSAFSAAHEEQWKLKEQ QLKVQIAQLETALKSDLTDNTEILDRLKTERQQNEKLVQENREL QKNGDLSFLVKVDSEINKDLERSMEELQATHAETVQELEKTRNM LIMQHKINKDYQMEVEAVTRKMENLQQDYELKVEQYVHLLDIRA ARIHKLEAQLKDIAYGTKQYKFKPEIMPDDSVDEFDETTHLERG ENLFEIHINKVTFSSEVLQASGDKEPVTFCTYAFYDFELQTTPV VRGLHPEYNFTSQYLVHVNDLFLQYIQKNTITLEYHQAYSTEYE TIAACQLKFHEILEKSGRIFCTASLIGTKGDIPNFGTVEYWFRL RVPMDQAIRLYRERAKALGYITSNFKGPEMQSLSQQAPKTAQL SSTDSTDGNLNELHITIRCCNHLQSRASHLQPHPYVVYKFFDFA DHDTAIIPSSNDPQFDDHMYFPVPMMDLDRYLKSESLSFYVFD		i		LOLOKOVOTOTYPOVHTOAOPSVOROFWDDAOVSVORDEOTURO
VGTQVSMEEIQNESACGLDVGECENRAREMPGVWGAGGSLKVTI LQSSDSRAFSTVPLTPVFRPSDSVSSTPANTSTPSKQALQFFCY ICKASCSSQGEFQDHMSBPQHQQRLGEIQHMSQACLLSLLPVPR DVLETEDEEPPPRRWCNTCQLYYMGDLIQHRRTQDHKIAKQSLR PFCTVCNRYFKTPRKFVEHVKSQGHKDKAKELKSLEKEIAGQDE DHFITVDAVGCPEGDEEEEBDEDEEEIEVEEELCKQVRSRGDIS REEWKGSSTYSPNTAYGVDFLVPVMGYICRICHKFYHSNSGAQL SHCKSLGHFENLQKYKAAKNPSPTTRPVSRRCAINARNALTALF TSSGRPPSQPNTQDKTPSKVTARPSQPPLPRRSTRLKT TSSGRPPSQPNTQDKTPSKVTARPSQPPLPRRSTRLKT TSSGRPPSQPNTQDKTPSKVTARPSQPPLPRRSTRLKT ANENAGLQECPRKGIKFQDADVAETPHPMFTKYGNSLLEEARGE IRNLENVIGSQRGQIEELEHLAEILKTQLRRKENBIELSLLQLR EQQATDQRSNIRDNVEMIKLHKQLVEKSNALSAMEGKFIQLQEK QATTLKISHDALMANGDELNMQLKECRLKCCSLEKQLHSMKPSER RIBELQDRINDLEKERELLKENYDKLYDSAFSAAHEEQWKLKEQ QLQVLQLQLETALKSDLTDKTEILDRLKTERDQNEKLVQENREL QLQVLEQKQQLDBLKKRIKKIKLYNQENDINADELSEALLLIKAQKE QKNGDLSFLVKVDSEINKDLERSMRELQATHAETVGELEKTRNM LIMQHKINKDYQMEVEAVTRKMENLQQDYELKVEQYVHLLDIRA ARIHKLEAQLKDIAYGTKQYKFKPEIMPDDSVDEFDETITLERG ENLFEIHINKVTFSSEVLQASGDKEPVTFCTYAFYDFELQTTPV VRGLHPEYNFTSQYLVHVNDLFLQYIQKNTITLEVHQAYSTEYE TIAACQLKFHEILEKSGRIFCTASLIGTKGDIPNFGTVEYWFRL RVFMDQAIRLYRERRKALGYITSNFKGPEMQSLSQQAPKTAQL SSTDSTDGNLNELHITRCCNHLQSRASHLQPHPYVVYKFFDFA DHDTAIIPSSNDPQFDDHNMYFPVPMMDLDRYLKSESLSFVYFD	1 1	Í		PHTOPOVSLIA PEOTPUTUTUCCI EMPRODAURA CCCMERMI DOD
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EQQATDQRSNIRDNVEMIKLHKQLVEKSNALSAMEGKFIQLQEK QRTLKISHDALMANGDELNMQLKEQRLKCCSLEKQLHSMKFSER RIEELQDRINDLEKERELLKENYDKLYDSAFSAAHEEQWKLKEQ QLKVQIAQLETALKSDLTDKREILLDRLKTERDQDREKLVQENREL QLQYLEQKQQLDBLKKRIKLYNQENDINADELSEALLLIKAQKE QKNGDLSFLVKVDSEINKDLERSMRELOATHAETVQELEKTRNM LIMQHKINKDYQMEVEAVTRKMENLQQDYELKVEQYVHLLDIRA ARIHKLEAQLKDIAYGTKQYKFKPEIMPDDSVDEFDETIHLERG ENLFEIHINKVTFSSEVLQASGDKEPVTFCTYAFYDFELQTTPV VRGLHPEYNFTSQYLVHVNDLPLQYIQKNTITLEVHQAYSTEYE TIAACQLKFHEILEKSGRIFCTASLIGTKGDIPNFGTVEYWFRL RVFMDQAIRLYRERAKALGYITSNFKGPEHMQSLSQQAPKTAQL SSTDSTDGNLNELHITIRCCNHLQSRASHLQPHPYVVYKFFDFA DHDTAIIPSSNDPQFDDHMYFPVPMMNDLDRYLKSESLSFYVFD	!	· ·		TENT FENT COORDES AND THE TENT
QRTLKISHDALMANGDELNMQLKEQRLKCCSLEKQLHSMKFSER RIEELQDRINDLEKERELLKERWYDKLYDSAFSAAHEEQWKLKEQ QLKVQIAQLETALKSDLTDKTEILDRLKTERDQNEKLVQENREL QLQYLEQKQQLDBLKKRIKLYNQENDINADELSEALLLIKAQKE QKNGDLSFLVKVDSEINKDLERSMRELQATHAETVQELEKTRNM LIMQHKINKDYQMEVEAVTRKMENLQQDYELKVEQYVHLLDIRA ARIHKLEAQLKDIAYGTKQYKFKPEIMPDDSVDEFDETIHLERG ENLFEIHINKVTFSSEVLQASGDKEPVTFCTYAFYDFELQTTPV VRGLHBEYNFTSQYLVHVNDLPLQYIQKNTITLEVHQAYSTEYE TIAACQLKFHEILEKSGRIFCTASLIGTKGDIPMFGTVEYMFRL RVFMDQAIRLYRERAKALGYITSNFKGPEHMQSLSQQAPKTAQL SSTDSTTGNLNELHITIRCCNHLQSRASHLQPHPYVVYKFFDFA DHDTAIIPSSNDPQFDDHMYFPVPMMVDLDRYLKSESLSFYVFD		•		TRIVEDRY TOSURGQIEELEHLAEILKTQLRRKENEIELSLLQLR
RIEELQDRINDLEKERELLKENYDKLYDSAFSAAHEEQWKLKEQ QLKVQIAQLETALKSDLTDKTEILDRLKTERDQNEKLVQENREL QLQYLEQKQQLDBLKKRIKLYNQENDINADELSEALLLIKAQKE QKNGDLSFLVKVDSEINKDLERSMRELQATHAETVQELEKTRNM LIMQHKINKDYQMEVEAVTRKMENLQODYELKVEQYVHLLDIRA ARIHKLEAQLKDIAYGTKQYKFKPEIMPDDSVDEFDETIHLERG ENLFEIHINKVTFSSEVLQASGDKEPVTFCTYAFYDFELQTTPV VRGLHPEYNFTSQYLVHVNDLPLQYIQKNTITLEVHQAYSTEYE TIAACQLKFHEILEKSGRIFCTASLIGTKGDIPMFGTVEYMFRL RVFMDQAIRLYREKAKALGYITSNFKGPEHMQSLSQQAPKTAQL SSTDSTTGNLNELHITIRCCNHLQSRASHLQPHPYVVYKFFDFA DHDTAIIPSSNDPQFDDHMYFPVPMMMDLDRYLKSESLSFYVFD	·			EQUATIONS NIEDNYEMIKLHKOLVEKSNALSAMEGKFIOLOEK
QLKVQIAQLETALKSDLTDKTEILDRLKTERDQNEKLVQENREL QLQYLEQKQQLDELKKRIKLYNQENDINADELSEALLLIKAQKE QKNGDLSFLVKVDSEINKDLERSMRELQATHAETVQELEKTRIM LIMQHKINKDYQMEVEAVTRKMENLQQDYELKVEQYVHLLDIRA ARIHKLEAQLKDIAYGTKQYKFKPEIMPDDSVDEFDETIHLERG ENLFEIHINKVTFSSEVLQASGDKEPVTFCTYAFYDFELQTTPV VRGLHPEYNFTSQYLVHVNDLPLQYIQKNTITLEVHQAYSTEYE TIAACQLKFHEILEKSGRIFCTASLIGTKGDIPMFGTVEYMFRL RVFMDQAIRLYRERAKALGYITSNFKGPEHMQSLSQQAPKTAQL SSTDSTDGNLNELHITIRCCNHLQSRASHLQPHPYVVYKFFDFA DHDTAIIPSSNDPQFDDHMYFPVPMMMDLDRYLKSESLSFYVFD	}	,	'	QRTLKISHDALMANGDELNMQLKEQRLKCCSLEKQLHSMKFSER
QLQYLEQKQQLDBLKKRIKLYNQENDINADELSEALLLIKAQKE QKNGDLSFLVKVDSEINKDLBRSMRELQATHAETVQELEKTRNM LIMQHKINKDYQMEVEAVTRKMENLQQDYELKVEQYVHLLDIRA ARIHKLEAQLKDIAYGTKQYKFKPEIMPDDSVDEFDETIHLERG ENLFEIHINKVTFSSEVLQASGDKEPVTFCTYAFYDFELQTTPV VRGLHPEYNFTSQYLVHVNDLFLQYIQKNTITLEVHQAYSTEYE TIAACQLKFHEILEKSGRIFCTASLIGTKGDIPNFGTVEYWFRL RVFMDQAIRLYRERAKALGYITSNFKGFEHMQSLSQQAPKTAQL SSTDSTDGNLNELHITIRCCNHLQSRASHLQPHPYVVYKFFDFA DHDTAIIPSSNDPQFDDHMYFPVPMMMDLDRYLKSESLSFYVFD				RIEELQDRINDLEKERELLKENYDKLYDSAFSAAHEEQWKLKEQ
QLQYLEQKQQLDBLKKRIKLYNQENDINADELSEALLLIKAQKE QKNGDLSFLVKVDSEINKDLBRSMRELQATHAETVQELEKTRNM LIMQHKINKDYQMEVEAVTRKMENLQQDYELKVEQYVHLLDIRA ARIHKLEAQLKDIAYGTKQYKFKPEIMPDDSVDEFDETIHLERG ENLFEIHINKVTFSSEVLQASGDKEPVTFCTYAFYDFELQTTPV VRGLHPEYNFTSQYLVHVNDLFLQYIQKNTITLEVHQAYSTEYE TIAACQLKFHEILEKSGRIFCTASLIGTKGDIPNFGTVEYWFRL RVFMDQAIRLYRERAKALGYITSNFKGFEHMQSLSQQAPKTAQL SSTDSTDGNLNELHITIRCCNHLQSRASHLQPHPYVVYKFFDFA DHDTAIIPSSNDPQFDDHMYFPVPMMMDLDRYLKSESLSFYVFD			. [QLKVQIAQLETALKSDLTDKTEILDRLKTERDQNEKLVQENREL
QKNGDLSFLVKVDSEINKDLERSMRELQATHAETVQELEKTRNM LIMQHKINKDYQMEVEAVTRKMENLQQDYELKVEQYVHLLDIRA ARIHKLEAQLKDIAYGTKQYKFKPEIMPDDSVDEFDETIHLERG ENLFEIHINKVTFSSEVLQASGDKEPVTFCTYAFYDFELQTTPV VRGLHPEYNFTSQYLVHVNDLFLQYIQKNTITLEVHQAYSTEYE TIAACQLKFHEILEKSGRIFCTASLIGTKGDIPNFGTVEYWFRL RVPMDQAIRLYRERAKALGYITSNFKGPEHMQSLSQQAPKTAQL SSTDSTDGNLNELHITIRCCNHLQSRASHLQPHPYVVYKFFDFA DHDTAIIPSSNDPQFDDHMYFPVPMMMDLDRYLKSESLSFYVFD	i i			QLQYLEQKQQLDBLKKRIKLYNQENDINADELSEALLLIKAOKE
LIMQHKINKDYQMEVEAVTRKMENLQQDYELKVEQYVHLLDIRA ARIHKLEAQLKDIAYGTKQYKFKPEIMPDDSVDEFDETIHLERG ENLFEIHINKVTFSSEVLQASGDKEPVTFCTYAFYDFELQTTPV VRGLHPEYNFTSQYLVHVNDLJFLQYIQKNTITLEVHQAYSTEYE TIAACQLKFHEILEKSGRIFCTASLIGTKGDIPNFGTVEYWFRL RVPMDQAIRLYRERAKALGYITSNFKGPEHMQSLSQQAPKTAQL SSTDSTDGNLNELHITIRCCNHLQSRASHLQPHPYVVYKFFDFA DHDTAIIPSSNDPQFDDHMYFPVPMMMDLDRYLKSESLSFYVFD	- 1			QKNGDLSFLVKVDSEINKDLERSMRELQATHAETVQELEKTRNM
ARIHKLEAQLKDIAYGTKQYKFKPEIMPDDSVDEFDETIHLERG ENLFEIHINKVTFSSEVLQASGDKEPVTFCTYAFYDFELQTTPV VRGLHPEYNFTSQYLVHVNDDLFLQYIQKNTITLEVHQAYSTEYE TIAACQLKFHEILEKSGRIFCTASLIGTKGDIPNFGVEYMFRL RVPMDQAIRLYRERAKALGYITSNFKGPEHMQSLSQQAPKTAQL SSTDSTDGNLNELHITIRCCNHLQSRASHLQPHPYVVYKFFDFA DHDTAIIPSSNDPQFDDHMYFPVPMMMDLDRYLKSESLSFYVFD				LIMQHKINKDYQMEVEAVTRKMENLQQDYELKVEQYVHLLDIRA
ENLFEIHINKUTFSSEVLQASGDKEPUTFCTYAFYDFELQTTPV VRGLHPEYNFTSQYLVHVNDLPLQYIQKNTITLEVHQAYSTEYE TIAACQLKFHEILEKSGRIFCTASLIGTKGDIPNFGTVEYWFRL RVFMQDAIRLYRERAKALGYITSNFKGPEHMQSLSQQAPKTAQL SSTDSTDGNLNELHITIRCCNHLQSRASHLQPHPYVVYKFFDFA DHDTAIIPSSNDPQFDDHMYFPVPMMVDLDRYLKSESLSFYVFD	1		ļ	ARIHKLEAQLKDIAYGTKQYKFKPEIMPDDSVDEFDETIHLERG
VRGLHPEYNFTSQYLVHVNDLPLQYIQKNTITLEVHQAYSTEYE TIAACQLKFHEILEKSGRIFCTASLIGTKGDIPNFGTVEYMFRL RVFMDQAIRLYRERAKALGYITSNFKGPEHMQSLSQQAPKTAQL SSTDSTDGNLNELHITIRCCNHLQSRASHLQPHPYVVYKFFDFA DHDTAIIPSSNDPQFDDHMYFPVPMMMDLDRYLKSESLSFYVFD	ľ		ļ	ENLFEIHINKVTFSSEVLOASGDKEPVTFCTYAFYDFELOTTDU
TIAACQLKFHEILEKSGRIFCTASLIGTKGDIPNFGTVEYWFRL RVPMDQAIRLYRERAKALGYITSNFKGPEHMQSLSQQAPKTAQL SSTDSTDGNLNELHITIRCCNHLQSRASHLQPHPYVVYKFFDFA DHDTAIIPSSNDPQFDDHMYFPVPMNMDLDRYLKSESLSFYVFD		1	ĺ	VRGLHPEYNFTSOYLVHVNDLFLOYIOKNTITLEVHOAVETEVE
RV?MDQAIRLYRERAKALGYITSNFKGPEHMQSLSQQAPKTAQL SSTDSTDGNLNELHITIRCCNHLQSRASHLQPHPYVVYKFFDFA DHDTAIIPSSNDPQFDDHMYFPVPMNMDLDRYLKSESLSFYVFD	- 1	1	Į.	TLAACOLKFHEILEKSGRIFCTASLIGTKONIONEGTVOUMEN
SSTDSTDGNLNELHITIRCCNHLQSRASHLQPHPYVVYKFFDFA DHDTAIIPSSNDPQFDDHMYFPVPMNMDLDRYLKSESLSFYVFD	- 1	Ì	j	RV2MDOAIRLYRERAKALGVITCHEVGDEUMOGI COORDUMAGI
DHDTAIIPSSNDPQFDDHMYFPVPMNMDLDRYLKSBSLSFYVFD	l		1	SSTDSTDGNI NELUTTID CONTI CORR CUI CRIMINALI CORRECTION CONTINUE C
DSDTQENIYIGKVNVPLISLAHDRCISGIFELTDHQKHPAGTIH	1	1		DHDTAT I PSCHOODDDUMY BOUNDARDS BOUNDARDS
DEDIGENTITIER VNVPLISEAHDRCISEIFELTDHOKHPAGTIH	- 1	ł	ł	DSDTOENTYTCHARUDI ICI AUDOGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
				PPP-55-111GKANASDISPWHDKCI2GILKFLDHÖKHbYGLIH

WO 01/53312

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
I	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ļ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ľ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	ocque.nee	\=possible nucleotide deletion,
<u> </u>	1		VILVERAL DECOMPOSITION
			VILKWKFAYLPPSGSITTEDLGNFIRSEEPEVVQRLPPASSVST
1			LVLAPRPKPRQRLTPVDKKVSFVDIMPHQSDVSQEGSVDEVKEN
ľ		}	TEKMQQGKDDVSLLSEGQLAEQSLASSEDETEITEDLEPEVEED
i			MSASDSDDCIIPGPISKNIKQPSEKIRIEIIALSLNDSQVTMDD
1		ł	TIQRLFVECRFYSLPAEETPVSLPKPKSGQWVYYNYSNVIYVDK
ļ	J		ENNKAKRDILKAILQKQEMPNRSLRFTVVSDPPEDEQDLECEDI
Į.			GVAHVDLADMFQEGRDLIBQNIDVFDARADGEGIGKLRVTVEAL HALQSVYKQYRDDLEA
6346	2921	533	
			QDRRLLRLELQKTCQPTSTMSGSHTPACGPFSALTPSIWPQEIL
ļ			AKYTOKEESAEQPEFYYDEFGFRVYKEEGDEPGSSLLANSPLMB
1 .	i		DAPORLRWOAHLEFTHNHDVGDLTWDKIAVSLPRSEKLRSLVLA
1			GIPHGMRPQLWMRLSGALQKKRNSELSYREIVKNSSNDETIAAK
			QIEKDLLRTMPSNACFASMGSIGVPRLRRVLRALAWLYPEIGYC
İ			QGTGMVAACLLLFLEBEDAFWMMSAIIEDLLPASYFSTTLLGVQ
ŀ			TDQRVLRHLIVQYLPRLDKLLQEHDIELSLITLHWFLTAFASVV
			DIKLLRIWDLFFYEGSRVLFQLTLGMLHLKEEELIQSENSASI
J			FNTLSDIPSQMEDAELLLGVAMRLAGSLTDVAVETQRRKHLAYL
			IADQGQLLGAGTLTNLSQVVRRRTQRRKSTITALLFGEDDLEAL
1			KAKNI KQTELVADLREAILRVARHPQCTDPKNCSVVSRQLPGLL
			PNTALTPPTPLVGLYSLWQELTPDYSMESHQRDHENYVACSRSH
			RRRAKALLDFERHDDDELGFRKNDIITIVSQKDEHCWVGELNGL
1			RGWFPAKFVEVLDERSKEYSIAGDDSVTEGVTDLVRGTLCPALK ALFEHGLKKPSLLGGACHPWLFIEEAAGREVERDFASVYSRLVL
1	Ì		CKTEPI.DECGNU TREEL I VENICOLDUMTURALUM CARDUMT
1			CKTFRLDEDGKVLTPEELLYRAVQSVNVTHDAVHAQMDVKLRSL ICVGLNEQVLHLWLEVLCSSLPTVEKWYQPWSPLRSPGWVQIKC
1			ELRVLCCFAFSLSQDWELPAKREAQQPLKEGVRDMLVKHHLFSW
			DVDG
6347	2921	533	QDRRLLRLELQKTCQPTSTMSGSHTPACGPFSALTPSIWPQEIL
			AKYTQKEESAEQPEFYYDEFGFRYYKEEGDEPGSSLLANSPLME
1		•	DAPQRLRWQAHLEFTHNHDVGDLTWDKIAVSLPRSEKLRSLVLA
1			GIPHGMRPQLWMRLSGALQKKRNSELSYREIVKNSSNDETIAAK
1 1	i		QIEKDLLRTMPSNACFASMGSIGVPRLRRVLRALAWLYPEIGYC
1 1	i		QGTGMVAACLLLFLEEEDAFWMMSAIIEDLLPASYFSTTLLGVQ
	•		TDQRVLRHLIVQYLPRLDKLLQEHDIELSLITLHWFLTAFASVV
1 !	j	İ	DIKLLLRIWDLFFYEGSRVLFQLTLGMLHLKEEELIQSENSASI
í	Į.		FNTLSDIPSQMEDAELLLGVAMRLAGSLTDVAVETQRRKHLAYL
			IADQGQLLGAGTLTNLSQVVRRRTQRRKSTITALLFGEDDLEAL
]	ļ		KAKNIKQTELVADLREAILRVARHFQCTDPKNCSVVSRQLPGLL
]]		[PNTALTPPTPLVGLYSLWQELTPDYSMESHQRDHENYVACSRSH
į į	•	[RRRAKALLDFERHDDDELGFRKNDIITIVSQKDEHCWVGELNGL
į l			RGWFPAKFVEVLDERSKEYSIAGDDSVTEGVTDLVRGTLCPALK
			ALFEHGLKKPSLLGGACHPWLFIEEAAGREVERDFASVYSRLVL
			CKTFRLDEDGKVLTPEELLYRAVQSVNVTHDAVHAQMDVKLRSL
1	}		ICVGLNEQVLHLWLEVLCSSLPTVEKWYQPWSFLRSPGWVQIKC
1	1	İ	ELRVLCCFAFSLSQDWELPAKRBAQQPLKEGVRDMLVKHHLFSW
L			DVDG
6348	3	3679	AGAEKCFVTLLACFLAKQQNKYKYEECKDLIKSMLRNELQFKEE
1	ł	1	KLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGRDASRSLN
	1	1	EHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQKLSPENDN
	ł	1	DDDEDVQVEVAEKVQKSSSPREMQKAEEKEVPEDSLEECAITCS
I	·		NSHGPCDSNQPHKNIKITFEEDEVNSTLVVDRESSHDECQDALN
· !		ł	ILPVPGPTSSATNVSMVVSAGPLSGEKAAINILEINEKLRPQLA
ĺ	1	ļ	EKKQQFRNLKEKCFLTQLACFLANQQNKYKYEECKDLIKFMLRN
1	j	ļ	ERQFKEBKLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGR
			DASRSLNEHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQK
			LSPENDNDDDEDVQVEVAEKVQKSSAPREMPKAEEKEVPEDSLE
		L	

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, P=Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i	amino acid	sequence	Codon, /-possible nucleotide deletion,
L	sequence	•	\=possible nucleotide insertion)
			ECAITCSNSHGPYDSNQPHRKTKITFEEDKVDSTLIGSSSHVEW
1			EDAVHIIPENESDDEEEEEKGPVSPRNLQESEEEEVPQESWDEG
1	ļ	i	YSTLSIPPEMLASYKSYSSTFHSLEEQQVCMAVDIGRHRWDQVK
į			KEDHEATGPRLSRELLDEKGPEVLQDSLDRCYSTPSGCLELTDS
			CQPYRSAFYVLEQQRVGLAVNMDEIEKYQEVBEDODPSCPRLSR
ļ			ELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGOPYSSAVYSLER
1	· ·		QYLGLALDVDRIKKDQEEEEDQGPPCPRLSRELLEVVEPEVLOD
1	l i		SLDRCYSTPSSCLEOPDSCOPYGSSFYALBEKHVGFSLDVGRIE
	1		KKGKGKKRRGRRSKKERRRGRKEGEEDQNPPCPRLSRELLDEKG
1			PEVLQDSLDRCYSTPSGCLELTDSCQPYRSAFYILEQQRVGLAV
		•	DMDEIEKYQEVEEDQDPSCPRLSGELLDEKEPEVLQESLDRCYS
1	<u>†</u>		TPSGCLELTDSCQPYRSAFYILEQQRVGLAVDMDEIEKYQEVEE
i			DODPSCPRLSRELLDBKEPEVLQDSLGRCYSTPSGYLELPDLGQ
			PYSSAVYSLEEQYLGLALDVDRIKKDQEEEEDQGPPCPRLSREL
ł	1		LEVVEPEVLQDSLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKH VGFSLDVGBIEKKGKGKKRRGRRSKKERRRGRKEGEEDQNPPCP
1	1		RLNSMLMEVEEPEVLQDSLDICYSTPSMYFELPDSFQHYRSVFY
			SFEEEHISFALYVDNRFFTLTVTSLHLVFQMGVIFPQ
6349	3	3679	AGAEKCFVTLLACFLAKQQNKYKYEECKDLIKSMLRNELQFKEE
	ŀ		KLAEQLKQAEELRQYKVLVHSQERELTOLREKLREGRDASRSIN
ļ	į	•	EHLQALLTPDEPDKSQGQDLQEQLAEGCRLAOHLVOKLSPENDN
		•	DDDEDVQVEVABKVQKSSSPREMQKAEEKEVPEDSLKECAITCS
			NSHGPCDSNQPHKNIKITFEEDEVNSTLVVDRESSHDECODALN
1			ILPVPGPTSSATNVSMVVSAGPLSGEKAAINILEINEKLRPQLA
			EKKQQFRNLKBKCFLTQLACFLANQQNKYKYEECKDLIKFMLRN
	,		EROFKEEKLAEOLKOAEBLROYKVLVHSQERELTQLREKLREGR
1 .			DASRSLNEHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQK
1 1			LSPENDNDDDBDVQVEVAEKVQKSSAPREMPKAEEKEVPBDSLE ECAITCSNSHGPYDSNQPHRKTKITFEEDKVDSTLIGSSSHVEW
1 1			EDAVHIIPENESDDEEEEEKGPVSPRNLQBSEEEEVPQESWDEG
1			YSTLSIPPEMLASYKSYSSTFHSLEEQQVCMAVDIGRHRWDQVK
			KEDHEATGPRLSRELLDEKGPEVLQDSLDRCYSTPSGCLELTDS
1	ļ		CQPYRSAFYVLEQQRVGLAVNMDEIEKYQEVEEDQDPSCPRLSR
			ELLDEKRPEVLQDSLGRCYSTPSGYLELPDLGOPYSSAVYSLRE
ł			QYLGLALDVDRIKKDQEEEEDQGPPCPRLSRELLEVVEPEVLOD
			SLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKHVGFSLDVGETE
		ŀ	KKGKGKKRRGRRSKKERRRGRKEGEEDONPPCPRLSRELLDEKG
<u> </u> .].		PEVLQDSLDRCYSTPSGCLELTDSCQPYRSAFYILEOORVGLAV
		ĺ	DMDEIEKYQEVEEDQDPSCPRLSGELLDEKEPEVLQESLDRCYS
	1		TPSGCLELTDSCQPYRSAFYILEQQRVGLAVDMDEIEKYQEVEE
			DQDPSCPRLSRELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQ
	Í		PYSSAVYSLEEQYLGLALDVDRIKKDQEEEEDQGPPCPRLSREL
			LEVVEPEVLQDSLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKH VGFSLDVGEIEKKGKGKKRRGRRSKKERRRGRKEGEEDQNPPCP
	1	ļ	RLNSMLMEVEEPEVLQDSLDICYSTPSMYFELPDSFQHYRSVFY
	ļ		SFEEEHISPALYVDNRFFTLTVTSLHLVFQMGVIFPQ
6350	3	3679	AGAEKCFVTLLACFLAKQQNKYKYEECKDLIKSMLRNELQFKEE
		. 1	KLAEQLKQAEELRQYKVLVHSQERELTOLREKLREGRDASRSIN
	ì	· .	EHLQALLTPDEPDKSQGQDLQEQLAEGCRLAOHLVOKLSPENDN
	·	İ	DDDEDVQVEVAEKVQKSSSPREMQKAEEKEVPEDSLEECAITCS
		[NSHGPCDSNQPHKNIKITFEEDEVNSTLVVDRESSHDECODALN
			ILPVPGPTSSATNVSMVVSAGPLSGEKAAINILEINEKLRPOLA
		}	EKKQQFRNLKEKCFLTQLACFLANQONKYKYEECKDLIKFMLRN
ł		1	ERQFKEEKLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGR
ł			DASRSLNEHLQALLTPDEPDKSQGQDLQEQLAEGCRLAOHLVOK
· <u></u>			LSPENDNDDDEDVQVEVAEKVQKSSAPREMPKAEEKEVPEDSLE

SEQ	Predicted	Predicted end	l mino acid accord
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H-Histidine, I-Isoleucine, K-Lysine,
]	corresponding	to first	L=Leucine, M=Methionine, N=lenaragine
	to first	amino acid	P=Proline, Q=Glutamine R=Arginine
i	amino acid	residue of	S=Serine, T=Threonine, V=Valine
ł	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown *-Shop
1	amino acid	sequence	Codon, /=possible nucleotide deletion
	sequence		\=possible nucleotide insertion)
	1.	ļ	ECAITCSNSHGPYDSNQPHRKTKITFEEDKVDSTLIGSSSHVEW
			EDAVHIIPENESDDEEEEEKGPVSPRNLOESEEREVDORSWORG
1			YSTLSIPPEMLASYKSYSSTFHSLEEQQVCMAVDIGRHRWDQVK
			KEDHEATGPRLSRELLDEKGPEVLQDSLDRCYSTPSGCLELTDS
1			CQPYRSAFYVLEQQRVGLAVNMDEIEKYQEVEEDQDPSCPRLSR
1			ELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQPYSSAVYSLEE
ŀ	1	1	QYLGLALDVDRIKKDQEEBEDQGPPCPRLSRELLEVVEPEVLQD
ŀ			SLDRCYSTPSSCLEOPDSCOPYGSSFYALEEKHVGFSLDVGEIE
l	ļ		KKGKGKKRRGRRSKKERRRGRKEGEEDQNPPCPRLSRELLDEKG
l			PEVLQDSLDRCYSTPSGCLELTDSCQPYRSAFYILEQQRVGLAV DMDEIEKYQEVBEDQDPSCPRLSGELLDEKEPEVLQESLDRCYS
l			TPSGCLELTDSCQPYRSAFYILEQQRVGLAVDMDEIEKYQEVEE
l			DQDPSCPRLSRELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQ
·			PYSSAVYSLEEQYLGLALDVDRIKKDQEEEEDQGPPCPRLSREL
]			LEVVEPEVLQDSLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKH
			VGFSLDVGEIEKKGKGKKRRGRRSKKERRRGRKEGEEDQNPPCP
1 1			RLNSMLMEVEEPEVLQDSLDICYSTPSMYFEL.PDSFOHVPCURV
6351			SFEEHISFALYVDNRFFTLTVTSLHLVFOMGVTRDO
6351	1291	319	REARRITERSQLGRMLVVEVANGRSLVWGAEAVOALRERIGUGG
			RTVGALPRGPRQNSRLGLPLLLMPEEARLLAFTGAVTLVSAPPD
			DSRHHSLALTSFKRQQEESFOEOSALAARARETERORILEKITE
			GQAAKKQKLEQASGASSSOEAGSSOAAKEDETSDGOASGEOVEA
			GPSSSQAGPSNGVAPLPRSALLVOLATARPRPVKAPPLDUDG
}			KDWPHAGRPAHELRYSIYRDLWERGFFLSAAGKFGGDFLVVDGD
i	,		PLRFHAHYIAQCWAPEDTIPLQDLVAAGRLGTSVRKTLLLCSPQ
6352	235	923	PDGKVVYTSLQWASLQ
		223	WSEWLSPCHAAKCKGLSMLRITMKTRAISLAADATEFVQGRSAP
1	İ		AMARSLVHDTVFYCLSVYQVKISPTPQLGAASSAEGHVGQGAPG
i i	1		LMGNMNPEGGVNHENGMNRDGGMIPEGGGGNQEPRQQPQPPPEE PAQAAMEGPQPENMQPRTRRTKFTLLQVEELESVFRHTQYPDVP
J	ŀ		TRRELAENLGVTEDKVRVWFKNKRARCRRHQRELMLANELRADP
			DDCVYIVVD
6353	65	672	RFAGAGATPEARARPPDVQAAEEEKEMDLPDSASRVFCGRILSM
j			VNTDDVNAIILAQKNMLDRFEKTNEMLLNFNNLSSARLQQMSER
)		•	FLHHTRTLVEMKRDLDSIFRRIRTLKGKLAROHDEAFGWIDERC
1			FLEEEDEDPIPPSTTTTIATSEOSTGSCDTSPDTVSDS1.SDCFP
6354	255		DLSHVQPGSPAINGRSQTDDEEMTGE
0354	965	510	PSLRPMEPTRDCPLFGGAFSAILPMGAIDVSDLRPVPDNOEVEC
	}		HPVTDQSLIVELLELQAHVRGEAAARYHFEDVGGVOGADANUR (
	1		SVQPLSLENLALRGRCOEAWVLSGKOOIAKENOOVAKDUTLUON
6355	158	1665	LLKLPQYQTDLLLTFNQPP
	450	1662	RGSSAAFRGSGLRGAMIRRVLPHGMGRGLLTRRPGTRRGGFSLD
ļ			WDGKVSEIKKKIKSILPGRSCDLLODTSHLPPRHSDVVIVGCGV
			LGLSVAYNLKKLESRRGAIRVLVVERDHTVSOASTGLGVGGIGO
[QFSLPENIQLSLFSASFLRNINEYLAVVDAPPLDLRFNPSGYLL
]	LASEKDAAAMESNVKVQRQEGAKVSLMSPDQLRNKFPWINTEGV
ŀ			ALASYGMEDEGWFDPWCLLQGLRRKVQSLGVLFCQGEVTRFVSS
	}	ŀ	SQRMLTTDDKAVVLKRIHEVHVKMDRSLEYQPVECAIVINAAGA
		1	WSAQIAALAGVGEGPPGTLQGTKLPVEPRKRYVYVWHCPQGPGL
	Ĭ	i	ETPLVADTSGAYFRREGLGSNYLGGRSPTEQEEPDPANLEVDHD
- 1	1		FFQDKVWPHLALRVPAFETLKVQSAWAGYYDYNTFDQNGVVGPH
	1	ļ	PLVVNMYFATGFSGHGLQQAPGIGRAVAEMVLKGRFQTIDLSPF LFTRFYLGEKIQENNII
6356	354	633	TGLTSSCLPLQVMMTKRTKDMGKFSSVTVSTIDEEEEEIEAREV
	į.	1	PROPERTY
ļ	I	t t	ADSYAQNAKVIEKQLERKGMSKRRLQELAELEAKKAKMKGTLID

Deginning	SEO	Predicted	Predicted end	
No:				Amino acid segment containing signal peptide
cortesponding cofired				Glutamic Roid Rubbons - 1 - 2 - 2 - 2
corresponding to first amino acid residue of residue of amino acid residue of amino acid sequence acid sequence				W-Wightiding T Inclusions (G=Glycine,
to first amino acid residue of amino acid residue of amino acid anino acid sequence 6357 2 915 GLEANMALIVECTRECONIC, V-VALISHE, V-TYCTOSINE, X-DURNOUM, *-Stop COMO, /-possible nuclectide deletion, \	ı			Leleucine Memorbionine Nullenger
sequence seq			1	P=Proline O-Glutamine D-Danisine,
residue of amino acid sequence	1			Seserine T-Throning W-Waline,
amino acid sequence Codon, /-possible nuclectide insertion	ł			W=Tryptophan V=Tyrogina V=Thhana + at
Sequence N-possible nucleotide insertion		amino acid		Codon. /=possible nucleotide dolotion
6361 615 156 GLIANMALURVURNOTSI SOWVEYCSKI IPVSPTQGGGRALS RYSOWPONSOSQA GOGGSQEDIO IQUARKYHTISTYTKOSP QPVSEKVGAFTKI ISAMSPTGELKYSKMIKI IAALRAYTSCVEK TDFEEFFLACOMDPTSNSWLITLIHUWACUNENGESGKYM CRII VAFWWEDVQDGCRWMGVPYILLKRWILHTHEYAALIQYI DEGILSDHOHGLAALBRETFSINKECEPPRILELLIVERGYGYL DEGILSDHOHGLAALBRETFSINKECEPPRILELLIVERGYGYL OBGILSDHOHGLAALBRETFSINKECEPPRILELLIVERYGYOTY DEGILSDHOHGLAALBRETFSINKECEPPRILELLIVERYGYOTY OBMOGDILLTGGVEHRPLUENNOGILKOHSFTYNDEGI AISKTAVAPIERVKLLLOVQHASKOTAADKOYKGYTETGIAR AISKTAVAPIERVKLLLOVQHASKOTAADKOYKGYTETGIAR REFRIGLGDCUVKITKSDGI RGLYQGFSVSVQGI I YRAAYROKY DIAKAGALDPIKKTHIVVSWIMIAQTYTAVAQVSYSPTTYRROW MOSGARGABIMYTGTYDCVRKIFPEDGCKAFFKGAMGNULROMG GAFVULVIDELKKYI 6359 98 1086 VCRQEEERMKEDCLESHYPISDSKSIOKSELLGLLKTYNCYHE GKSFGCLHREERGTHI IEGLIANAGLRAFIRLAYOGDREGUYHL PSTSWWPREPSCPLKEPSPQNONITAQGFSIOPVIKABSSTOS GPLERAERAQUMRIKSBASCANGAPKPKGARAGNIKRROM GAFVULVIDELKKYI GKSGCCHARRESCETI IEGLIANAGLRAFIRLAYOGDREGUYHL PSTSWWPREPSCPLKEPSPQNONITAQGFSIOPVIKABSSTOS GPLERAERAQUMRIKSBASCANGAPKPKGARAGNIKRROM GAFVULVLUBLKAVI GKSGCCHARRESCETI IEGLIANAGLARIPTULQVITALLINKRY EDOGSFFALIVIYHERGGRYKKLOECPYPLISRILHOPCEKIARIP LIMBALLGGVEYHEVAQYIKFENYULDSFVEKLKEEEREI IKLI MKPQALRIJHOLGGUVEKA MKPQALRIJHOLGGUVEKA FLYNKULSVEGSTULLERGGRYKLOECPYPLISRILHOPCEKIARIP LIMBALLGGVEYHEVAQYIKFENYULDSFVEKLKEEEREI IKLI MKPQALRIJHOLGGUVEKA REPSCALGCHCALAPOAGNIRGREFHGUHALTRSTHRGKPMSIMQ FRADTAGNVTLKHGGSELI I LPRORVOGSC REPSCALGOLGHCALAPOAGNIRGREFHGUHALTRSTHRGKPMSIMQ FRADTAGNVTLKHGGSELI I LPRORVOGSC REPSCALGOLGHCALAPOAGNIRGREFHGUHALTRSTHRGKPMSIMQ FRADTAGNVTLKHGGSELI I LPRORVOGSC REPSCALGOLGHCALAPOAGNIRGREFHGUHALTRSTHRGKPMSIMQ FRADTAGNVTLKHGGSELI I LPRORVOGSC REPSCALGOLGHCALAPOAGNIRGREFHGUHALTRSTHRGKPMSIMQ FRADTAGNVTLKHGGSELI I LPRORVOGSC REPSCALGOLGHCALAPOAGNIRGREFHGUHALTRSTHRGKPMSIMQ LARVYLSSVOGLAUVATILLYTHANSHRKHTUGALGILAULA GHANGARAGNITEGRAFHATTAGAI FFLUTAKAGAPMSIMA FRADTAGNITHAURAGNITHAURAGNITHAURAGNITHAURAGNITHAURAGNITHAURAGNITHAURAGNITHAURAGNITHAURAGNITHAURAGNITHAURAGNITHAURAGNITHAURAGNITHAURAGNITHAURAGNITHAURAGNITHAURAG		sequence		\=possible pucleotide insertion)
RTSOMPOWSGSQACGGSSQIPGIDIQLINKYHTTRKLSTTKSCYEK QPVERVCAFIKI IRAMPGTGLYSYSKKKIKIARMYTGCVEK TDFEFFIRCOMPDTFNSWFLITLLHUNKCLVEMKQSGRSFGKYKY CRIIVISHMENDVOGAGRWAMGUPIKKRMILTHVANLGY DEGILSDDHGLAAALMRTFSNIKCEDPRHELLUFEVRKQIQTL DEMMSGDLLIDGEVHRPLUENSPOLIKKRNILTHVANLGY DEGILSDDHGLAAALMRTFSNIKCEDPRHELLUFEVRKQIQTL DEMMSGDLLIDGEVHRPLUENSPOLIKKRNILTHVANLGYGGIAA AISKTAVAPIERV KLLLQVGHASKQIAALMOYKGIVDCIVERIF EQGVLSFKRGALMANIRAFRKKYKXDIJGGADAM AISKTAVAPIERV KLLLQVGHASKQIAALMOYKGIVDCIVERIF EQGVLSFKRGALMANIRAFRKKYKXDIJGGADAMANIKRMG GFREYDVLUDELKKVI DTAKGGLDDPKNITHVVSMMIAQTVTAVAGVSYPPDTVRRMM MOSGRGADIMTGTVDCWKRIFDBGGKAFFGAMSNVLRGMG GAFVUVLUDELKKVI FORGEEMKEDELDESHVYISDGKSIOKGELLGLLKTYNCVHE GKSFQLRHREBEGTLIIEGLINIAMGLREPIRLQMQDDREQUMI BYSTSWHPRRSCLELESHDVNORTAGGGSIOVENKASSTOSS GPLERABERAQLMRYKSDASCMSORRPKCRAPGEAQRIRRHFS INGHYNIKKSVEVLERBSPQNORTAGGGFSVAVGGIIRHREST REGORSFFALVIVUESGERTLKUCGEVPLIGRILHOHDINERSSTOSS GPLERABERAQLMRYKSDASCMSORRPKCRAPGEAQRIRRHFS INGHYNIKKSVEVLERBSGVAVRINGGERSTLANGGGIGILKTYNCVHE EDGPSFFALVIVUESGERTLKUCGEVPLIGRILHOHDINERSSTOSS GPLERABERAQLMYKSDASCMSORRPKCRAPGEAQRIRRHFS INGHYNIKKSVEVLERBSGVAVRIDGSVEKKKEEBERSIIKH MKRQALATINLQRLEQUVBAW GASALTHUGREGUVBAW AFGRERGFFFTAVLKARAGERVAATSTITNDGIGIN PAOTAGNIVFLEGSERFTTAVLKYABERVAATSTITNDGIGIN PAOTAGNIVFLEGGERFFTAVLKYABERVAATSTITNDGIGIN PAOTAGNIVFLEGGERFFTAVLKYABERVAATSTITNDGIGIN PROTINTELDDSSVAVPLIGATIANSTILSVERNOGVETGIMAA AFGRERGRITSGERFFTAVLKYABLIUL GHLVVSIALALLGKVCHIRLAGSKOPRAYFTKTWILLDLIALLG GHLVVSIALALLGKVCHIRLAGSKOPRAYFTKTWILLDLIALLG GHLVVSIALALLGKVCHIRLAGSKOPRAYFTKTWILLDLIALLG GHLVVSIALALLGKVCHIRLAGSKOPRAYFTKTWILLDLIALLG GHLVVSIALALLGKVCHIRLAGSKOPRAYFTKTWILLDLIALLG GHLVVSIALALLGKVCHIRLAGSKOPRAYFTKTWILLDLIALLG CHLVVSIALALLGKVCHIRLAGSKOPRAYFTKTWILLDGBUHLIVSK PFLIMIUSGILLAVGRAYLIKSALITARJAIFTHROGBUHLIVSK PFLIMIUSGILLAVGRAYLIKSALITARJAIFTHROGBUHLIVSK CHLVVSIALALLGKVCHIRLAGSKOPRAYFTKTWILLDLIALLG RETEGSSFFRENDSAMESTULIKRNILALAGROVILLALAGSKOPRA ASQMTDSSALLAVGRAYLIKSTAGALTINGTVULD SGGGVTHAVPIYEGFRAPHSIMBIDIAGROVSELLALLARROV	6357	2	915	GLIRNMALLVRVIRNOTSTSOWVRVCSPLIRVERTOCOCDENIC
QPVERKVGAFTKIIBAMGFTGPLKYSKKIKIAALRRYTSCVEK TDFFEFFFRCKOMPTTRINSFILTLHUNGKGRISGKSKYK CRIIVIHMMEDVQQRGRMGWNPYLIKKNMILMTNHFYAALIGY DEGILSDDMIGLAALLRFTFRNKCEDPRHLEVYPKGIOJYL DSMIGDLLLTGEVSKRPLVERKPQSILKPHGFTYNDEGI AISKTAVAPIERVELLLOVQHASKQIAADKOYKGIVGCIVRIPK SQGVLSFRKGRLANVIRKYPDALADKOYKGIVGCIVRIPK CQRUSFYRGRIANVIRKYPDALAPTATKORIAADKOYKGIVCIVRIPK CQRUSFYRGRIANVIRKYPDALAPTATKAADVAKSGITA AISKTAVAPIERVELLLOVQHASKQIAADKOYKGIVCIVRIPK CQRUSFYRGRIANVIRKYPDALAPTATKAADVAKSGITA CQRUSFYRGRIANDITAVYPDALAPTATKAADVAKSGITA REFRGLGDCLVKITKSGOIRGLKQGFSVSVQGITIYKAAYFGOV DTAKKOHLDPKNITHLVVSWMIAGTTVAAVGVVSYPFDTVRRRWM MQSGRGADIMYTGTVDCOMKTIFRDEGGKAFFKGAMSINVLRRMG GASTQLRHREEGETLITIGGLMIAMGTRRYIELDMCDDREQVHI GKSFGLARINEEGETLITIGGLMIAMGTRRYIELDMCDDREQVHI PSTSWMPRRPSCPLKESPSQNGNITAGGPSIGAPKHABSSTDSS GPLEEAEEAPQLMRTKSDASCAMGARFKCARAGRIRKTHRSP LMRADLGVEVPHSVAQYTKFEMPVLDSFVEKLKEEBEREITLIT INGHYNIKTSVFTPAYGSVTNAVNSTMTTLQVITLLLINKFRV EDGPSFFALIVIVBSGERTKLKDCSYPLISTHLOMDDDREQVHI LMRADLGVEVPHSVAQYTKFEMPVLDSFVEKLKEEBEREITLIT MKKQARLITHAQALSQLVEKAP LMRADLGVEVPHSVAQYTKFEMPVLDSFVEKLKEEBEREITLITGDR RELPYKLSVYSETSPTAVALKPAEEFKVPAATSAITTNDGIGIN PAGTAANVFLKHGSELRI I PROBVOSC GREAPSPTILTSTHRRKSVSKTITLTSDB CRITTATTTLDGIGIN PAGTAMVFLKHGSELRI I PROBVOSC GREAPSRGITSDSFVEHPLAGARTASTHRRKSVSKTITLTSDB CRITTATTTLDGIGIN PAGTAMVFLKHGSELRI I PROBVOSC GREAPSRGITSDSFCHPT QGRCTFTPDOGTTHIQAGADALHPA NSTGINDIQETVRKTYVLII FROMGANDALAPATSTALTAGAITFTGFTRRKRWIGHTAGA APGRENGRITSDSFCHPT QGRCTFTPDOGTHIQACAAPGATCHOVACA APGRENGRITSDSFCHPT QGRCTFTPDOGTHIQACAAPGATCHOVACAAPGA	1			RTSOWPOMSOSOACGGSEOTPGTDTOLNEYVUTTPVLCTTVDCD
TDFFEFFLRCOMPDTFINSWELTTLLHUNGCLIVENKGGGGGGYM CRITVISHMENGDQGGGGWMGDVFLLKKNIHFYPALIGY DEGILSDHGLAAALMFFFNRKCEDPRHLELLUETYWGLOYL DSMIGDELLIGEVWRPLUEKRPGSILKHFSFTNDEGI 6358 2009 1040 ASDALBISJAPVLELSSKSAREPATHTEGISFAKDFLAGGTAN AISKTAVAPISHVLLLOQHASKQTAADKOYKGITDCLYIFK EGGVLSFWRGNLANVIRTFFTOALMFAKGYKKYIFLGGVDKHF COFREYFACNLASGGAAGTSLCTVFLDFARTRLAADVCKSGTE REFRGLGGLUKKTKSDGIRGUCGFSVSQGITIVRAAYRGVV DTAKGHLDPKNTHLVVSWHLAGVTIVAAGVVSYFPTVYRRMM MOSGRGGADINTYGTVDCMRKTFRDEGKAFFKGAMGNVLRGMG GAFVLLVDELKKVI 6359 98 1086 VCRGEBENKREDCLFSSWYFISDSKSTOKSELLGLLKTYNCYHE GKSFGLRHREEGTLITEGLLNTANGCRRFIRLDMODDEEQVHL PSTSWMPRRESCLKEPS PGNORNTYAGGSFGAGAGRIFHEFS INGHFYNIKTSVFTAYGSVTNYRVSTSWTTJCVLTLLINKRFN EDGPSFFALYTVHEGGERTKLKDCSYPLISRILHGPCEKIARIF INGHFYNIKTSVFTAYGSVTNYRVSTSWTTJCVLTLLINKRFN EDGPSFFALYTVHEGGERTKLKDCSYPLISRILHGPCEKIARIF INGHFYNIKTSVFTAYGSVTNYRVSTSWTTJCVLTLLINKRFN EDGPSFFALYTVHEGGERTKLKDCSYPLISRILHGPCEKIARIF INGHFYNIKTSVFTAYGSVTNYRVSTSWTTJCVLTLLINKRFN EDGPSFFALYTVHEGGERTKLKDCSYPLISRILHGPCEKIARIF INGHFYNIKTSVFTAYGSVTNYRVSTSWTTJCVLTLLINKRFN EDGPSFALYTVHEGGERTKLKDCSYPLISRILHGPCEKIARIF INGHFYNIKTSVFTAYGSVTNYRVSTSWTTJCVLTLLINKRFN EDGPSFALYTVHEGGERTKLKDCSYPLISRILHGPCEKIARIF INGHFYNIKTSVFTAYGSVTNYRVSTSWTTJCVLTLLINKRFN EDGPSFALYTVHEGGERTKLKDCSYPLISRILHGPCEKIARIF INGHFYNIKTSVFTAYGSVTNYRVSTSFTTSHLKDRCKFNSITKT MKFQALRITHURPLEGVTJATAGATTSHCHGERTKLT KFGALVSTSTLEGVTJATAGATTSHCHAGAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	1			OPVEEKVGAFTKI I KAMGFTGPI, KYSKWKIKI AAT DAYDOOURY
CRITYHPMEDVQQRRYMGVDYYLKRNNILMYNHYYARLIGY DEGILSDDHIGLAALLMFTPHRKCDPRHLEVYYRKIQYL DSMMGDDLLINGEVSMRPLVEXRYGSLIKPHSPTYNDBGL AISKTAVAPIEVVLELSSKSARPTYMTEGJSFAKEPTHAGGIFA AISKTAVAPIEVVLELUQVCHASKQIAAKOYKGIVDCUVLIFE COGVLSFWRGNLANVIRTFPTQALBFAFKOKYKGIFLGVOKDHT OFRRYFAGNILASGGAGASTSLCYVFDDFARTRLAADVGKSGTE REFRGLGDCLVKITKSDGIRGLYQFFSVSVQGIIYRAAAYROV DTAKKGHLDPFKATHLVVSWHIAQTVTAVAQVVSYPPTYTRRMM MQSGRGADINYTGTVDCWKKITRDEGGKAFFKGAMSNVLRGMC GAFVLVLVDELKKVI 6359 98 1036 VCRGEESKMKEDCLPSSRVPISDSKSIOKSELLGLLKTYNCYHE KOSFOLRRIEBEGTILIGGLINAGGGRRIPLGMQDDEEQVHL PSTSWMPREPSCDLKEPSPDQMCNITAGGPSIOPVHKAESSTDSS GPLEBEAERAPGLMFRISDASCMSQRRPKCRAPGGARIRHERFS INGHYNHKTSVFTPAYGSVTWVRWISTMTTLQVIITLLINKFRW EDOPSEFALITVHIESGERTKLKDCSYPLISRILIGHQCDDEEQVHL PSTSWMPREPSCDLKEPSPDQMCNITAGGPSIOPVHKAESSTDSS GPLEBEAERAPGLMFRISDASCMSQRRPKCRAPGGARIRHERFS INGHYNHKTSVFTPAYGSVTWVRWISTMTTLQVIITLLINKFRW EDOPSEFALITVHIESGERTKLKDCSYPLISRILIGPCEKLARIF IMREQALARITMLQRLEQLVEAK 6360 1 345 GTRGAVPSTLEESVULPFRSCRVFWINSGTTMSKVSFKITLTSDP RLPYKVLSVPESTPETAVLKFAAREFKVPAATSAITTNDGIGIN PAGTAGNVFIKMSSELRI IPROFVOSC 6361 615 158 RPGLGGLGHCKLAFQOKORRKCRPHGERJALTESTHRGKEMSIMG FKDTLMTLEVINSSFVAPLGAJTAVASTLSYBUODEFTGINA APGRWRRGJINSGFCHPIQGRCTPTPDDGETLHIQAGDALMLPA NSTGIMDIGFTVKKTVLII 6362 350 1576 TTMDGSHSAARKLQOLPFTSSSAVSEASFSYKENLIGALLAYF CHLVVSIALMALOXYCHIRLAGSKDPRAYKYKTWMUGLEHILG ELGVASVARAPIDSJULVTTATAGAIFYLIKKMKKPD LRRYLISPVCCGLAVVGTYLLVTFARNSHEKMTGENVTHHLVSK PFLIMUMENILIFCLLIFYTKRKNNIVVLULAGSMVTV TVAVAAGHLVLSIQGNILQLDYPIFYVMFVCWATAVAYQAARLOQ ASQMYDSSLLTAAVGTUSTATAGAIFYLIKKKPDDVHLTCHAPL NPRKHSKABAVFFFTTNYVALDISSRVILAGSGVIKAGFNJ DIPKYCPRIVYGROCLGTPSEEHPULITGAPL NPRKHERABVFFFTTNYVALDISSRVIKAGFAG DIPKYCPRIVYGROCLGTSEEHPULITGAPL NPRKHERABVFFFTTNYVALDISSRVIKKGFAFAG DIPKYCPRIVYGROLLSSVKKLAPAVILSANDL RTHELGSSFFRERDSAMESYDVIANGGVULDGSSEHFKLEPAL NPRKHERABVFFFTTNYVALDISSRVIKKGFAFAG DIPKYCFRIVYGROLLSSVKKLAPAVILSANDL RTHELGSSFFRERDSAMESYDVIANGGROUNGRENINGRAPG DIPKYCFRIVYGROLLSSVKKLAPAVILSANDL RTHENSSFFILVERFFTTNYNDLLSSKAPLERPL NPRHEIGIVKOMNINGERIKGVYSKOQLGTSSEHPULITERPL NPRHEI	ļ			TDFEEFFLRCOMPDTFNSWFLITILHWWNCLJPMVORCDCCVVM
DEGILADHIGHARALMETPENRICCEDPRICHELLULYPYRUGIQIYL SSMAGEDILLINGSVARPIUENSPASILKAPSTINDEGI ASDALHSISAPVIRLISSRSAARPATHTEGAISFARDFIAGGIAA ASDALHSISAPVIRLISSRSAARPATHTEGAISFARDFIAGGIAA AISKTAVAPISRKALIADVORASKOIAABOKVIDCIVAPIK EOGULSFREGRIANVIRYPPOALMERAKOKVIQIPLGGVOKHT OPRKYRAGAILASGAAGATSLCPVYPLDPARTRIAADVOKKIT OPRKYRAGAILASGAAGATSLCPVYPLDPARTRIAADVOKKIT OPRKYRAGAILASGAAGATSLCPVYPLDPARTRIAADVOKKIT OPRKYRAGAILANTANGOVSYPEPTURREM MQSGRAGADIMYTGYDOKKITROBGGARPFKGAMSINVLRGME GAFULVLDELKKVI ORVERDEKMIKATORDOKNITAGOSIGIALLIKTYNCYHE GKSFOLHREEGOTLIIBGILANIAGGRARPIRLDMODDEGUVIL PSTSMMPRRESCILKEPSPOMOKNITAGOSIGIALLILIKTYNCYHE GKSFOLHREEGOTLIIBGILANIAGGRARPIRLDMODDEGUVIL PSTSMMPRRESCILKEPSPOMOKNITAGOSIGIALLILILATIPS INGHFUNKINSDACMSGRRYKCAAGGRARIRIFFS INGHFUNKINSDACMSGRRYKCAAGGRARIRIFFS INGHFUNKINSDACMSGRRYKCAAGGRARIRIFFS INGHFUNKINSDACMSGRRYKCAAGGRARIRIFFS INGHFUNKINSDACMSGRRYKCAAGGRARIRIFFS INGHFUNKINSDACMSGRRYKCAAGGRARIRIFFS INGHFUNKINSDACMSGRRYKCAAGGRARIRIFFS INGHFUNKINSDACMSGRRYKCAAGGRARIRIFFS INGHFUNKINSDACMSGRRYKCAAGGRARIRIFFS INGHFUNKINSDACMSGRRYKCAAGGRARIRIFFS INGHFUNKINSDACMSGRRYKCAAGGRARIRIFFS INGHFUNKINSDACMSGRRYKCAAGGRARIRIFFS INGHFUNKINSDACMSGRRYKTHINGHGENIKAT KECALARLUTHLORLOQUEAK APOGRARICITSGRSCHIPHOOLOGIALLIP PAGTAGONYPLKAGSELRI IPRORVOSC GTEGAPSGRTGASGRCHIPHOOLOGIALLIP PROTAGONYPLKAGSELRI IPRORVOSC OHANNOSTINDIGSTVAKTYULIL GHUVYSIALALQXYCHIRLAGSCDPRAYKYKTTWINGLIPLALLI ELAVASVARAPISLIVULSAVAVAGALGIATIFGAKDAMIVV VANAAGAULULSIOONIOLDYPIPYVMCVANATAVQARILGE ELAVASVARAPISLIVULSAVAVATATITICISKKKKOM VERVLENTIKA ASQAYDSSLIASVOYILLITTIATRAGIFYLDFIGSDUHHOUT VANAAGAULULSIOONIOLDYPIPYVMCVANATAVQARILGE IRVENSSAFELVERITURALTITATAGAIFYLDFIGSDUHHOUT ALGCLIAFIGUVELITRIKKEY IPREPY ISMAAMPROGNOMMIDKOM TOPSILASSTSTALENDONISEIYAPATLEVMQERGGRASGAG VPYKVLEHTIKA ASQAYDSSLIASVOYILDOSTIATIVARACU ORPHYSPERMININGAACHIPTARIAGADVARDRAGONIDRI RTHIGSSFFRREDSSAMESYDVIANOGVUDOSGAVIKAGOPAG DIPKYCPRIVYOYAPAGALGOIPTSEEHPULITARIAD NPRKHERAABVYFFTTNIVALISEDHVULTARIADOR TIRIGGSTHAPFITORFITINDALISIANAATARTTOVULD SGGGUTHAVPITGEFTHNIVALISHISHAVA	ł	İ		CRIIVHFMWEDVOORGRVMGVNPYII.KKNMTI.MTNUEVAATI.GV
6358 2009 1040 ASDALHSLEAPPURELNSRAPATMTEGAISFAKOPLAGGIAA AISKTAVAP IERVELLLOQUHASKOTADKOYKGIVUGT VRIPK COGNLSFMERILADUR TYPPTOLAIMAPREVKOI PLOGOVICHT OPREY PAGRILASGGAAGATSLCFVYPLDPARTRIAADVCKSGTE REFFREIGDCLVKITKSDGIRGIAGGEVSVGGIITYRAYFGUY DTAKGRIPDPRINTHIVVSMMIAQTVTAVAGVVSYPPDTVRRRM MQSGRKSADINYTSTUDCHRKITFEBEGGKAFFKGAMSHVLRGMC GAFVULVUDELKKVI 6359 98 1086 VCRQEEEKKKEDCLPSSHPYISDSKSIQKSELIGLLKTYNCYHE GREFGLOLGKERSPONGNITTAGGESIQPHIKASSTOSS GPLERAEERPOLIMTRISASCMSCRPRKCRAPGEAGRIRHIRES INGHYNHKTSVFTPAYGSVTNWAWSTWTTLQVLITLLINKPRV EDGDSFALIYVHESGERTKLKDCEYPLISAILIGGCEKTARII MKRQALRITMQALEGUVEAK 6360 1 34S GTRRAVPSTLEEVVLPPRSGCEVPHINSITINSKVSFKITLTSDP RLPYKVLSVPESTPFTAVLKFAAEFKVDASTAIITTGGIGIN PAGTAGNVYLKHGSELRI IPRDRVGSC 6361 615 158 RPGLGGLQHCKLAPDAGNNECRFHGELHAITRSTHRGKFMSIMG FROITHTELPDSSDAVALGADIAANTASTHRGKFMSIMG APGRWRQITTSQEFCHPIQGRCTFTDDGETLHIQAGDALMLPA NSTGINDTGEVKKTYVLILL 6362 350 1576 TTMOGSHSAALKLQQLPPTSSSAVSEASFSYKENLIGALLAIF GHLVVSTALAILOXYCHIRLAGSKOPRAYFKTKYMMGLIFLINGIG ELGVPASYAFAPISLIVVLSVASVIASIAGIIFICEFEMKPKDF LRRYVLSVCGGLAVCTYLLVTFANSHERMTGGHTHLGY ALGCLIAFLAVFLITRNRKKZIFPEYISDERMHOMMIDKOM TVOPBLKARSSYGALENDNISEIYAPATLPVMGEHGSRSASG VPYWLERITKKB RYPMEHGIVKONNOMERI WQVVSKODQUTFGEBEHPULGPAD NPRKNERBASVYALSINGOQUTFALTERAQVYLIPDGS TIEIGPSRFAAPFLLFRPDLIGESSGGIHEVLVFAIQKSDMIRGTRYLGE PRINSSEFEIVKAIKERGCVISNONOMETHICERAQVYLIPDGS TIEIGPSRFAAPFLIFRPDLIGGSTLFREGOVYLIPDGS TIEIGPSRFAAPFLIFRPDLIGGSTLFREGOVYLIPDGS TIEIGPSRFAAPFLIFRPDLIGGSTLFREGOVYLIPDGS TIEIGPSRFAAPFLIFRPDLIGGSTLFREGOVYLIPDGS TIEIGPSRFAAPFLIFRPDLIGGSTLFREGOVYLIPDGS TIEIGPSRFAAPFLIFRPDLIGGSTLFREGOVYLIPDGS TIEIGPSRFAAPFLIFRPDLIGGSTLFREGOVYLIPDGS TIEIGPSRFAAPFLIFRPDLIGGSTLFREGOVYLIPDGS TIEIGPSRFAAPFLIFRPDLIGGSTLFREGOVYLIPDGS TIEIGPSRFAAPFLIFRPDLIGGSTLFREGOVYLIPDGS TIEIGPSRFAAPFLIFRPDLIGGSTLFREGOVYLIPDGS TIEIGPSRFAAPFLIFRPDLIGGSTLFREGOVYLIPDGS PRYNKRERAABAVFFTTRVDALFIJENGAUSLSJATGGRTTGVVUD SOGOVTHAVPIVEGFAAPHSINRIDIAGROVSFILETERAQVYLIPDGS DPHSSSEFEIVKALISINGOVETIETERAQVYLIPDGS DPHSSSEFEIVKALISINGOVETIETERAQVYLIPDGS DPHSSSEFEIVK	İ			DEGILSDDHGLAAALWRTFFNRKCEDPRHIELIAVEVUDVOTOVI.
ASSALHSLSAPVIELISSRSARRPATMTEGALISFAKDPLAGGIAA AISKTAVAP IERVELLIQUOVIANSKOILADVIGIUDGU VRIPK EOGYLSFMRGNLANVIRYPTOALINFAFKDKYKOI PLGGVDKHT OPRKYFRGRULANVIRYPTOALINFAFKDKYKOI PLGGVDKHT REFRGLGDCLVKITKSBGIRGLYGGFSVSVGGI I YRAAYRGVV DTAKGRLEDPENTHIVVSKMIAQTVTAVAGVVSYPPGTVARRM MOSGRKGADINTYTOTUOKRIKTPEDEGGKFFKGAMSHVLIRGMG GAFVIVLYDELKKVI CVRQBEEKKREDCLPSSHVPISDSKSIOKSELLGLIKTYNCYHE GKSFGLRHREEGGILIEGLINIAMGLRRPIRLOMODDEGUYHL GKSFGLRHREEGGILIEGLINIAMGLRRPIRLOMODDEGUYHL FSTSWMPRRPSPCCILKEPSPONONITJAGGFOYHKABSSTDSS GPLEBAEEAPQLMRTKSDASCMSQRRPKCRAPGEAGRIRRIRFS INGHYNHKISVSTTATYSUTSTUTUVASSITTTLQVLILLINKFRV EDGPSSFALVIVHESGERKKLGCEYPLELHGGCEKLARIF LMRADLGVEVPHEVAGYIKFEMVEVDSFVELKEBEBERIIKLT MKRQALRITHAQALEQLVEAK 6360 1 345 GTRGAVPSTLEEVVLDSPRSCRVFMINGTTMSKVSFKTLTSDF RAPTAGNVFLKHGSELRI I PPDRVGSC AFGAVPSTLEEVVLDSPKSCRVFMINGTTMSKVSFKTLTSDF RAPTAGNVFLKHGSELRI I PPDRVGSC 6361 6361 615 158 RPGGGGLGHCALARPGAGNRRCRFHGRIHALTRSTHRGKPMSIMQ PKDTLNTPLPDSSPVAVELGAPIAVASTLSVERINDOVETGIMAC APGRWRQTTSQBFGHFIQGRCTFTPDDGETLHIQAGDALMLPA AFGRWRQTTSQBFGHFIQGRCTFTPDDGETLHIQAGDALMLPA AFGRWRQTTSQBFGHFIQGRCTFTPDDGETLHIQAGDALMLPA AFGRWRQTTSQBFGHFIQGRCTFTPDDGETLHIQAGDALMLPA FRYNLSSVGCGLAVVGTYLLVTFARNSHVRTWRWGLFLIMLIG ELGVPASYAPAPLSLIVPLSAVSVEASFTYKTWMIGLIALIAF GHLVVSILALIAGSXDPRAFFTKYTWWGRNTUNLIGALIAFF ALGCLIAFLGVFLITTRNKKZFIPFFTYSMDAMPGMOMMIDKGM TVOPSILARSYGVLESTTLATAGAGTPTGGEVTHIUGHTUNLT ALGCLIAFLGVFLITTRNKKZFIPFFTSMDAMPGMOMMIDKGM TVOPSILARSYGVLESTTLATAGAGTPTGGEVDHILICH ALGCLIAFLGVFLITTRNKKZFIPFFTSMDAMPGMOMMIDKGM TVOPSILARSYGVLESTTLATAGAGTPGGEVTLKAPGAF DOLPKYCPPNYVGRPKHVWAMGALGEGIPTGGRAEEHRGLLSI RPFWBHGIUVGNMDMERINGINGSVIKAGFAG DOLPKYCPPNYVGRPKHVWAMGALGEGIPTGGRAEHRGLLSI RPFWBHGIVGNMDMERINGINGSVIKAGFAG DOLPKYCPPNYVGRPKHVRWAGGALEGGIPTGGRAEHRGLLSI RPFWBHGIVGNAMDMERINGINGSVIKAGFAG DOLPKYCPPNYVGRPKHVRWAGGALEGGIPTGGRAEHRGLLSI RPFWBHGIVGNAMDMERINGOTYSKGOLGTSERHPULTERAPDY HPRKNRBRAABVFFTTNOVALPINFINGMONSTFIRMYLTRAPOR PRINKRBRAABVFTTTNOVALPINFINGMONSTFIRMYLTRAPOR DOLPKYCSPFTRUKAALISHQNOGTISTERPOVILDEAPL NRRKRBRAABVFTTTNOVALPINFINGMONSTFIRMYLTRAP	l.			DSMNGEDLLLTGEVSWRPLVEKNPOSILKPHSPTVNDRGI.
AISKTAVAP IERVKLLIQVÇHASKQIADKYKGIPLGEVOKHT BEGGLISFIRGILADVIRYPTQALINFAFRQYKQIPLGEVOKHT GPRYPAGRILASGGAAGATSLCPVPPLDPARTRLAADVGKSGTE REFEGLOCUVLITKSDGIRGLYQGFSVSVQGIITKAAYRGVV DTAKGHLPDPKNTHIVVSMILAQTVTAVAGVUSYPPDTVRRRM MQSGRKSADINYTGTVDCKRKIFEBEGGRFFKGAMSHVLRGMG GAFVULVUDELKKVI GAFVULVUDELKKVI GAFVULVUDELKKVI GAFVULVUDELKKVI GRAFVILVIDELKEVI GRAFGLARIBEEGGTLIIEGLLINIAMGIRAFIRLOMGDDREQVHL PSTSWMPRPSCPLKEPSPQNGNITAQGPSIQPVHKABSSTDGS GPLEEAEBAPQLMRTKSDASCMSQRPKCRAFGEAGRIRRIRFS INGHFINIKTSVETPAYQSVITNVAVSITATLQVILLLINKFRV EDGPSSFALVIVIESGERTKLKDCEVPLISSILIGGCEKIARII IMKEQALGUVEVBVAQVILKPSPVDLOSTKLEBEEGILIKI MKEQALRITULQRLEQLVEBK G160 1 345 GTRGAPPSIEEVVLEPRSCRVFMILIGGTTMSKVSFKITLTSDP RLPYKVLSVPSSTPFTAVLKFAAEEFKVPAATSAIITNDGIGIN PAQTAGNVFLKHGSELRIIPDRAVSGSC AFGRENGRITTGSFCHPTGGRCFFFGBLHALTRSTHRGKPMSIMQ FKDTLINTFLEDSSPAVVLIGAPIAVASTLSVERINDGVSTGIMAC AFGRENGRITTGSFCHPTGGRCFFFGBLHALTRSTHRGKPMSIMQ FKDTLINTFLEDSSPAVVLIGAPIAVASTLSVERINDGVSTGIMAC AFGRENGRITTGSFCHPTGGRCFFFGBLHALTRSTHRGKPMSIMQ FKDTLINTFLEDSSPAVVLIGAPIAVASTLSVERINDGVSTGIMAC AFGRENGRITTGSFCHPTGGRCFFFFGBLHALTRSTHRGKPMSIMQ FKDTLINTFLEDSSPAVVLIGAPIAVASTLSVERINDGVSTGIMAC AFGRENGRITTGSFCHPTGGRCFFFGBLHALTRSTHRGKPMSIMQ FKDTLINTFLEDSSPAVVLIGAPIAVASTLSVERINDGVSTGIMAC AFGRENGRITTGSFCHPTGGSCTPFTGGRCFFFTGBLHALTRSTHRGKPMSIMQ FKDTLINTFLEDSSPAVVLIGAPIAVASTLSVERINDGALLAIF CHLVVSIALINLQXYCHIRLAGSKOPRAYFTKTWMLGLFIMLUS GLHVVSIALINLQXYCHIRLAGSKOPRAYFTKTWMLGLFIMLUS FFLLMMLVSILLVSIALIVVSIASAIGGIFTGKEMKPKDF LRRYVLSFVGGLAVVGTYLLVTFARNSHANNIVVILLLVALLIGSMTVV TVXAVAGHLVISTGGNLGUPFTFVMVVATAVAYQAAPLSQ ASMYDSSLLASVGYTLSTTTATTAGAIFYLDPIGGDVLHICVF ALGCLIAFLGVFLTFTRAVKSIPPEPTSWAAVAYQAGAPLSQ ASMYDSSLLASVGYTLSTTTATTAGAIFYLDPIGGBVLHICVF ALGCLIAFLGVFLTFTRAVKSIPPERFYNVARYAHVAYAYQAAPLSQ ASMYDSSLLASVGYULSTGARMHSIMRIDAGROVSFRIRLYTERAPL RYMBHGIVKONNOMERINGVYVSKOOLOTSGRIPVLUFAPLO NPRKKRERAABVFFFTTNVALFINGMOUNGSGVIKAGFAG DQIPKYCPRYVARPKHVRWAGALEGGIFTGFKAEERHGLLSI RYPMEHGIVKONNOMERINGVYVSKOOLOTFSERHPULLTGAPL RYTSMIGGSILASLDTFKKMWSKKEVEEDGARSILRKTF ARTHGS	6358	2009	1040	ASDALHSLSAPVLRLSSRSAARPATMTEOAISFAKDRLAGGTAA
BOGYLSFWEGHLANUTRYFPTOALNFAFRDRYKGIFLGGUNDHT OPRHYFAGHLASGGAAGRISLGFYNPIDAGFRIADADVEKSGTE REFRGLDCLVKITKSDGIRGLYGGFSVEVGGIIVERAAYPGUV DTAKGKLIPPDRITHIVVSWMLAGTVTAVAGVUSTE REFRGLDCLVKITKSDGIRGLYGGFSVEVGGIIVERAAYPGUV DTAKGKLIPPDRITHIVVSWMLAGTVTAVAGVUSTERAM MQSGRKGADIMYTGTVDCMRKIFPDEGGKAFFKGAMSNVLRGMM GAFVLULIDELKKVI 6359 98 1086 VCRGEESKMERDCLFSSHVPISDSKSIQKSELLGLLKTYNCYHE GKSFOLRHREEGGILIEGLINIAMGLREPIRLQMQDDREQVHL PSTSWMPRRFSPCJLKEPS PORNITAGGFOEDAGRIRDIKEFS INGHVYNIKTSVPTPAAYGSVITNURVMSTTTLQMYDDREQVHL LINGHFYNIKTSVPTPAAYGSVITNURVMSTTTLQMYDDREQVHL LINGHFYNIKTSVPTPAYGSVITNURVMSTTTLLINKPRV EDGPSFALYIVHESGERTKLKDCEYPLISILINGFCEKIARIF LMEADLGVEVPHVAQYIKFEMPVLDSFVEKLKEBEBERIIKLT MKRQALRITMLQKLEGLVEAK 6360 1 345 GTRGAVPSTLEEVVLDFRSCRVFWINISGITMSKVSFKITLTSDP RADTAGNVFLKHGSELRIIPPDRGSC PROLIGHOLGALAFDAGNKRCFFRGELHALTFSTHRGKPMGIMG PROTIANTPLEPDSS PVAVPLGAPLAVATSALSVERNDGVETGIMAC APGRWRRQITSQBFCHPIQGCTPTPDDGETLHIQAGALMLPA NSTGIMDIQETVAKTYVLIL 6361 6362 350 1576 TIRLDGSHSAALKLQOLPFTSSSSAVEASFSYKENLIGALLAFF GHLVVSILALALGXYCHIRLGSSUPPARTYKTWWLGLFIMLLG ELGVPASVAPAPLISLIVPLSAVSVIASAIIGIIFIXEKWKKDF LRRYVLSFVGCGLAVVGTYLLVTFARNSKMTGNVTRHLVSR PFLLMMLVBILLSTGCNLGLDYFTSFRTWGRONTPHLVSR PFLLMMLVBILLSTGCNLGLDYFTSFRTWGRONTPHLVSR PFLLMMLVBILLSTGCNLGLDYFTSFRTWGRONTPHLVSR PFLLMMLVBILLSTGCNLGLDYFTSFRTWGRONTPHLVSR PFLLMMLVBILLSTGCNLGLDYFTSFRTWGRONTPHLVSR PFLLMMLVBILLSTGCNLGLDYFTSFRTWGRONTPHLVSR PFLLMMLVBILLSTGCNLGLDYFTSFRTWGRONTPHLVSR PFLLMMLVBILLSTGCNLGLDYFTSFRTWGRONTPHLVSR PFLLMMLVBILLSTGCNLGLDYFTSFRTWGRONTPHLVSR PFLLMMLVBILSTGCNLGLDYFTFTNDFGEDVLHICGF ALGCLIFLSVFLITTRNKKRIPFFTTNVPALFISMGAVLSLYATGRTTGVVLD SGGGVTRAPFITEGFRAPHLIFTRDLIGESGGIHBGLLSI RYPMEHGIVKONNDMERINGVYVSKODLOFFSERHVLIFREGT DPHSSSEFFUKALIFREGTVALFREGT PRESSEFFUKALIFREGTVALFREGT PRESSEFFUKALIFREGTVALFREGT PRESSEFFUKALIFREGTVALFREGT PRESSEFFUKALIFREGTVALFREGT PRESSEFFUKALIFREGTVALFREGT PRESSEFFUKALIFREGTVALFREGT PRESSEFFUKALIFREGTVALFREGT PRESSEFFUKALIFREGTVALFREGT PRESSEFFUKALIFREGTVALFREGT PRESSEFFUKALIFREGTVALFREGT PRENKRERABAVFFTETNVALFISHGNGUNSFILKTFGT PRESSE				AISKTAVAPIERVKLLLOVOHASKOIAADKOYKGTVDCTVRTPK
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REFRICTOCLVKITKSDGIRGLYQGFSVSVQGIITYRAAYBQUV DTAKGMLDPKNTHIVVSWMIAQTVTAQVGVSYPPDTVRRRM MQSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSWVLRGMG GAFVLVLYDELKKVI OVERGEERMKEDCLDSSHVPISDSKSIQKSELLGLLKTYNCYHE GKSFQLRHAEESGTLIIEGLLMIAWGLRFIRLOMDDREQVHL PSTSWMPRPSCPLKESPDNONITAGOPSIQPVHARASSTDSS GPLEEABEAPQLMRTKSDASCMSQRRPKCRAPGEAQRIRRHEFS INGHFYNHKTSVFTPAYGSVTNVRVNSTMTILQVILLLINFRRV EDDPSSFALYIVHBSGERTKLKDCSFYDLISRILHGPCSKLARIF LMBADLGVSVPHEVAQYIKPEMPVLDSFVSKLKEEBEREIIKLI MKFQALRITMLQRIEGUVEAK 6360 1 345 GTRGAVPSTLESVVLPPBSGCVFWIHISGTTMSKVSFKITLTSDP RLPYKVLSVPSTDFTAVLKFABEFKVDAGTAINTDGIGIN PAQTAGNVFLKHGSELRIIPRDRVSG FREIGGLOHCALAPQAGNRRCFHGRLHAITRSTHRGKPMSIMQ FKDTLMTLPDSSSVAVPLGAPIAVASTLSVERINGGVFTGIWAC APGRWRRQITSQBFCHFIQGRCTPPDDGETLHIQAGDALMLPA NSGINDIGTSVRKTVYLLL 6362 350 1576 TIMDGSHSARLKLQQLPPTSSSSAVSEASFSYKENLIGALLAIF GHLVVSIALALQXYCHIRLAGSKDPRAYFFTTWHALGLFLMLLG GHLVVSIALALQXYCHIRLAGSKDPRAYFFTTWHALGLFLMLLG GHLVVSIALALQXYCHIRLAGSKDPRAYFFTTWHALGLFLMLLG GHLVVSIALALQXYCHIRLAGSKDPRAYFFTTWHALGLFLMLLG FLAVFASVAPAPLSLIVHYFYKSKNANUFULLLVALLGSMTVV TVKAVAGMLVLSIQGNLQLDYPIFYVMFVCMVATAVYQAAFLSQ ASQMYDSSLLASVYTLSTTAATAGAFYLDTGEDVLHICMF ALGCLIAFLGVFILTRNKKIPPEPFIVILLLLAGMTVV TVKAVAGMLVLSIQGNLQLDYPIFYVMFVCMVATAVYQAAFLSQ ASQMYDSSLLASVYTLSTTAATAGAFYLDTGEDVLHICMF ALGCLIAFLGVFILTRNKKIPPEPFIVILLLEAPLL NPRKREERAAEVFFETTNVPALFISMQAVLSLVARGRTGVVVLD SGGGVTHAVPIYRGFMPMSIKMICHAGNVARRGTRTGVVLD NPRKNEERAAEVFFETTNVPALFISMQAVLSLVARGRTGVVLDDG TTEIGPSFRAPELLFRPDLIGESFSGIHEVLVFARGKSTMDLR RTLEFSNIVLSGSSTLFKGFGGRALSSVKLAPKDVVKRTSAPQE RYSTWIGGSILASLDTFKKMWSKKEYSEDGASHIRKTF RTLEFSNIVLSGSSTLFKGFGGRALSSVKLAPKDVVKRTSAPQE RYSTWIGGSILASLDTFKKMWSKKEYSEDGASHRKTFI RYPMEHGIVKDWNDMERIMQVYYSKDQLQTFSBEHPVLLTRAPQU NPRKNEERAAEVFFFTFNVPALFISMQAVLSLVATGRTTGVVLD SGCGVTHAVPIVEGFPMYGARGALGSDIFFICPKABEHRGLLSI RYPMEHGIVKDWNDMERIMQTVYSKDQLQTFSBEHVLLTRAPQU RYSTWINGSSTLASSPFPREDSSAMSSYDVIANGAVLSLVATGRTTGVVLD SGCGVTHAVPIVEGFPMYGARGALGSDIFFICPKABEHRGLLSI RYPMEHGIVKDWNDMERIMQTVYSKDQLGTFSBEHVLLTRAPQ DPHSSSEPERTUKARGRAMSSYDVIANGAUSLSVATGRTTGVVLD SGCGVTHAVPIVEGFAMFISTMRIDIAGRDUSRPLRIVL	1	<u> </u>		OFWRYFAGNLASGGAAGATSLCFVYPLDFARTRLAADVGKSGTR
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GKSFQLRHREEGTLIIBGLIIAMGLRPPIRLQMQDREUMH PSTSWMPRRPSCPLKEPSPQNGNITAGGSIQPVIKARSSTDS GPLEEAERAPQLMRYKSDASCMSQRIRRHRFS INGHFYNHKTSVFTPAYGSVTNVRVNSTMTTLQVLTLLLNKFRV EDGPSEFALIVHREGGRTKLKDCEYPLISRILHGPCEKLARIF IMBADLGVEVPHEVAGYIKFRENVPLDSFYGEKLKEEEREIIKLIT MKKPQALRLTHLORLEQLVEAK GTGRGAVPSTLEEVVLPPRSCRVFWIHIGTTMSKVSFKITLJTSDP RLPYKVLSVPESTPFTAVLKFAREEFKVPAATSAIITNDGIGIN PAGTAGNVFLHKGSELRIIPRDRVGSC 6361 615 158 RFGLGGLGCHCALAPDGANRRCERFHGRLHALTRSTHRGKPMSIMQ FKDTLMTPLPDSSPVAVPLGADIAVASTLSVERHDGVETGIMAC APGRWRRQITSGSEFCHFIQGRCTFTPDDGGTLHIQAGDALMLPA NSTGIWDIQETVRKTYVLII 6362 350 1576 TINDGSHSARLKJQQLPTSSSSAVSEASFSYKENLIGALLAIF GHLVVSIALNLQXVCHIRLGSKDPAYFKTKTWLGLFLMLIG ELGVFASVAFAPLSLIVPLSAVSVIASAIIGIJFIKSKMFXDP LRYVLISFVGCGLAVVGTYLLVTFAPNSHEKMTCENVTRHLVSM PFLLYMLVSILIFCLLIYFYKERNANNIVVLLLVALLGSMTVV TVKAVAGMLVLSIGGNLQLDYPIFYVMFVVWATAVVQAAFISQ ASGMYDSSLIASVGYLISTTIATTAGAIFYLDFIGEDVLHICMF ALGCLIAFIGVFLITRNRKKJIFPEPYISMDAMPGMONMHDKGM TVOPBLKASFSYGALENNDNISEIYAPATLFVMQEHEGRRSASG VPYRVLENTKKR 6363 21 1201 RRTRLGSSFPRRRDSSAMESYDVIANQPVVIDNGSGVIKAGFAG DQIPKYCPPNVVGRPKHVRVMAGALEGDIFIGFRAEEHRGLLSI RYPMBEIGIVKOWNDMERIMQVVSKDQLQTFSBEHPVLLTEAPL NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYRGFRAPHSIMRIDIAGRDVSRFLELVILGSDMDLR RTLFSNIVLSGGSTLFKGFGDRLLSEVKKLAPKDVKKIRISAPQE RLYSTWIGGSILASLDTFKKRWVSKKEYEBDGARSIHKRTF ODIPKYCPPNVVGRPKHVRWMGALEGDIFIGFRAEEHRGLLSI RYPMEIGIVKOWNDMERIMQVVYSKDQLOTFSBEHPVLLTBAPL NPRKNERSABEPFETFNVPALFISMQAVISLYATGRTTGVVLD SGDGVTHAVPIYRGFRAPHSIMRIDIAGRDVSRFLELVIRKEGY DPHSSSEPEIVKAIKERACYLSINPQKDETLEEKAQYVLEDGS TREIGGSFFRRPDSSAMESYDVIANQPVVIDNGSGVIKAGFFAG DQIPKYCPPNVVGRPKHVRWMSKKEYEBDGARSIHKRTF RTRLGGSFFRRPDSSAMESYDVIANQPVVIDNGSGVIKAGFFAG DQIPKYCPPNVVGRPKHVRWMSKKEYEBDGARSIHKTF RTRLGGSFFRRPDSSAMESYDVIANQPVVIDNGSGVIKAGFFAG DQIPKYCPPRVVGRPKHVRWMGALEGDIFIGFRAEHRGLLSI RYPMEHGIVKOWNDMERIMQVVYSKDQLOGFSEEHPCULVER SGDGVTHAVPIYRGFAMPHSIMRIDIAGROVSLYATGRTTGVVLD SGDGVTHAVPIYRGFAMPHSIMRIDIAGROVSLYATGRTTGVVLD SGDGVTHAVPIYRGFAMPHSIMRIDIAGROVSLYATGRTTGVVLD SGDGVTHAVPIYRGFAMPHSIMRIDIAGROVSLYATGRTTGV	L			GAFVLVLYDELKKVI
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GPLEEAEEAPQLMRTKSDASCMSQRRPKCRAPGEAQRIRRHRFS INGHFYNHKTSWYTPAYGSTMTVAVMSTMTTLQVLTLLINKFRV EDDPSEFALYIVHESGERTKLKDCBYPLISHLINGPCEKLARIF LMEADLGVEVPHEVAQYINFEMPVLDSFVEKLKEEBEREIIKLT MKFQALRITHLQRLEQLVEAK MKFQALRITHLQRLEQLVEAK MKFQALRITHLQRLEQLVEAK RLPYKVLSVPESTPFTAVLKFAAEEFKVPAATSAIITNDGIGIN PAQTTAGNVFIKHGSELRIIPROVGSC 6361 615 158 RPGLGQLQHCALAFQAGNRRCRFHGRLHALTRSTHRGKPMSIMQ FKDTLNTPLPDSSPVAVPLGAPIAVASTLSVERNDGVETGIWAC AFGRWRQITSGSEGTHFIQGRCTFTPDDGETLHIQAGDALMLPA NSTGINDIQGTVRKTYVLIL 6362 350 1576 TIMDGSHSAALKLQQIPTSSSSAVSEASFSYKENLIGALLAIF GHLVVSIALNLQKYCHIRLAGSKDPRAYFTKTWWLGLFIMLLG ELGVFASYAFAPLSLIVPLSAVSVIASAIIGIIFIKEKWKPKDF LRRYVLSFVGCGLAVVGTYLLVTFAPNSHERMTGENVTHALVSW PFILLYMLVSILIFCLLLYFYKEMINIVVLILLVALLGSMTVV TVXAVAGMLVLSIQGNLQLDYPIFYVMFVCMVATAVYQAFLSQ ASQMYDSSLLASVGYILSTTIALTAGAIFYLDPIGEDVLHICMF ALGCLIAFIGVFLITRNKKY: 1PFEPYISMDAMPGMQNMHDKGM TVQPBLKASFSYGALENNDNISEIYAPATLPVMQEBHGSRSASG VYPKVLHTYKKE DDIPKYCFPNYVGRPKHVWAGALEGDIFIGFKASEHRGLLSI NPRKNERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRVSFFLRLVLRKEGY DPHSSSEFEIVKA KERRCYLS PROKETHERVAYYLPDGS TIEIGPSRFRAPFILFRPDLIGEESEGIHEVLVFAIQKSDMDLR RTLFSNIVLGGSTLAGLDTFKKMWYKKEYEDGARSHRKTF ELSTWIGGSILAGLDTFKKMWYKKEYEDGARSHRKTF ODIPKYCFPNYVGRPKHVWAGALEGDIFIGFKAEEHRGLLSI RTPMERGISVLOMDMERINGVYVSKODQLOTFSEEHPVLLTEAPL NPRKNERAAEVFFETFNVPALFISMQAVLSLVATGRTTGVVLD SGDSVTHAVPIYEGFAMPHSIMRIDIAGRUSGFLIRKTF PLYSTWIGGSILAGLDTFKKMWYKKEYEDGARSHRKTF PLYSTWIGGSILAGLDTFKKMWYKKEYEDGARSHRKTF ODIPKYCFPNYVGRPKHVWAGALEGDIFIGFKAEEHRGLLSI RTPMERGISVKDMIMMERINGVYVSKOQLOTFSEEHPVLLTEAPL NPRKNERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGOGVTHAVPIYEGFAMPHSIMRIDIAGRUSGFLIRLYLREGY DOIPKYGFPNYVGRPKHVWAGALEGDIFIGFKAEEHRGLLSI RTPMERGISVKDMIMMERINGVYVSKOQLOTFSEEHPVLLTEAPL NPRKNRRAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGOGVTHAVPIYEGFAMPHSIMRIDIAGRUSGFLIRLYLREGY DFHSSSEFEIVKALKERACYLSLNDQKDSTFLERLYLREGY DFHSSSEFEIVKALKERACYLSLNDOKDSTLETKRAQYYLDGGS DFHSSSEFEIVKALKERACYLSLNDOKDSTLETKRAQYYLDGGS DFHSSSEFEIVKALKERACYLSLNDOKDSTLETKRAQYYLDGGS				GKSFQLRHREEEGTLIIEGLLNIAWGLRRPIRLOMODDREOVHL
INGHYNHKISUTIPAYGSUTNIVUNSTMITLQUILILLINKPRU EDGPSFALVIVIESGERTKLKDCEYPLISRILHGPCEKIARIF LMEADLGUEVPHEVAQYIKFEMEVLDSFYEKLKEBEEREIIKLI MKRÇALRITHLQRLEGLUEAK GTRGAVPSTLEEVVLPPSCERVEWHISGTTMSKVSFKITLTSDP RLPYKULSVPESTPFTAVLKFAAEEFKVPAATSAIITNDGIGIN PAQTAGNVFLKHGSELRIIPRDRVGSC 6361 615 158 RPGLGQLQHCALAPQAGNRRCRPHGRLHALTRSTHRGKBMSIMQ FKDTLNTPLPDSSDVAVPLGAPTAVASTLSVEHNDGVETGIWAC APGRWRRQITSQEFCHFIQGRCTFTPDDGETHHQAGDALMLPA NSTGINDIGSTVKKTVVLIL GHLVVSIALLALAF GHLVVSIALLALAYCHIRLAGSVDPRAYPKTKTWWLGLALAIF GHLVVSIALLALAYCHIRLAGSVDPRAYPKTKTWWLGLFLMLLG LGVPASYAPAPILSLIVPLSAVSVIASAIIGIIFIKEKKPKDF LRRYVLSFVGCGLAVVGTVLLVTFAPNSHEKMTGRNVTHHLVSW PFLLYMLVRIILFCLLLYFYERNANNIVVILLIVALLGSMTVV TVKAVAGMLVLSIQGNLQLDYPIFYVMPVCMVATAVQAAFLSQ ASGMYDSSLIASVGYLISTTIATAGAIFYLDFIGEDVLHICMF ALGCLIAFLGVIITNNKKY, PIPPFYISMDAMPGMQMMHNKGM TVQPBLKASFSYGALENNDNISEIYAPATLPVMQEEHGSRSASG VPYRVLEHTKKE 6363 21 1201 RRTRLGSSFFRRRDSSAMESYDVIANQPVVIDNGSGVIKAGPAG DQIPXYCFPNYVGRPKHVRVMAGALEGIFTOPKAEEHRGLLSI RYPMBGIVKDMNDMERIWQVYSKDQLQTFSEEHPVLLTEAPL NPRKNRERAABVFFFTTNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRIVLRKEGY DPHSSSEPFIIVKAIKERGYSINPQKDETLETEKAQYYLDGS TIEIGPSRFRAPELLFRODLIGERSEGHHEULVFAIQKSDMDLR RTLFSNIVLSGGSTLFKGFGDRLLSEVKKLAPKDVKIRISAPQE RLYSTWIGGSTLASLADTPKKMVKKEYEEGGARSIHKKTF DQIPXYCFPNYVGRPKHVRVMAGALEGIFTGPKAEEHRGLLSI NPRKNRERAABVFFFTTNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRIVLRKEGY DPHSSSFFEIVKAIKALSLADTPKKMVKKYEEGGARSHIRKTF RTPMEHGIVKOMMDMERIWGVYYSKDOLOFTSEEHPVLLTEAPL NPRKNRERAAEVFFFTFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRIVLEREGY DPHSSSFFEIVKMINDMERIWGVYYSKDOLOFTSEEHPVLLTEAPL NPRKNRERAAEVFFFTFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRIVLEREGY DPHSSSFFEIVKAIKARGAVLSINPQKOETLETEKKAQVYLDGS GDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRIVLEREGY DPHSSSFFEIVKAIKARGAVLSINPQKOETLETEKKAQVYLDGG GDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRIVLEREGY DPHSSSFFIYARAIKARGAVLSINPQKOETLETEKKAQVYLDGG GDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRIVLEREGY DPHSSSFFEIVKAIKARAGVITERADTIVLRKEGY DPHSSSFFIYM	l I	,		PSTSWMPRRPSCPLKEPSPONGNITAOGPSIOPVHKAESSTDSS
EDGPSFFALYIVIESGERTKLKDCEYPLISRILHGPCEKIARIF LMEADLGUEVPLEVAQYIKFEMPVLDSFVEKLKEEBEREIIKLT MKFQALRLTMLQRLEQLVERK 6360 1 345 GTRGAVPSTLEEVVLIPRSCRVEWHISGTMSKVSFKITLTSDP RLPYKVLSVPSSTPFTAVLKRABEFKVPAATSAIITNDGIGIN PAQTAGNVFLKHGSELRIIFRDRVGSC 6361 615 158 RPGLGQLOHCALAPQAGNRRCRFHGRIHALTRSTHRGKPMSIMQ FKDTLMFPLPDSS PVAVPLGADIAVASTLSVEHNDGVETGIWAC APGRWRRQITSQBFCHPIQGCTFTPDDGETHHIQAGDALMLPA NSTGIMDIGETVKKTYVLIL 6362 350 1576 TTMDGSHSAALKJQQDPPTSSSSAVSEASFSYKENLIGALLAIF GHLVVSIALNLQXYCHIRLAGSKDPRAYFKTKTWMLGLFLMLIG ELGVFASYAFADISLIVPLSAVSVIIASAIIGIIFTIKEKWKPKDF GHLVVSIALNLQXYCHIRLAGSKDPRAYFKTKTWMLGLFLMLIG ELGVFASYAFADISLIVPLSAVSVIIASAIIGIIFTIKEKWKPKDF LRRYVLSFVGCGLAVVGTTULTVFADNSEKHAMGENVTHHLVSW PFLLYMLVBIILFCLLLYFYKEKNANNIVVILLLVALLGSMTVV TVKAVAGMUVLSIQGALQUDYPIFYVMFVCMVATAVYQAAFLSQ ASGMYDSSLIASGYGYLISTITAGAIFFUDFIGEDVHLICMF ALGCLIAFLGVFLITRNRKKPIPPFYISMDAMPGMOMMHDKGM TVQPBLKASFSYGALENNDNISSIYAPATLPVMQEHGSRSASG VPYRVLEHTKKB 6363 21 1201 RRTRLGSSFPRRDSSAMESYDVIANQPVVIDNGSGVIKAGFAG DDIPKYCFPNYVGRPKHVRVMAGALEGDIFIGPKAEEHRGLISI RYPMBEGIVKOMDMERIUGVYVSKDOLOTFSEEHPVLLITRAPL NPRKNRERABEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRIVLRKEGY DFHSSSEFFIVKAIKERAGYLNPQNDETERKAQVYLDDGS TIEIGPSRFRAPELLFRDDLIGESEGIHEVLVFAIQKSDMDLR RTLFSNIVLSGGSTLFKFGFGDRLLSEVKLAPKDVKIRISAPQB ELYSTWIGGSILASLDTFKKMWVSKKEYEGOARSIHKKTF RTPSNIVLSGGSTLFKFFGDRLLSEVKLAPKDVKIRISAPQB ELYSTWIGGSILASLDTFKKMWVSKKEYEGOARSIHKKTF DQIPKYCFPNYVGRYKHVWNAGALEGIFIGPKAEEHRGLISI RYPMEHGIVKOMMDERIUGVYYSKDOLOTFSESHPVLLITRAPL NPRKHRERAAEVFFETFNVPALPISMQAVLSLYATGRTTGVVLD SGGSVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRIVLEREGY DFHSSSEFFIVKAIKERAFYLJENGGOFFGERHPGLLTSAPL NPRKHRERAAEVFFETFNVPALPISMQAVLSLYATGRTTGVVLD SGGSVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRIVLEREGY DFHSSSEFFIVKAIKERGYLJSINPQKOETLETKKAQVYLDGS SGGSVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRIVLEREGY DFHSSSEFFIVKAIKERGYLJSINPQKOETLETKKAQVYLDGS SGGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRIVLEREGY DFHSSSEFFIVKAIKERGYLJSINPQKOETLETKKAQVYLDGS SGGVTHAVAIKERGYLJSINPQKOETLETKKAQVYLDGGS				GPLEEAEEAPQLMRTKSDASCMSQRRPKCRAPGEAQRIRRHRFS
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GHLVVS IALNLQKYCHIRLAGSKDPRAYFKTKTWWLGLFLMLLG ELGVFASYAPAPLSLIVPLSAVSVIASAIGIIFIKEKWKPKDF LRRYVLSFVCGGLAVVGTYLLVTFAPNSHEKMTGENVTRHLVSW PFILYMLVEI ILFCLLLYFYKEKNANNIVVLLLLVALIGSMTVV TVKAVAGMLVLS IQGNLQLDYPIFYVMFVCMVATAVYQAAFLSQ ASGMYDSSLIASVGYILSTTIAITAGAIFYLDPIGEDVLHICMF ALGCLIAFIGVFLITRNRKK? IPPEPYISMDAMPGMOMMHDKGM TVQPBLKASFSYGALENNDNISEIYAPATLPVMQEEHGSRSASG VPYRVLEHTKKB 6363 21 1201 RRTRLGSSFPRRDSSAMESYDVIANQPVVIDNGSGVIKAGFAG DQIPKYCFPNYVGRPKHVRVMAGALEGDIFIGPKAEEHRGLLSI RYPMBHGIVKDWNDMERIWQYVYSKDQLQTFSEEHPVLLTEAPL NPFKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS TIEIGPSRFRAPFLLFRPDLIGESSGGHEVLVFAIQKSDMDLR RTLFSNIVLSGGSTLFKGFGDRLLSEVKKLAPKDVKIRISAPQE RLYSTNIGGSILASLDTFKKMWVSKKEYEEDGARSIHRKTF BQIPKYCFPNYVGRPKKWWVSKKEYEEDGARSIHRKFF DQIPKYCFPNYVGRPKKWWVSKKEYEEDGARSIHRKFF DQIPKYCFPNYVGRPKHVRVMAGALEGDIFIGPKAEEHRGLLSI RYPMEHGIVKDWNDMERIWQYVYSKDQLQTFSEEHPVLLTEAPL NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRPLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS	6362	350	1576	TTMDGSHSAALKLOOLDDTSSSSAVSFASESVERILTCALLAYE
ELGYFASYAFAPLSLIVPLSAVSVIASAIIGIIFIKEKWKPKDF LRRYVLSFYGCGLAVVGTYLLVTFAPNSHEKMTGENVTRHLVSW PFLLYMLVBIILFCLLLYFYKEKNANNIVVILLLVALLGSMTVV TVKAVAGMULSIQGNLQLDYPIFYVMFVCMVATAVYQAAFLSQ ASQMYDSSLIASVGYILSTTIAITAGAIFYLDFIGEDVIHICMF ALGCLIAFLGVFLITRNRKKPIPFPPYISMDAMPGMONMHDKGM TVQPELKASFSYGALENNDNISEIYAPATLPVMQEEHGSRSASG VPYRVLEHTKKE RRTRLGSSFPRRDSSAMESYDVIANQPVVIDNGSGVIKAGFAG DQIPKYCFPNYVGRPKHVRVMAGALEGDIFIGPKAEEHRGLLSI RYPMEHGIVKDWNDMERIWQYVYSKDQLQTFSEEHPVLLTEAPL NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS TIEIGPSRFRAPFLLFRPDLIGEESEGIHEVLVFAIQKSDMDLR RTLFSNIVLSGGSTLFKGFGDBLLSEVKKLAPKDVKIRISAPQE RLYSTWIGGSILASLDTFKKMWVSKKEYEDGARSIHRKTF BQIPKYCFPNYVGRPKHVRVMAGALEGDIFIGPKAEEHRGLLSI RYPMEHGIVKDWNDMERIWQVYYSKDQLQTFSEEHPVLLTEAPL NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGGGYTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLDGS	1	· · ·		GHLVVSIALNLOKYCHIRLAGSKDBBAVFVTVTWWIGIEL MILIC
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TIEIGPSRFRAPELLFRPDLIGEESEGIHEVLVFAIQKSDMDLR RTLFSNIVLSGGSTLFKGFGDRLLSEVKKLAPKDVKIRISAPQE RLYSTWIGGSILASLDTFKKMWVSKKEYEDGARSIHRKTF 6364 21 1201 RRTRLGSSFPRRRDSAMESYDVIANOPVVIDNOSGVIKAGFAG DQIPKYCFPNYVGRPKHVRVMAGALEGDIFIGPKAEEHRGLLSI RYPMEHGIVKDWNDMERIWQYVYSKDQLQTFSEEHPVLLTEAPL NPRKNRBRAAEVFFETFNVPALPISNQAVLSLYATGRTTGVVLD SGGGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPOKDETLETEKAOYYLPDGS		Í		SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY
RTLFSNIVLSGGSTLFKGFGDRLLSEVKKLAPKDVKIRISAPQE RLYSTWIGGSILASLDTFKKMWVSKKEYEEDGARSIHRKTF 6364 21 1201 RRTRLGSSFPRRRDSAMESYDVIANQPVVIDNGSGVIKAGFAG DQIPKYCFPNYVGRPKHVRVMAGALEGDIFIGPKAEEHRGLLSI RYPMEHGIVKDWNDMERIWQYYSKDQLQTFSEEHPVLLTEAPL NPRKNRERAAEVFFETFNVPALPISMQAVLSLYATGRTTGVVLD SGGGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLEFTEKAQYYLPPGS		}		DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS
RLYSTWIGGSILASLDTFKKMWVSKKEYEEDGARSIHRKTF 6364 21 1201 RRTRLGSSFPRREDSAMESYDVIANQPVVIDNGSGVIKAGFAG DQIPKYCFPNYVGRPKHVRVMAGALEGDIFIGPKAEEHRGLLSI RYPMEHGIVKDWNDMERIWQYVSKDQLQTFSEEHPVLLTEAPL NPRKNRERAAEVFEFFNVPALPISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLEFTEKAQYYLPDGS				TIEIGPSRFRAPELLFRPDLIGEESEGIHEVLVFAIQKSDMDLR
RRTRLGSSFFRRRDSSAMESYDVIANQPVVIDNGSGVIKAGFAG DQIPKYCFPNYVGRPKHVRVMAGALEGDIFIGPKAEEHRGLLSI RYPMEHGIVKDWNDMERIWQYVYSKDQLQTFSEEHPVLLTEAPL NPRKNRERAAEVFFFFNVPALFISMQAVLSLVATGRTTGVVLD SGGGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLEFTEKAQYYLPDGS	.	·		KTLFSNIVLSGGSTLFKGFGDRLLSEVKKLAPKDVKIRISAPQE
DQIPKYCFPNYVDGRPKHVRVMAGALEGDIFIGPKAEEHRGLLSI RYPMEHGIVKDWNDMERIWQYVYSKDQLQTFSEEHPVLLTEAPL NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS	6364		120	RLYSTWIGGSILASLDTFKKMWVSKKEYEEDGARSIHRKTF
RYPMEHGIVKDWNDMERIWQYVYSKDQLQTFSEEHPVLLTEAPL NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS	0204	21	1201	RRTRLGSSFPRRRDSSAMBSYDVIANQPVVIDNGSGVIKAGFAG
NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS			1	
SGOGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS]]	
DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS		İ	i	NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD
DEHSSSEFEIVKAIKERACYLSINPOKDETLETEKAQYYLPDGS TIEIGPSRFRAPELLFRPDLIGEESEGIHEVLVFAIQKSDMDLR	1	•		SGAGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY
TISIGPSRFRAPELLFRPDLIGEESEGIHEVLVFAIQKSDMDLR	[1		DRHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS
				TIBIGPSKFKAPELLFRPDLIGEESEGIHEVLVFAIQKSDMDLR

SEQ	Predicted	Predicted end	Dmino poid coment contributes in the
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Clutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
	<u> </u>		RTLFSNIVLSGGSTLFKGFGDRLLSEVKKLAPKDVKIRISAPOE
İ	•		RLYSTWIGGSILASLDTFKKMWVSKKEYEEDGARSIHRKTF
6365	234	1989	KHKSRASCAARAQAFGPSREREVHSRFRSGLRRLGESNSGCCTM
	-	-/-/	ASMGTLAFDEYGRPFLIIKDQDRKSRLMGLEALKSHIMAAKAVA
			NTMRTSLGPNGLDKMMVDKDGDVTVTNDGATILSMMDVDHQIAK
			LMVELSKSQDDEIGDGTTGVVVLAGALLEEAEQLLDRGIHPIRI
ł	ĺ		ADGYEQAARVAIEHLDKISDSVLVDIKDTEPLIQTAKTTLGSKV
			VNSCHRQMAEIAVNAVLTVADMERRDVDFELIKVEGKVGGRLED
			TKLIKGVIVDKDFSHPQMPKKVEDAKIAILTCPFEPPKPKTKHK
			LDVTSVEDYKALQKYRKEKFEEMIQQIKETGANLAICQWGFDDE
			ANHLLLQNNLPAVRWVGGPEIELIAIATGGRIVPRFSELTAEKL
1			GFAGLVQEISFGTTKDKMLVIEQCKNSRAVTIFIRGGNKMIIEE
			AKRSLHDALCVIRNLIRDNRVVYGGGAAEISCALAVSQEADKCP
!			TLEQYAMRAFADALEVIPMALSENSGMNPIQTMTEVRARQVKEM
			NPALGIDCLHKGTNDMKQQHVIETLIGKKQQISLATQMVRMILK
			IDDIRKPGESEE
6366	257	1898	GNKEGAHSSTFWVLLS1FLGAVAMLCKEQGITVLGLNAVPDILV
		2030	IGKFNVLEIVQKVLHKDKSLENLGMLRNGGLLFRMTLLTSGGAG
1			MLYVRWRIMGTGPPAFTEVDNPASFADSMLVRAVNYNYYYSLNA
			WLLLCPWWLCFDWSMGCIPLIKSISDWRVIALAALWFCLIGLIC
1			QALCSEDGHKRRILTLGLGFLVIPFLPASNLFFRVGFVVAERVL
			YLPSVGYCVLLTFGFGALSKHTKKKKLIAAVVLGILFINTLRCV
1			LRSGEWRSEEQLFRSALSVCPLNAKVHYNIGKNLADKGNOTAAI
1			RYYREAVRLNPKYVHAMNNLGNILKERNELQEAEELLSLAVQIQ
1			PDFAAAWMNLGIVQNSLKRFEAAEQSYRTAIKHRRKYPDCYYNL
1			GRLYADLNRHVDALNAWRNATVLKPEHSLAWNNMIILLDNTGNL
1			AQAEAVGREALELIPNDHSLMFSLANVLGKSQKYKESEALFLKA
			IKANPNAASYHGNLAVLYHRWGHLDLAKKHYEISLQLDPTASGT
1			KENYGLLRRKLELMOKKAV
6367	287	1934	SIGFPVMLVLSILLYTCEMFQDSVAFEDVAVSFTQEEWALLDPS
1 1			QKNLYRDVMQETFKNLTSVGKTWKVQNIEDEYKNPRRNLSLMRE
1			KLCESKESHHCGESFNQIADDMLNRKTLPGITPCESSVCGEVGT
į i			GHSSLNTHIRAD'IGHKSSBYQEYGENPYRNKECKKAFSYLDSFQ
			SHDKACTKEKPYDGKECTETFISHSCIQRHRVMHSGDGPYKCKF
1			CGKAFYFLNLCLIHERIHTGVKPYKCKQCGKAFTRSTTLPVHER
			THTGVNADECKECGNAFSFPSEIRRHKRSHTGEKPYECKQCGKV
[]			PISFSSIQYHKMTHTGEKPYECKQCGKAFRCGSHLQKHGRTHTG
		•	EKPYECRQCGKAFRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCA
			SQLQIHERTHSGEKPHECKECGKVFKYFSSLRIHERTHTGEKPH
]			ECKQCGKAFRYFSSLHIHERTHTGDKPYECKVCGKAFTCSSSIR
j i			YHERTHTGEKPYECKHCGKAFISNYIRYHERTHTGEKPYOCKOC
	1		GKAFIRASSCREHERTHTINR
6368	1	327	RPVPAKLNPRSWPRTAGALPLRPPPLTMAVFHDEVEIEDFQYDE
1	i		DSETYFYPCPCGDNFSITKEDLENGEDVATCPSCSLIIKVIYDK
[DQFVCGETVPAPSANKELVKC
6369	1	1745	AGCCRDTRFPTPRGPGSLCHNFCRSAACTVTRTIHGSPREDTGT
	1	·	PRSREMMFQDSVAFEDVAVSFTQEEWALLDPSQKNLYRDVMOET
		İ	FKNLTSVGKTWKVQNIEDEYKNPRRNLSLMREKLCESKESHHCG
			BSFNQIADDMLNRKTLPGITPCESSVCGEVGTGHSSLNTHIRAD
	J		TGHKSSEYQEYGENPYRNKECKKAFSYLDSFQSHDKACTKEKPY
	1	l	DGKECTETFISHSCIQRHRVMHSGDGPYKCKFCGKAFYFLNLCL
[ļ		IHERIHTGVKPYKCKQCGKAFTRSTTLPVHERTHTGVNADECKE
ľ			
İ	}	j	CGNAFSFPSEIRRHKRSHTGEKPYECKQCGKVFISFSSIQYHKM THTGEKPYECKQCGKAFECCEULQVUGBTUTCEVDYBGDQCGVZ
			THTGEKPYECKQCGKAFRCGSHLQKHGRTHTGEKPYECRQCGKA FRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCASQLQIHERTHSG
			EKPHECKECGKVFKYFSSLRIHERTHTGEKPHECKOCGKAFRYF
			DATE CONTRACTOR OF A PROPERTY

Deginning nucleotide location corresponding continue c	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Autoration Corresponding	ID	li .		(A=Alamine C-Cysteine D-Asparia A-13 n
Cocation Corresponding Co first College Colleg	NO:			Glutamic Acid. F=Phenylalanian C-Clusies
Labertine Labe	ĺ	location		H=Histidine TaTsoleucine V-Lucine
P-Proline, Q-Glutamine, R-Arginine, Serine, T-Pireonine, V-Valine, serine amino acid sequence Serine, T-Pireonine, V-Valine, w-Tryosine, X-Unknown, *-stop Codon, /-possible nucleotide deletion, Codon, /-possible nucleotide deletion, N-Pireonine, V-Valine, w-Tryosine, X-Unknown, *-stop Codon, /-possible nucleotide deletion, N-Pireonine, V-Valine, w-Tryosine, X-Unknown, *-stop Codon, /-possible nucleotide insertion SILIMIERITHGENEY ECKICKAF ISNYIRYHERTHTGENEY SIRIMIERITHGENEY CKCKCKAF ISNYIRYHERTHTGENEY CKCKCKAF ISNYIRYHERTHTGENEY CKCKCKAF ISNYIRYHERTHTGENEY CKCKCKAF ISNYIRYHERTHTGENEY CKCKCKAF ISNYIRYHERTHTGENEY CKCKCKAF ISNYIRYHERTHTGENEY CKCKCKAF ISNYIRYHERTHTGENEY CKCKCKAF ISNYIRYHERTHTGENEY CKCKCKAF ISNYIRYHERTHTGENEY CKCKCKAF ISNYIRYHERTHTGENEY CKCKCKAF ISNYIRYHERTHTGENEY CKCKCKAF ISNYIRYHERTHTGENEY CKCKCKAF ISNYIRYHERTHTGENEY CKCKCKAF ISNYIRYHERTHTGENEY CKCKCKAF ISNYIRYHERTHTGENEY CKCKCKAF ISNYIRYHERTHTGENEY CKCKCKAF ISNYIRYHERTHTGENEY CKCKCKAF ISNYIRYHERTHTGENEY CKCKCKAF ISNYIRYHERTHSGENEY CKCKCKAF ISNYIRYHERTHSGENEY CKCKCKAF ISNYIRYHERTHSGENEY CKCKCKAF ISNYIRYHERTHSGENEY CKCKCKAF ISNYIRYHERTHSGENEY CKCKCKAF ISNYIRYHERTHSGENEY CKCKCKAF ISNYIRYHERTHSGENEY CKCKCKAF ISNYIRYHERTHSGENEY CKCKCKAF ISNYIRYHERTHSGENEY CKCKCKAF ISNYIRYHERTHSGENEY CKCKCKAF ISNYIRYHERTHSGENEY CKCKCKAF ISNYIRYHERTHSGENEY CKCKCKAF ISNYIRYHERTHSGENEY CKCKCKAF ISNYIRYHERTHSGENEY CKCKCKAF ISNYIRYHERTHSGENEY CKCKCKAF ISNYIRYHERTHSGENEY CKCKCKAF ISNYIRYHERTHSGENEY C		corresponding	to first	L=Leucine. M=Methionine N=Asnaragine
smino acid residue of amino acid sequence ship ssible nucleotide deletion, % possible nucleoti		to first	amino acid	P=Proline, O=Glutamine, R=Arginine
amino acid anino acid acquence Sequence	1	amino acid	residue of	S=Serine, TaThrequine, VaValine
sequence Sequence	1	residue of	amino acid	WaTryptophan, YaTyrosine, Xalinknown *-Gton
Sequence N-possible nucleotide insertion		amino acid	sequence	Codon, /=possible nucleotide deletion
SSLIAHBERTHTGENYJEKUGIKAPTGESSTEYHERTHTGENGY EKKICKAPISHYRYBERHTGERYPQCKQCKAPITASSCRE HERTHTIR FULSEQRIKTETYNPESPGIGGRAANAGRPTAGAGLIERLILGGG ALVGGLEPVTHTTPANAGNASKTHELSLYELHRTPQEAIMGGTE LAVPSRSHISHKUPCICLOKLANTHTIKECHHRFCSDCIVTALI SCHWEGGTCRKLUVSKASIRPPHPTAALISKITERSPEYRAHQD RVLIRLSRLHNQAHASSTEELLMQAHHRAGNVERPIPSGOGG RVLIRLSRLHNQAHASSTEELLMQAHHRAGNVERPIPSGOGG SSVATGGGTGGVGGASSEDGGDRGGTLGGGTLGPPSPPGAG PPERGGELELVFRPPHLLVEKKEEVCTHYVETTGATVDHISKY LAURIALBERRQQDEAGSPGGGGGABDTGGGTLGPPSPPGAG SSVATGGGTGGVGGASSEDGGDRGGTLGGGTLGPPSPPGAG PPERGGELELVFRPPHLLVEKKEEVCTHYVETTGATVDHISKY LAURIALBERRQQDEAGSPEPGGRGAADTGGTLGPPSPPGAG GOPPERAPSISLEVSPERQTYTI THAGGGAPTTHAGTVDHISKY LAURIALBERRQQDEAGSPEPGGRGAADTGGTLGPPSPPGAG GOPPERAPSISLEVSPERQTYTI THAGGGAPTTHAGTVDHISKY LAURIALBERRQQDEAGSPEPGGRGAADTGGTLGPPSPPGAG GOPPERAPSISLEVSPERQTYTATAGGGAPTHAGTVDHISKY LAURIALBERRQQDEAGSPEPGGRGAADTGGTLAPSPPGAG GOPPERAPSILEVSPERQTHAGGGAPTHAGGAPTHAGTAGTUSHLEV LIKNYLEKSALISTELSVLHNEFSPSPEPKEKGFEKKKE LINNNFENALCREEKEYLECHMERIKAMGDPLEKLGFGDLTSC KSEAKK 6372 2141 625 RVSALASBGKAEERYKKLEDLLEKSFSLVKRFSLGPVWGWWSH LKGYILKKSALISTELSVLHNEFSPSPETRRGGEVWGRIMG VGKNWLDDWLGPTRIFLERTRAVIYCTLRAELHALMOLDVG ELCTVDFCHKFTWCLDACTREPFVDSKRARELGGFLOVKXGG GULGDLSHILCOPPAINTLASTYPHLOELWOGPTLPDGDPDL LLERLIALGQGAMMLISGUPFRIFLERTRAUSTUTLERLEHALMOLDVG ELCTVDFCHKFTWCLDACTREPFVDSKRARELGGFLOVKXGG GULGDLSHILCOPPAINTLASTYPHLOELWOGPTLPDGDPDL LLERLIALGGAAMMLISGUPFREHAGETLTEFTWFLORGARGAWAN APSKLEALGGALEFTGGGGAVAEUTSGCLEKERGLDCHWGBDL VYHNTOKKLDARELFSTSLTESTRINGEVTLIFSFTWAGGAPATHAGA APSKLEALGGALEFTGGGGAVAEUTSGCLEKERGLDCHWGBDL VYHNTOKKLDARELFSTSLTENSTYNGLGEKUNGTHAGAA APSKLEALGGALEFTGGGGAVAEUTSGCLEKERGDLOCKAGG GAARPSGPPPGGGGAAGAGGAGAGGAGAGGAGGAGGAGGAGGAGAGGAADAGAA ARSTPALERIPHTAGATTTIJFSTTWAGGAPAGATTRGG GAARPSGPPPGGGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	ŀ	sequence	-	\=possible nucleotide insertion\
6370 1711 329 FUSEQUESTENTERS FIGURGANAGERTAGACIDELLIGES ALVOGRAPHTEN AND ASSET MELEST PER SECUL AND ASSET AND ASSET AND ASSET				SSLHIHERTHTGDKPYECKUCYKAPTCSSCTDVUEDTUTCEVDV
6370 1711 329 FVLSEQRIETERTWPESPGLGRGAAAAGARTAGAGLLRILLGCG ALVGGRFYTHTTPANAQNASKTWELSLYELHRTDGER HUGHE IAVSPRSLHSELMCPICLUMKIMTMTKECKLERFCSDCTYTALR SONKECPTCRIKUVSKRSLRPDENDALISKIYPERSENCTYTALR SONKECPTCRIKUVSKRSLRPDENDALISKIYPERSENCTYTALR SONKECPTCRIKUVSKRSLRPDENDALISKIYPERSENCTYTALR SONKECPTCRIKUVSKRSLRPDENDALISKIYPERSENCTYTALR SONKECPTCRIKUVSKRSLRPDENDALISKIYPERSENCTYTALR SONKECPTCRIKUVSKRSLRPDENDALISKIYPERSENCTYTALR SONKECPTCRIKUVSKRSLRPDENDALISKIYPERSENCTYTALR RVIKUSGRSPGEGEGODGDVSDSADBAGDEAPGRADG RVLIRISRIHMCOLSSESDAGDGEGOGGAGG SSVSTGGGOTGGOGGAGGGAGG GSVSTGGOTGCOCASSEDGRGGTLGGOTGLPFSPFORS PPEPGGEIELVFRPHPLLVEKGEYCOTROUTTURAFVOHISK LALRILLBERGQQEAGRGGTGGGAGGGAGG GOPEPRALPSISEVSKRYTIVIAPGGGAFTLANSITLELVME KRWKVSRPLELCYAPTKOPK KRWKVSRPLECVSRPTKERSTELSTWANGCEVSCH KRYKVSRPLECVSRPTKERSTELSTWANGCENSTALL LARDELSTAGSSLTVALLELGOOLONGALTERSTUND LALLAGGAADDHIDSQVFKRPKMSVELITRILDRIANSLAD LALBERALGKALPPTGGGGAAVKELYSOLGEKLEGDDRKKSPLO DYTHOVOKLABERCHYSTSPHENSTRELSKELEDDLAGGIT-LALHIPRV APSKLEALGKALPPTGGGGAAVKELYSOLGEKLEGDDRKKSPLO QAAFFALLELDSVAPABUL LARDELSTAGSSLTARTVANTELTSKKELEDDLOVQAKORSYDAL VHICKGGLINVAATAAVWAASKGQGALSERLSSTMODITTIRGD GAAFFALDELDSVAPABUL 6374 535 105 KKFFCSYLSTSSEFFSSTRHISCPFHTFCHYTSSTIFLSSTEDIS CPHTFCHYTSSTIFLSSKELEDDLOVQAKORSYDAL VHIGKGGLINVAATAAVWAASKGGALSERLSSTMODITTIRGD GAAFFGGPPPGGGGAGGAAKGCPTTSSKLEDCOTTAGSKELT SCHALTAVADHILFFLATTSTSKELEDDLOVQAKORSYDAL VHISROVSSMCCOTHNINLISCOPTTSSTTYTSSTIFLSSTDIS CPHTFCHYTSSTIFLSSTEDDSCPTTTSCTYTSSTIFLSSTDIS CPHTFCHYTSSTIFLSSTEDDSCPTTTSCTYTSSTIFLSSTDIS CPHTFCCHYTSSTIFLSSTEDDSCCOTTHTSSTIFLSST NICHTAGATATATATATATATATATATATATATATATA	į			ECKHCGKAFISNYIRYHERTHTGEKPYOCKOCGKARIDAGGCER
ALVOGREP VINITIPANGANS KIVALISTYLEHEPOEN MIDSTE I AVSPRSLHSSLMCPICLDMLMRIMITITECLHERCSDCIVTALE SONNECPTCREKKUSKRSLEHEPDENDELIST KYRESEYBAHGD RVLIRISRLHNQGALSSSIEGGENGAMRRAGRVERP I PGSDCT TIMSGGGES DEGEGEGDGED SUSSBAPDGASPGRPGGGGAG SSVGTGGGTGGVGGGAGSEDSGDRGGTLGGTLGPSPPGAPS PPEPGGEISLVFRPRHLLVERGEYCYTRYVLYTIONATVDHLSKY LALBIALBERGOQGAGSEDGAGSGTLGGGTLGPSPPGAPS PPEPGGEISLVFRPRHLLVERGEYCYTRYVLYTIONATVDHLSKY LALBIALBERGOQGAGSEDGAGSTLGGGTLGFSPPGAPS PPEPGGEISLVFRPRHLLVERGEYCYTRYVLYTIONATVDHLSKY LALBIALBERGOQGAGSEDGAGSGTLGGGTLGFSPPGAPS PPEPGGGISLVFRPRPHLVERGEYCYTRYVTONATVDHLSKY LALBIALBERGOQGAGSEDGAGSTLGGGTLGFSPPGAPS PPEPGGGISLVFRPRPHLVERGYCTTURGATVDHLSKY LALBIALBERGOQGAGSEDGAGSTLGGGTLGFSPGAGG DOPEPALPSLEGVSKYKTITALAGGGAFTTLANGELLVENE KRWKYSRPLELCYAPYROPK GYMMSTANNFCRIKCHTSPPPTLANGELVENE KRWKYSRPLELCYAPYROPK LANDNFENALCRIESSESLLVKMFSLOPVWCVMKK LANDNFENALCRIESSESLLVKMFSLOPVWCVMKK LANDNFENALCRIESSESLLVKMFSLOPVWCVMKK LANDNFENALCRIESSESLLVKMFSLOPVWCVMKK LANDYLDERGKALFTGLGAUNTFSSPSTERGGEVVQRLTRM VGKNVKLYDMVLOFLRTHFLARTSVHTCHLGRLVGGTLBGNSGDL LLKGYLLKKSALFSTELGVLHNFSSSPSTREGGEVVQRLTRM VGKNVKLYDMVLOFLRTHFLARTSVHTCHLGRLVGGTLBGNSGDL LLKRLALGGAGADNIDSGOVERSPMSVELICHGWKKGGE GULGDLSHILCDEFAINTLALSTVEHLGELVGGTLBGNSGDL LLADEFALEDFCSSLFDGFFLTASFTKENDENGTLFHLNSPLUD DYTENVDOKLDAEEKAPVSVPNTLDESSTREDGEDLIFLHSDRUCH VYLHITKGRNNALLRELPGIVSTFBDLAFGUTFLARGLALHLHLHRR APSKLEALGKALEPTGGGGAVKELYSGJGEKLEGLDHKKFSPA APSKLEALGKALEPTGGGGGAVKELYSGJGEKLEGLDHKKFSPA APSKLEALGKALEPTGGGGGAVKELYSGJGEKLEGLDHKKFSPA APSKLEALGKALEPTGGGGGAVKELYSGJGEKLEGLDHKKFSPA LADEFALEDFCSSLFFGFFTTCTVTSTFTLSTTDHSCTTHLARGLAL LADEFALEDFCSSLFFGFFTTCTVTSTFTLSTTDHSCTTHA WILLSPYTKGSSLLYRKFVHFTLSSKEKETDDCLVQAKORSYDAL VHEKRGLIVAAAAVAAASKGGGALSERLASFTLSSTEDHS CPHTFCTYTSSTTJSTSTDHSCTTHTCNYTTSTIPLSSTEDHS CPHTFCTYTSSTTJSTSTDHSCTTHTCNYTTSTIPLSSTEDHS CPHTFCTYTSSTTJSTSTDHSCTTHTCNYTTSTIPLSSTEDHS CPHTFCTYTSSTIPLSSTEDHSCOTTHTCNYTTSTIPLSSTEDHS CPHTFCTYTSSTTJSTSTDHSCOTTHTCNYTTSTIPLSSTEDHS CPHTFCTYTTSSTTJSTSTDHSCOTTHTCNYTTSTIPLSSTEDHS CPHTFCTYTTSSTTJSTSTDHSCOTTHTCNYTTSTIPLSSTEDHS CPHTFCTYTTSSTTJST	İ			HERTHTINR
ALVGGRPYTHTPANAQNASKTWELSLYELHRTPGEAUMOTE INVSPRENIESLEMCPICUMKINTHTKECHERFCSDCIVTALE SONKECPTCRKKUVSKRSLRPDENPALISKTYPSBREVFAHOD RVLITEISLINGCOLSSISTEGELMOMMERGUREPIGEGOG RVLITEISLINGCOLSSISTEGELMOMMERGUREPIGEGOGG SSVSTGGGGTGGGGGDGDVSDSADDAPGPARRPRGGAGG SSVSTGGGGTGGGGGGDGDVSDSADDAPGPARRPRGGAGG SSVSTGGGGTGGGGGGGGGGGGGGGGGGGGGGGGGGG	6370	1711	329	FVLSEORLRTERTWPRSPGLGRGAAAAGAPTAGAGLLPLLLGCG
INVSPRSLHSELMCPICLDMLMSTHTTRECLURESCECTUTALE SONNECPTERKEN/USKSLENGEPDENPIOLAISKY PREBEVERAGIO RVLIRISRIHHNQGALSSSIEGGERMGAMHRAGRUNDED PROSECTOR RVLIRISRIHHNQGALSSSIEGGERMGAMHRAGRUNDED PROSECTOR SVOTGGGTGGVGGGAGSEDGDRGGTLGGTLGPSPPDADE PPERGGEIELVERPRIPLLIVERGYCOTTYVETTGATVDHLSKY LALIK LALERROQQEAGERGGFGGGASDTGGPDGCGGGGGGGAGGG DOPSEPALSEGVSEKQYTTYTAPGGGATTLAGSTLILEUNDE KFWKVSRPLELCTAPTKOPE 6371 3 288 GVARMSTARNFGTKSFORPFDERGSFFLDHLGECKSFKEKFMKC LINNSTENALGRESSKEVLESCRMERKLMQEPLEKLOFFDCTSC KSEAKK 6372 2141 625 RVSALASSGKABERYKKLEDLLEKSFSLVKMFSLQPVWKCYMKI LPKVPEKKLKLVVADKELYRACAVEVRGUMODNOALFGDEVSF LLKGYLLEKSSALFSTELSVLNNFFSSPSKTEDCFUNGVKKGGE LDKVYEKKLKLVVADKELYRACAVEVRGUMODNOALFGDEVSF LLKGYLLEKSSALFSTELSVLNNFFSSPSKTEDCFUNGVKKGGE GUVLGDLSHILCDEPA INTLALSTVEHLOELVGOSTLPRDSPDLL LLIKALALGGAMDVIDGGVVKSP PMSTVELITRFLEPHASPLD DYTFHVUDKLPAEEKAPVSYPHTLDESFYKLOELGRAGEVGUT TVLHTKGRRKGNALIKLIPGLVETTGDLAFGD ITLHLIGGNAL LADEFALEDFCSSLEDGFFILDSFPVBKRABELFUNGKRAGEVGILV VVLHTKGRRKGNALIKLIPGLVETTGDLAFGD ITLHLIGNAL LADEFALEDFCSSLEDGFFILDSFPKENNHARARKLILHLIPGHAF AFSKLEALGKALEFTGGSGENKELTSOLGEKLEGLDHKKFSPA QAAETPALEDFLSSVPAPAB 6373 67 711 PSRRARASPARLDAWSWITSELVULTFGLYVPAYYSVKAVKSK DIKEYVKMWWINTIFALTTATETTFDI PLCGGRMAGEVGILV WILLSPYTKGSSLLYRKFVHFTLSSKEKEIDDCLVOAKORSYDAL VHCKRGLIVAAATAAVANASKOGGALSEEKRESTMODLTTIRGG GAPAPSGPPPGGGRASCKHOLTSSTIPLSSTRIDHS CPHHTCHYTSSTIPLSSTRIDHSCPTHTFCCNYTSSTIPLSSTRIDHS CPHHTCHYTSSTIPLSSTRIDHSCPTHTTCCNYTSSTIPLSSTRIDH SCHHTCHYTTSSTIPLSSTRIDHSCPTHTTCCNYTSSTIPLSSTRIDH CPHHTCHYTTSSTIPLSSTRIDHSCPTHTTCNYTSSTIPLSSTRIDH SCHHTLTCHYTTSSTIPLSSTRIDHSCPTHTTCNYTSSTIPLSSTRIDH CPHHTCHYTTSSTIPLSSTRIDHSCPTHTCCNYTSSTIPLSSTRIDHS CPHHTCHYTTSSTIPLSSTRIDHSCPTHTCCNYTSSTIPLSSTRIDHS CPHHTCHYTTSSTIPLSSTRIDHSCPTHTCNYTSSTIPLSSTRIDHS CPHHTCHYTTSSTIPLSSTRIDHSCPTHTCCNYTSSTIPLSSTRIDHS CPHHTCHYTTSSTIPLSSTRIDHSCPTHTCCNYTSSTIPLSSTRIDHS CPHHTCHYTTSSTIPLSSTRIDHSCPTHTCCNYTSSTIPLSSTRIDHS CPHTTCHYTTSSTIPLSSTRIDHSCPTHTCCNYTSSTIPLSSTRIDHS CPHTTCHYTTSSTIPLSSTRIDHSCPTHTCHYTPHAGCVAA IRGSVNEKIRDLHFCHTTSSTRIPHGGGGGGDECHALAGROSEMNIL SGRNUKMMERSHUPUNN	1			ALVGGLRPVTMTTPANAONASKTWELSLYELHRTDOFATMDGTE
SONKECPTCRKKLVSKRSIRPDPNFDALISKIYPSSREFEHAND RVILTISRIHINQALISSI EEGLEMAMRURUPRI PIGSDOT TTMSGGGE PEGEGDGEDVSSDEAPDSAPGURPRI PIGSDOT TTMSGGGE PEGEGDGEDVSSDEAPDSAPGURPRI PIGSDOT SVSTGGGGTGGVGGGAGGGEDGGGBGGGGGGGGGGGGGGGGGGGGGGGGGGG				IAVSPRSLHSELMCPICLDMIKNTMTTKRCLHPRCSDCTVTALP
RVLIRISRIHMQQALSSSIEGGLEMQAMRKAQRURPH JFGSDOT TTMSGGGR GFGEGGDGEDVSBSBAPDSAPGAPGARGAGGAGG SSVSTGGGTGVGCGGSBDGGTLGGGTLGGGTLGPSPPBAPS PPBFGGE IELVFRPHPLUEKGEYCQTRYWKTTQNATVDHLSKY LALRIALERRQQQBAGEPGGPGGGAGGAGGAGG DOPEPALPSLEGVSEKQYTIYIAPGGAPTTLMGSLTLELVNE KWRLVSRPLELCYAPYTDDK 6371 3 288 GVANMSTANNFGTRSFQPAPPDKSSFPLDHLGECKSFKEFKKFMK KSEAK 6372 2141 625 GVANMSTANNFGTRSFQPAPPDKSSFPLDHLGECKSFKEFMKFMK KSEAK 6372 LIKU 625 RVSALASBGKGERYKKLEDLLEKSFFLWFBLGPVMCVUKH LPKVPEKKLKLVMADKELYRACAVEVRRGIUQDNOALFGDEVSF LLKQYLLEKSSALFSTELSVLHNFFSPSFKTRRGGEVVQRITRM VGRIVELIVDMVLOFFLATIFLETKRIVHYLTTLABELLMSHDLDUV EICTVDPCHKFTMCLDACTREREVDSKRARBLGGFLDGVKGOG OVLGDLSMILCDPFAINTLATSTVHLGGEVGGSTLPRDSFDLL LLELLALGGGAMMTDSQVFKBFKGVELTRFLIMMSFLVD DYTRIVDGVLPAEKAPYVPNTIPSSFFKLGGRMAGEVGLV VVLHITKGRINNALLRLDEGLVETPGDLAFGDIFLHLLTGNLAL LADEFALEDFCSSLFGGFFLTASFRKENVHRARLLLIHLHPRV APSKLBALGKALEPTGGSGGAVKELYSGLGEKLEGLDDRKKSPA QAAETPALELELSSVAPAPL 6373 67 711 PSRARASBFALZAMVSHITSRLVULIFGTLYPAYYSYKKVKEK DIKRYVKMMWHIFALFTTAEFITDIFLCAPPTYYLKIAFVA WLLSPYTKGSSLLYRKFYHPTLSSKKERIDDLTVOAKORSYDAL VHCKRGILNVAATAAVMAASKGGALSERLESSIMDDLTTRGG GAPAPSGGPPPGGGRASKCHOPMSGASASSASSSGTA 6374 535 2105 HKLFCSYLTSEFPSSTRHSCPTHTFCNYTSSTFLSSTRDHS CPHHTFCNYTSSTFILSSTRHSCPTHTFCNYTPSTFLSSTRDHS CPHHTFCNYTSSTFILSSTRHSCPTHTFCNYTPSTFLSSTRDHS CPHHTFCNYTSSTFILSSTRHSCPTHTFCNYTPSTFLSSTRCHSC PAGACGTRAGGAMKGRSGGATALLLKCGAGEDAVERVINGH SCQHLITAVADHLFKIKTTSNELGBFRSALELDTPSMTAGQVA IEGGVMEKTRORGADHTFOTLDDGSGVULVENWERRFDINGQH SCQHLITAVADHLFKIKTTSNELGBFRSALELDTPSMTAGQVA IEGGVMEKTRORGADHTFOTLDDFSGVULVENWERRFDINGQH SCGHLITAVADHLFKIKTTSNELGBFRSALELDTPSMTAGQVA IEGGVMEKTRORGADHTVTGDEKGGFLDDHAGPTARVAUL GKNRLINGESSTLLFLTTGDEKGGGLFLLAGPPASVETLIGGTVABVL GKGRAKKGRFRGGGGATAMSRT 1 1535 ANMAATRPVLEFAGCGGRERCWHPSRSSBHGGGGLAMSGT CPRRFRGGGGGATAMSRT 1 1535 ANMAATRPVLEFAGCGGERCKMPSRSSBHGGGGGLAMSGT FVAAPPLIFAGGALAGGATATANGFRGGGGGFLOLLEDGR FORRAFGGGGATATANGFRGTAGGGGGGCLLEDGR FVAAPPLIPATTARAFKYHLUGBVASSLVDMLGRKNSCVLFSLTY SLCCLTKLSQDYFVLLVGRALGGGSTTLLEPGRAFVILLEPURF FUAAPPLIFATSPRAMTHEHVER HPPRABVIPATRARAFWHILGH	1			SGNKECPTCRKKLVSKRSLRPDPNFDALISKIVPSPREVEAHOD
TTMSCGGE PCGEGOCEDVSSDAPGGAPGRAPKRPGGGAGG SSVGTGGGTGGVGGGGGGTGGP98 PPGAPS PPEFGGEIELVPRPHPLLVEKGEVCOTRYVKTTONATVDHLSKY LALRIALERQQGEAGFGGGGGAGGTGGP98 PGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	1	ł		RVLIRLSRLHNOOALSSSIEEGLRMOAMHRAORURRDIRGSDOT
SSVOTGGGTGVGCGGGSEDSGDRGTTLGGTLGGTLGGTLGGTLGGTLGGTLGGTLGGTLGGT	}	İ		TTMSGGEGEPGEGEGDGEDVSSDSAPDSAPGPAPKPDPGGGAGG
PPERGGEIELVERPHPLLUSKGECOTTRYKETIONTOHINES. LARIALBERRQQQEAGEGEGGGGAGGGGAGG DOPEPALPSLEGVSERQYTITIAPGGGAPTTLNGSLTLELVNE KPHVSSPPLELCXAPTKOPK GVANMSTANNFOTKSFODRPPDKGSFPLDHLGECKSFKEKSMKC LHINNFENALCKESKEYLECKMERKLMLQEPLEKLGFGDLTSG GVANMSTANNFOTKSFODRPPDKGSFPLDHLGECKSFKEKSMKC LHINNFENALCKESKEYLECKMERKLMLQEPLEKLGFGDLTSG KSEAKK SEAKK LHINNFENALCKESKEYLECKMERKLMLQEPLEKLGFGDLTSG G372 2141 625 RVSAIASEGKAERYKKLEDLLEKSFSLVKNFSLDPVNMCVMKT LPKVPEKKLKLMJANGKLYRACAVEVRGUMQDNOALFGDEVSP LLKGYILEKESALFSTELSVLHNFFSPSPKTRRQGEVORLTKM VGRNVKLIDMVLGFLRTLFLRITRNYHYCTLRAELLMSLHDLDVG EICTVDPCHKFTMCLDACTREFFVDSKERGGFLDGVKKGGG OVLGDLSMILCDPRINTLALSTVUHLQELVGGETLPRDSPDLL LLEALLAGGAMMNISQVFKEPRERELGGFLDGVKKGGG OVLGDLSMILCDPRINTLALSTVUHLQELVGGETLPRDSPDLL LLABELALGGAMMNISQVFKEPRERELGGFLDGVKKGGG OVLGDLSMILCOPRAINTLALSTVUHLQELVGGETLPRDSPDLL LADEFALEDGSTANDSVFKEPRERELGGFLDGVKKGGG OVLGDLSMILCOPRAINTLALSTVUHLQELVGGETLPRDSPDLL LADEFALEDGSTANDSVFKEPRERELGGFLDGVKKGGG OVLGDLSMILCOPRAINTLALSTVUHLGELVGGETLPRDSPDLL LADEFALEDGSVERVELYSQLGEKLEGLDHRKPSLV APSKLERLGGSKARGVKELYSQLGEKLEGLDHRKPSLV APSKLERLGGSKARGVKELYSQLGEKLEGLDHRKPSLR APSKLERLGGSKARGVKELYSQLGEKLEGLDHRKFSSPA UNFOKEGLEVLEFTANDSVILTSGVERSTANDSTVILTSLAND VHFCKRGLGVAATAAVWARASKGGGALSERLFSSSMODLTTIKGG GAPAPSGPPPPGSGRASGKHGQPKMRSASGESASSGTA KKLFCSYLSTSETESSTRUHSGPTHTSCNYTSSTFILSSTRDHS CPHTTCTAYTSTTFILSSTRDHSCPTHTFCNYTSSTFILSSTRDH SCCPTHTSCNYTSSTFILSSTRDHSCPTHTFCNYTSSTFILSSTRDH SCCPTHTSCNYTSSTFILSSTRDHSCPTHTFCNYTSPTILSSTD HSCCPTHTSCNYTSSTFILSSTRDHSCPTHTFCNYTSPTILSSTD HSCCPTHTSCNYTSSTFILSSTRDHSCPTHTFCNYTSPTILSSTD HSCCPTHTSCNYTSSTFILSSTRDHSCPTHTFCNYTSPTILSSTD HSCCPTHTSCNYTSSTFILSSTRDHSCPTHTFCNYTSPTILSSTD HSCCPTHTSCNYTSSTFILSSTRDHSCPTHTFCNYTSPTILSSTD HSCCPTHTSCNYTSSTFILSSTRDHSCPTHTFCNYTSPTILSSTD HSCCPTHTSCNYTSSTFILSSTD HSCCPTHTSCNYTSSTFILSSTD HSCCPTHTSCNYTSSTFILSSTD HSCCPTHTSCNYTSSTFILSSTD HSCCPTHTSCNYTSSTFILSSTD HSCCPTHTSCNYTSSTFILSSTD HSCCPTHTSCNYTSSTFILSSTD HSCCPTHTSCNYTSSTFILSSTD HSCC				SSVGTGGGGTGGVGGGAGSEDSGDRGGTLGGGTLGPPRPPGAPS
LALRIALERRQQQEAGEFGGFGGASDTGGGAGGG DOPEEPALPSIESUSERVERQYTITJAFGGGAFTTLNGSLTLELIVNE KFWKVSRPLELCYAPTKDPK GVANMSTANNFOTKSFGDFRPFDKGSFFPLDHLGGEKSFKEKSMK LHANNFENALCRKESKEYLECKMERKLMLGEPLEKLGFGDLTGG KSEAKK 6372 2141 625 RVSA1ASEGKAEERYKKLEDLLEKSFSLVKMPSLQPVMCVMKR LPKVPEKKLKLWADKELYRACAVEVRRQINQDNOALFGDEVSP LLKQYILEKESALFSTLESVLINFFSPSPKTRRGGEVVQRITEN VGKNVKLYDMVLQFLRTLFLRTRNNVTCTLRAELMSLHDLDVG EICTVDPCHKFFWCLDACTRERFVDSKRARELQGFLDGVKKGGE OVLGDLSMILCDPFAINTLALSTVERLGVGGTVPDRSDFLL LLIKLALGGGAMMIDSQVFKEPMEVELITEFLEMLMSPLVD DYTFNVDQLIAPEEKAPVSYPNTLDESTFKLOGGRMACEVGIV YVLHITKQRNKNALLERLEGLVETTGDLARGDIFLHLTGNLAL LADEFALEDFCSSLFDGFFLTASPRKENVHRHALRLITHLHPRX APSKLEARJGKALEFTGGGGAVKELYGGEKKLEGLDHRKFSPA APSKLEARJGKALEFTGGGGAVKELYGGEKKLEGLDHRKFSPA OAASTPALBIPLPSVPAPAPL 6373 67 711 PSRAARASPARJAMVSHISELVVLTFGTLYBAYYSYKAVKSK DIKEYVKWMMYWIIFALFTTDIFLCWPFFYYELKTAFVA WLLSPYTKGSSLLYRKVUPTILSSKEKEIDDCLVQAKORSYDAL VHCKKGLUNVAATAAVMASKGGGALSERLGFSMODLTTIRGD GAPAPSGPPPBGGGASGGGHCGGFVKTSTSTTFLSSTRDHS CPHTTCNTTSSTTFLSSTRDHSCPTHTCNTSSTTFLSSTRDHS CPHTTCNTTSSTTFLSSTRDHSCPTHTCNTSPTITLSSTRDHS CPHATGCNTYSSTTFLSSTRDHSCPTHTCNTSPTITLSSTRDHS CPHATGCNTYSSTTFLSSTRDHSCPTHTCNTSPTITLSSTRDHS CPHATGCNTYSSTTFLSSTRDHSCPTHTCNTSPTITLSSTRDHS CPHATGCNTYSSTTFLSSTRDHSCPTHTCNTSPTITLSSTRDHS CPHATGCNTYSSTTFLSSTRDHSCPTHTCNTSPTITLSSTRDHS CPHATGCNTYSSTTFLSSTRDHSCPTHTCNTSPTITLSSTRD HSCHTTTSSTTPLSSTRDHSCPTHTCNTSPTITLSSTRDHS CPHATGCNTYSSTTFLSSTRDHSCPTHTCNTSPTITLSSTRDHS CPHATGCNTYSSTTFLSSTRDHSCPTHTCNTSPTITLSSTRDHS COMLITANADHLFKLKTTSSELGERFAGEGGALDHTSMTKLL OKNNINLERLAVNIAHSLRNSSPDWGCVVLLRRKEGDSFRMNI ANSIGSSTLLFTTVGBCGGGGLFLAGADVKKURGNTKILL OKNNINLLRLLAVNIAHSLRNSSPDWGCVVLLRRKEGDSFRMNI ANSIGSSTLLFTTVGBCGGGGLFLAGADVKKURGNTSKLL OKNNINLLRLLAVNIAHSLRNSSPDWGCVVLLRRKEGDSFRMNI ANSIGSSTLLFTTVGBCGGGGLFLAGADVKAURGNTSCUCFSTLY FLEGOLATLVYGGLASCTLLFSAFERGEGGLAWSRT CCGRPRRFGGGVVRGFTMLVTALARVGLASCTGLESRCRAK PPGRACSNPSFLBFQLDFYQVYTALARVGLASCTGLESRCRAK PPGRACSNPSFLBFQLDFYQVYTALARVGLASCTGLESRCRAK PPGRACSNPSFLBFQLDFYQVYTALARDGLAGFYAVE SLCCSLUTKLSQDYFVLLVGGRAGGGSTALLFSSPGAWIHEHVER HDFPAEW	1			PPEPGGEIELVFRPHPLLVEKGEYCOTRYVKTTGNATVDHI.QKV
BOPEPRALISLES/USERQYTIT/TAPE/GGAPTTLINGSLITLELVNE				LALRIALERROQQEAGEPGGPGGGASDTGGPDGCGGEGGACGC
6371 3 288 GYANNISTANNISTIKSFOPRIPPIKSSPPLDILGECKSFKEXMK LUNNNFENALCRKESKEYLECRMERKLMLQEPLEKLGFGDLTSG KSEAKK 6372 2141 625 RVSAIASEGKAEERYKKLEDLLEKSFSLVKMPSLQPVVMCVMKN LPKVPEKKLKLVAADKELYRACAVEVRRQIMQDNQALFGDEVSP LLKQYLLEKSSALFSTELISJLINFSSPKTRQGEVVQRLTRM VGKNVKLYDMVLQFLRTLFLRTRNVHYCTLRAELLMSLHDLDVG EICTVDPCHKFTWCLDACIREREVDSKRARELQGFLDGVKKGGE QVLGDLSMILCDPFAINTLALSTVHLQELVQGETLGDGVKKGGE QVLGDLSMILCDPFAINTLALSTVHLQELVQGETLGDGVKKGGE QVLGDLSMILCDPFAINTLALSTVHLQELVQGETLGDGVKKGGE QVLGDLSMILCDPFAINTLALSTVHLQELVQGETLGQLDGVKKGGE QVLGDLSMILCDPFAINTLALSTVHLQELVQGETLGQLDGVKKGGE QVLGDLSMILCDPFAINTLALSTVHLQELVQGETLGQLDGVKKGGE QVLGDLSMILCDPFAINTLALSTVHLQELVQGETLGQLDGVKKGGE QVLGDLSMILCDPFAINTLALSTVHLQELVQGETLGQLDGHKRQLDAL LADEFALEDFCSSLFDGFFLTASPRKENVHHRARKLIHLHPRV AFSKLERLQKALEPTGGSGEAVELVSQLGGETLGQLDHKRYSPA QAAETPALSLPLPSVPAPAPL 6373 67 711 PSRAARASPARLJANNSVIISRUVLIFGTLYPAYYSYKAVKSK DIKEYVKMMMYMITFALPTTAETFTDIPLCMPPFYYSLKIAFVA MLLSPYYKGGSLLYRKPVHPTLSSKEEDDCLVQAKORSYDAL VHFGKRGLNVAATAAANAASKOQALSERLEKSFGMQDLTTIRGD GAAPASGGPPPFGGGRASGKRIGQFKMSRASSSASSGTA 6374 535 2105 HKLFCSYISTSEFSSTTRHSCFTHFCCNYTSSTIFLSSTRDBS CPPHTFCNYTSSTIFLSSTRDHSCPTHTSCNYTSSTIFLSSTRDBS CPPHTFCNYTSSTIFLSSTRDHSCPTHTSCNYTSSTIFLSSTRDB CPPHTFCNYTSSTIFLSSTRDHSCPTHTFCNYTSSTIFLSSTRD SCHLTTAVADHLEKLKTTSWELGRFRSALEDTPSMTAGQVAA IEGGVBEXTRUFLVNNGELSLDDPEVQVSGRGLPDDHAGFIR VNIBGVDSNMCCGTHVSNLSDLQVIKLGTEKGKKNRTNLIFL GKNNLNLLRDLAVHAHSLENNSPDGGGVULHKREGDSFMMII ANEIGSETLLFLTVGDEKGGGLFLLAGPASVETLGFYABVL GKGAGKKGRFGGKATMMSRMEAQALLQVISTGSVABVL GKGAGKKGRFGGKATMMSRMEAQALLQVISTGSVABVL GKGAGKKGRFGGKATMMSRMEAQALLQVISTGSVABVL GCGRPRRPGQQVVRGPTMLVTAYLAFVGLLASCLGELSRCRAK PPGRACSNFSFLRFQLDFYQVFFLANDALGRKNSTVLEGVGSPVFLYBUTY SLCCLTKLSQDFFFLANGENTDRQRRFSRSHEGEGGLAAMSRT CPGRPRRPGQQVVRGPTMLVTAYLAFVGLLASCLGELSRCRAK PPGRACSNFSFLRFQLDFYQVFFLANDALGLGFVAPVIHEHVER HPPPABEWT PATFARAFWHVLIAVANGARABAVASWIGLGFVAP FVAAIPLLAARALALGRANHVILOVANGAVAAEAVASWIGLGFVAP FVAAIPLLAARALGRANHVILOVANGAVAAEAVASWIGLGFVAP FVAAIPLLAARALGRANHVILOVANGAVAAEAVASWIGLGFVAP SLCCSTKLSGDVFFLTYFLOVTFLOTTSTSPVARA	1			DGPEEPALPSLEGVSEKQYTIYIAPGGGAFTTLNGSLTI.RI.JUNE
6372 2141 625 RVSAIASEGKAERYKKLEDLLEKSFSLVKNFSLQPLVMCYMKKLEDLEKSFSLVKNFSLQPLVMCYMKKLEDLEKSFSLVKNFSLQPLVMCYMKKLEDLEKSFSLVKNFSLQPLVMCYMKKLEDLEKSFSLVKNFSLQPLVMCYMKKLEDLEKSFSLVKNFSLQPLVMCYMKKLEDLEKSFSLVKNFSLQPLVMCYMKKLEDLEKSFSLVKNFSLQPLVMCYMKKLEDLEKSFSLVKNFSLQPLVMCYMKKLEDLEKSFSLVKNPSLQPLVMCYMKKLEDLEKSFSLVKNPSLQPLVMCYMKKLEDLEKSFSLVKNDSDLTLKQYILEKSALFSTELSVLHNFFSPSKTRGGEVVQRLTERN VGKNVKIJVMULQFERTLFILKTRNVHYCHLARELMSLHDLDUG EICTVDPCHKFTWCLDACHERSFYSPKTRGGEVVQRLTERN VGKNVKIJVMULQFERTLFILKTRNVHYCHLARELMSLHDLDUG EICTVDPCHKFTWCLDACHERSFSPKTRGGEVVQRLTERN VGKNVKLJWNLQFTLYRHLGELVGGTLPRDSSPDLL LLERLLAGGAMVNIDSQVKERGVELTSTLYMMSFLVD DYTFNVDOKLPABEKAPVSYPNTLPSFTKKPLOGGTLARDSSPDL LLADEFALEDFCSLEDGFFTLASFNHTMATALLIHLHPRY APSKLERLOKALEPTGGSGERVKELTSOLGEKLEQLDHRKPSPA QAASTPALRILPJSVAPAPAPI. 6373 67 711 PSRAARASPARLPAMVSWITSFLVVLIFGTLYPAYYSYKAVKSK DIKRYVKMMMYWITFALFTTAETFTDIFLCMPFFYYSLKTAFVA WLLSPTYKGSSLIVKRVHPTLSKSKEIDDCLVQAKORSYDAL VHYCKRGLAVAATAAVAAASKGQALSERLRSFSMODLTTIRED GARPASPSPPDGASGASGKIGQFMSKRASESANSSGTA 6374 535 2105 HKLFCSYISTSEFFSSTRHBGCFHTFCNYTSSTTFLSSTRDHS CPTHTTCNYTSSTTFLSSTRDH SCPTHTSCN				KFWKVSRPLELCYAPTKDPK
LINNNFENALCRESSEYLECRMERKLMLQEPLEKLGFGDLTSC KSEAK KSEAK KSEAK RYSAIASBGKAEERYKKLEDLLEKSFSLVKMFSLQPVVMCVMKH LPKVPEKKLKLVYADAKELYRACAVEVRRQIMODNOALFGDBYSF LLKQYILEKSSALFSTELSVLHMFSSPKTRRQGEVVQRLTRM VGKNVKLYDMVLQFLRTLFLRTRNVHYCTLRAELLMSLHDLDVG EICTVDPCHKFTWCLDACIRERFVDSKRARELQGFLDGVKKGGE OVLGDLSMILCDPFAINTLALSTVHLQELVGGTLDGVKKGGE OVLGDLSMILCDPFAINTLALSTVHLQELVGGTLDGVKKGGE OVLGDLSMILCDPFAINTLALSTVHLQELVGGTLDGVKKGGE OVLGDLSMILCDPFAINTLALSTVHLQELVGGTLDGVKKGGE OVLGDLSMILCDPFAINTLALSTVHLQELVGTDGSPGLL LLIELLALGGGAMDKIDSQVFKBFKMEVSLITTFLPMLMSFLVD DYTRIVDQKLPABERGAPVSYDNTLPESTTKFLOEQRMACEVGLY YVLHITKQRNKNALLRLLPGLVETTGDLAFGDIFHLLITGNLAL LADEFALEDFCSSLEDGFFILASPRKENNHRALRLLHLHHPRV APSKLEALQKALEPFGGGGGADVKELYSOLGEKLEGLDHRKFSPA QAASTPALBILPLSVPAPAPL 6373 67 711 PSRARASPARLDAMVSWIISRLVVLIFGTLYPAYYSYKAVKSK DIKKYVKMMMYMIIFALFTTAETFTDIFLCMFFFYYSLKIAFVA WLLSPYTKGSSLLVRKFVHPTLSSKEKELDDCLVQAKDRSYDAL VHCKKGLNVAATAAVMASKGGABERLSFSMGDLTTIRGD GAPAPSGPPPPGGGRASGKHGQPKMSRSASSSASSGTA 6374 535 2105 HKLFCSYISTSFFSSTRHSGFTHTFCNYTSSTIFLSSTRDHS CPHTTCNYTSSTIFLSSTRDHSGPKTSCTYTSSTIFLSSTRDHS CPHTTCNYTSSTIFLSSTRDHSGPKTSTTFLSSTTDHS CPHTTCNYTSSTIFLSSTRDHSGPKTSTTFLSSTTDHS CPHTTSCNYTSSTIFLSSTRDHSGPKTSTTFLSSTTDHS CPHTTSCNYTSSTIFLSSTRDHSGPKTSTTFLSSTTDHS CPHTTSCNYTSSTIFLSSTRDHSGPKTSTTFLSSTTDHS SGQHLITAVADHLFKLKTTSWELGFRSAIELDTPSMTAEQVAA LEGSVWEKIRDRLPMVREISLDDPEVEQVSGRGLPDDHAGPIR VNIEGVDSNNCCGTHVSNLSDLQVIKLIGGTEKKKNRTNLIFL SGRRVLKMMERSHGTEKALTALLKCGABDH+VAVKIQNSTKIL QKNNLMLRDLAVNIAHSLRNSPDGGVVLLHRKEGDSFFMMII ANBIGSETLLFLTVTGDEKGGGLFLLAGPPASVETLGPRVAEVL EGKGAGKKGRPQGKATMMSRRMEAQALLQVISTGSEAKS 1 1535 ANMAAATRPVELFBAGGGGREKEMSSRSHSGGGLAAMSRT CPGRPRRGQQVVRGPTMLVTAYLAFVGLLASCLGLELSRCRAK PPGRACSNPSFLRFQLDTTYQDEKGGREKEMSRSSHSHSGGGLAAMSRT CPGRPRRGQQVVRGPTMLVTAYLAFVGLLASCLGLELSRCRAK PPGRACSNPSFLRFGLDTYQVYFLALAADHLQAFTIYKLYQHYY FLEGGIALLVYCGLASTVLFGLVASSLVDMLGRKNSCVLFSLTY SLCCLTKLSQDYFYLLVGRALGGLSTALLFSRFAMYIHEHVER HPFPAEWTPATPARAPKHVLLLYALLGAVLTVVPSLEMTHSTSSP SLCSSLVIKRITSTRSFHLQPHILLSLAVLTVVPSLEMTHTSTSP	6371	3	288	GVANMSTAMNFGTKSFQPRPPDKGSFPLDHLGECKSFKEKFMKC
6372 2141 625 RVSATAGEGKAEERYKKLEDLLEKSFSLVKMPSLOPVVMCVMKH LPKVPEKKLKLVMADKELYRACAVEVRRQIMQDNQALFGDEVSP LLKQY LLEKSALFSTELSVLINFFSSPSTRRGGEVVQRITRM VGKMYKLYDMVLQFLKTELFRYSPKTRRGGEVVQRITRM VGKMYKLYDMVLQFLKTELFRYSPKTRRGGEVVQRITRM VGKMYKLYDMVLQFLKTELFRYSPKTRRGGEVVQRITRM VGKMYKLYDMVLQFLKTELFRYSPKTRRGGEVVQRITRM VGKMYKLYDMVLQFLKTELFRYNHYCTLRAELLMSLHDLDVG EICTVDPCHKFTMCLDACTREFPVDSKRARRLQGFLGGVKKQDE OVLGDLSMILCDPPAINTLALSTVRHLQELVGGETLPRDSSPDLL LLLRLALGQGANDM.DGQVFKBPKMEVELITRILPMLMSFLVD DYTFNVDQKLPAEEKAPVSYPMTLDESSTFYBLORQRMACEVGLY YVLHITKQRNKMALIRLLEGLUGTFGDLAFGDI FIHLITGNLAL LADEPALEDPCSSLFDGFFLTASPRKENVHRHALRLLIHLHPRV APSKLEALQKALEPTGQSGGAVKELVGEKLEQLDHKKPSFA QAAETPALBLPLSVVAPAPAPL 6373 67 711 PSRRARRSPARLDAMVSWITSELVVLIFGTLYPAYYSYKAVKSK MLLSPYTKGSSLLYRKFVHPTLSSKEKEIDDCLVQAKDRSYDAL VHFCKRGLAVAATAAVMAASKGQGALSERRSFSMDDLTTIRGD GAPAPSGPPPPGGGRASCKHGQPKMSRSAGSGASSGTA VHFCKRGLAVAATAAVMAASKGQGALSERRSFSMDDLTTIRGD GAPAPSGPPPPGGGRASCKHGQPKMSRSAGSGASSGTA UNFCKRGLAVAATAAVMAASKGQGALSERRSFSMDDLTTIRGD GAPAPSGPPPPGGGRASCKHGQPKMSRSAGSGASSGTA 6374 535 2105 HKLFCSYLSTSEPSSTRHSCPFHTFCNYTSSTIFLSSTRDHS CPTHTFCNYTSSTIFLSSTRDHSCPTHTFCNYTSSTIFLSSTRDHS CPTHTSCNYTSSTIFLSSTRDHSCPTHTFCNYTSSTIFLSSTRDHS CPTHTSCNYTSSTIFLSSTRDHSCPTHTFCNYPRPIIRLSSC CPABLQTEGSNOKKRBVLSGFQVVLEDTVLPPEGGGGDPDDRGTIN DISVLKNYRRGRGADHFYOTLDFGSQVLWLEDWERRPDHMQOH SQCHLTTAVADHLFKLKTTSWELGRFRSAIELDTPSMTAEQVAA IEQSVNEKIRDRLPNIVRELSLDDPEVEGVGGRGLDDDHAGGIR VNIBOVDSNMCCGTHVSNLSDLQVIKILGTERGKKNRTNLIFL SGRNVLKWMERSHGTEKALTALLKCGAEDHVEAVKKIQNSTKIL QKNINLILEDLAVHATHASLERNSGVVVLEDTVLPGGGGGLAMSSTT CPGRRRPGQQVVROPMLVTAVLAFFGLLASCLUGLELSRCRAK PPGRACSNPSFLRFQLDFYVQPFGRAGGLADAMSRT CPGRRRPGQQVVROPMLVTAVLAFFGLLASCLUGLELSRCRAK PPGRACSNPSFLRFQLDFYVQVYFLALAADLGAPTLYKLYCHYY FLEGGIALLYVCGLASTVVBCLAVSSLVDMLGRKNSCVLFSITY SLCCLTKLSQDYFVLLVGRALGGGSTALLSPAFMYTHEHVER HDFPBEWIPATFARAPSMIVLAVVAGAASSLVDMLGRKNSCVLFSITY SLCCLTKLSQDYFVLLVGRALGGGSTALLSPAFMYTHEHVER HDFPBEWIPATFARAPSMIVLAVVAGAASSLVASMIGLGPVAP FVAAIPLLALAGALLARMGENVDRQRAFRTCAGGICCLLSDR RVLLLGTTQAAFESVIFIFFYLLTHFYLDRAFFLISSFMAA SLLGSSLVRIATSK				LHNNNFENALCRKESKEYLECRMERKLMLOEPLEKLGFGD'TSG
LEKYPEKKLKUVADAKELIYACAVEVRRQIMONALIFGEVSE LLKQYILEKSALFSTELSVLINFFSPSPKTRRGGEVVQKLTRM VGKAVKLYDMVLOFLRTLFIRTNYVYCTLRAELLMSLHDLDVG EICTVDPCHKFTACLDACTREFFVDSKRARELQFFLGSVKKGE OVLGDLSMILCDEFAINTLALSTVEHLQELIVGOSTLPRDSPDLL LLELLALGGGADMIDISQVFRMEVELLTRIPHIMSPLVD DYTFNVDOKLPAEEKAPVSYPNTLPESFTKFLQEQRMACEVGLY YVLHITKQRNKNALIRLUFGLVETFGDLAFGDIFLHLLITGNLAL LADEFALEDCSSLFFGFFLTASPKEWVHRHALRLIHHLPRV APSKLEALQKALEPTGGGEAVKELYSQLGEKLEQLDHRKFSPA OAASTPALEBLPLSVVPAPAPL 6373 67 711 PSRARASPARLDAMVSWII SELVVLIFGTLYPAYYSYKAVKSK DIKSYVKWMYWIIFALFTTASTFTDIFLCMPFPYYBLKIAFVA WLLSPYKKGSLLYRKFVHPTLSSKEKEIDDCLVQAKDRSYDAL VHFGKRGLNVAATAAVMASKGGALSERLRSSMODLTIRGD GAPAPSGPPPGGGRASGKHGQPKNSKSASGSASSGSTA HKLFCSYISTSFFPSSTRHSCPTHTFCNYTSSTIFLSSTRDHS CPTHTFCNYTSSTIFLSSTRDHSCPTHTSCNYTSSTIFLSSTRDH HSCPTHTSCNYTSSTIFLSSTRDHSCPTHTSCNYTSSTIFLSSTRD HSCPTHTSCNYTSSTIFLSSTRDHSCPTHTFCNYPRPITRLSSC CPAELGTGSNGKKREVLSGFQVULDTVLPPEGGGDDDRGTIN DISULRVTRGEQADHPTQTPLDPGSQVLVRVDWERRFDHMQOH SCQHLITAVADHLFFLIKTTSWELGRFRASAELDTPSMTAEQVAA IEGSVMEKIRDELPVNVELSLDDPEVEQVSGREIPDDHAGFIR VVNIEGVDSHMCCGTHVSNLSDLQVIKILGTERGKNNTTNLIPL SGNRVLKWMERSHGTKALTALLKCGAEDHVEAVKKIQNSTKIL QRNNINLIRGLAVHIAHSLRNSPDWGGVVULHRKEGDSFFMII ANNIGSESTLIPLTVGDEKGGLFLLAGPDASVETLGPRVAEVL GEGGAKKGFPGGAKTMKSRRMAQAPPASVETLGPRVAEVL EGGGAKKGFPGGAKTMKSRRMENGALDQVISTQSAKE 6375 1 1535 AIMAAATRPVRIPEAGCGGRERCWNPSRRSHSGEGGLAANSRT CPGPRRRGQQVRGPTMLVTATLAFVGLASCLGLELSRCRAK PPGRACSNPSFLRFCDLFFQVYFLALAADWLQAPYLYKLLYGHYY FLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTY SLCCLTKLSQDYFULLVERALGGISTALLPSAFRAWYHHEHVER HPFPBEWIPATFARAPANNIVLAVVQAAAEAVASWIGLGFVAP FVAAIPLLALAGALARNWGENYDRQAPSRTCAGGIRCLLSDR RVLLLGTLQAAFESVIFIFFVFLMTPVLDFAGFLGISTSAFMYHHEHVER HPFPBEWIPATFARAPANNIVLAVVQAAAEAVASWIGLGFVAP FVAAIPLLALAGALARNWGENYDRQRAPSRTCAGGIRCLLSDR RVLLLGTLQAAFESVIFIFFVFLMTPFVLDFAGFLGISTSMAA SLLGSTURINTSKYHLQPWHLDLLSLAVULVULVELFMITFSTSP	ŀ			KSEAKK
LIKOYIEKKIJVANDICELVRACAVEVRO(IMODNOALFGEVVORITRM VGRIVKLYDMVLOFLERTELLSVLHINFSPSPKTRROGEVVORITRM VGRIVKLYDMVLOFLERTELLERTRINVHYCTLERBELLMSLHILDUG EICTVDPCHKFTMCLDACIRERFVDSKERRELGGFLIGVKKGGE OVLGDLSMILCOPPAINTLALSTVEHLQELVGGETLPRDSPDLL LLLRLALAGGANDMIDSQVFKEPKMEVELITRFLPMLMSFLVD DYTENVDGKLPAEEKAPVSYPHTLDESSTFELORORMACEVGLY YVLHITRGRIKMALIRLIGHGLVGTFGDLAFGDI FHLLTGNILL LADEFALEDPCSSLFDGFFLTASPRKENVHRHALRLLIHLHPRV APSKLEALQKALEPTGGSGEAVKELYSGLGEKLEGLDHRKFSPA OAAETPALELPJSVEAPAPL BYRAARSPARLSAMVSHITSRLVVLIFGTLYPAYYSYKAVKSK DIKEYVKMMMYWIIFALFTTAETFDIPLCMFFFYYEKLTAFVA WLLSPYTKGSSLLYRKFVHPTLSSKEKEIDDCLVQAKDRSYDAL VHFCKRGLANVAATAAVMAASKGGGLSERLESFSMQDLTTIRGD GAPAPSGPPPPPGSGRASGKHGQPKMSRSASESSSSTA 6374 \$35 2105 HKLFCSYISTSEPSSTRHSCCPTHTFCNYTSSTIFLSSTRDHS CPHTTFCNYTSSTIFLSSTRDHSCPTHTSCNYTSSTIFLSSTRDH SCPTHTFCNYTSSTIFLSSTRDHSCPTHTFCNYTPSTIFLSSTRDH SCPTHTSCNYTSSTIFLSSTRDHSCPTHTFCNYTPSTIFLSSTRDH SCPHTTSCNYTSSTIFLSSTRDHSCPTHTFCNYTPSTIFLSSTRDH SCPHTTSCNYTSSTIFLSSTRDHSCPTHTFCNYTPSTIFLSSTRDH SCPHTTSCNYTSSTIFLSSTRDHSCPTHTFCNYTPSTIFLSSTRDH SCPHTTSCNYTSSTIFLSSTRDHSCPTHTFCNYTPSTIFLSSTRDH SCPHTTSCNYTSSTIFLSSTRDHSCPTHTFCNYTPSPIRMTAEQVAA IEQSVNEKIRDLPVNVRELSLDDPEVEQVSGRGLPDDHAGFIR VVNIEOVDSNMCCGTHVSNLSDLQVIKILDTERGKKNRTNLIFL SGRRVLKMMERSHGTERALTALLTLETERGAPUNDHAUPAVA IEQSVNEKIRDLPVNVRELSLDDPEVEQVSGRGLPDDHAGFIR VVNIEOVDSNMCCGTHVSNLSDLQVIKILDTERGKKNRTNLIFL SGRRVLKMMERSHGTERALTALLGAGALDAUGAVKILQNSTVIL OKNNLNLLRDLAVHIAHSLRNSPDWGGVVILHRKEGDSEFMII ANBIGSESTLIFLTVGDEKGGGLFLLAGPPASVETLGFEVAVEVL GEKGAGKKGFFGGKATKMSRRMEQHLADQVISTGSAKS CCPGRERRGQVVRGPMUVTAVLAFVGLASCLGLEISRCRAK PPCRACSNESFLIRFCLDFTQVYFALLAADWLGAPVIJKLLYCHYY FLEGQIAILYVCGLASTVLFGLVSASLVDWLGRKNSCVLFSLTY SLCCLTKLSQDYFVLLVGRALGGLSTALLFSFRAMYHHEIVER HPFPAEMIPATFRARAWNINVLAVVAGVAAEAVASWIGLGFVAP FVAAIPLLAAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDR RVLLLGTLGAAFESVIFITFFTSSP	6372	2141	625	RVSAIASEGKAEERYKKLEDLLEKSFSLVKMPSLOPVVMCVMKH
LLKQYILEKESALFSTELSV.HHFFSPSPKTRQGEVVORLTEM VGKNYKLYDMVLOPLRTL.FLETRIVHYCTLRAELLMSLHDLDVG EICTVDPCHKFTWCLDACTRERFVDSKRARELQGFLLGVKKGGE OVLGDLSMILCDPAINTLALSTVHLUGLVGGETLGFNSPDLL LLELLALGGGADMMIDSQVFKBFKMEVELITFPLEMLMSPLVD DYTRIVDOKLPAEKAPVSYPNTLPESFTKFLQEQRMACEVGLY YVLHITKQRIKNALLRLLGOLVETFGDLAFGDIFTHLLTGNLAL LADEFALEDFCSSLFDGFFLTASPRKENVHRHALRLLIHLHPRV APSKLEALGKALFFTGGGGEAVKELYSQLGEKLEQLDHRKPSPA QAASTPALELPLPSVPAPAPL 6373 67 711 PSRARASFARLZAMVSWIISRLVVLIFGTLYPAYYSYKAVKSK DIKKYVKWMMYWIIFALFTTAEFFTDIFLCWPPFYYSELKIAFVA WLLSPYTKGSSLYKKFVHPTLSSKEKEIDDCLVQAKDRSYDAL VHFGKRGLNVAATAAWAASKGQGALSRALRSFSMQDLTTIRGD GAPAPSGPPPPGSGRASGKHGQPKMSRASESASSSGTA HKLFGSYLSTSEPPSSTRHSCFTHTFCNYTSSTIFLSSTRDHS CPTHTFCNYTSSTIFLSSTDHSCPTHTFCNYTSSTIFLSSTRDH SCPTHTSCNYTSSTIFLSSTDHSCPTHTFCNYTSSTIFLSSTRDH HSCPTHTSCNYTSSTIFLSSTDHSCPTHTFCNYTSTIFLSSTRD HSCPTHTSCNYTSSTIFLSSTDHSCPTHTFCNYPRPIIRLSSC CPAELQTEGSNGKKEVLSGFQVVLEDTVLPPEGGGQPDDRGTIN DISULRVTRRGEQADHFTQTPLDPGSQVLVRVDWERRFDHMQQH SCQHLITAVADHLFKLKTISWELGFFRASIELDTFSMTAEQVAA IEGSVEKKTRBLPVWKRELSLDDPEVEQVSGRGLPDHAGGIR VVNIEGVUSNMCCGTBVSNLSDLQVIKTLGTEKGKKNTINLIFL SGNRVLKWMERSHGTEKALTALLKCGAEDHVEAVKKILGNSTKIL QKNNINLIERLBAVH IAHSLRNSPDMGGVVILHRKSGDSEFMNII ANSIGSESTILFILTVCDEKGGGLFLLAGPASVETLGRVARVL EGKGAKKGFFGCKATKMSREGAGALLQDYISTGGSAKE CPGRRRFGQQVVRGFTWITAYLAFVGLLAGPLSVTGGSAKE CPGRRRFGQQVVRGFTWITAYLAFVGLLAGTGLESKCRAK PPGRACSNFSFLERFQLDFYVVTLALADMULQAPYLYKLYQHYY FLEGQIAILYVCGLASTVLFGLVASSLVDMLGRKNSCVLFSLTY SLCCLTKLSQDYFVLLVCRALGGLSTALLFSAFRAWYHEHVENER HDFPREWIPATFARAFNHVLVAVAGAABARANSMIGLGPVAP FVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDR RVLLLGGTQAFESVIPTFVFLWTFVLUPGLADAUSITFSTSP				LPKVPEKKLKLVMADKELYRACAVEVRRQIWODNOALFGDEVSP
VGKNYKLYDWYLOFLERTRUNYHCTLRABILNBLHDLDUG EICTVDPCHKFTWCLDACIRERFVDSKRARELQGFLIGVKKQGE OVLGDLSMILCDPFAINTLALSTVRHLQELVGGETLPRDSPDLL LLERLLAIGQGAMDM.IDSQVFKBPKMEVELITRFLPMLMSPLVD DYTFNVDOKLDABEKAPSVFNLTPESFTKPLQGGRMACEVGLY YVLHITKQRNKNALIRLLPGLVETFGDLAFGDIFLHLLIGNIAL LADEFALEDFCSSLFDGFFLTASPRKENVRRHALRLLIHHJPRV APSKLEALGKALFPTGGGEBAVKELYSQLGEKLEQLDHRKPSPA QAAETPALELPLPSVPAPAPL 6373 67 711 PSRARASPARLDAMWSWITSRLVVLIFGTLYPAYYSYKAVKSK DIKKEVKMMSWWIIFALFTTAEFFTDIFLCMPPFTYELKIAFVA WLLSPYTKGSSLLYRKFVHPTLSSKEKEIDDCLVQAKORSYDAL VHPCKKGLANVAATAAVMAASKGGALSERLRSFSMODLTTIRGD GAPPSGPPPPGSGRASGKHOKGPKMSRASESASSGTA 6374 535 2105 HKLFCSYISTSEFPSSTRHHSCPTHTFCNYTSSTIFLSSTRDH CPTHTFCNYTSSTIFLSSTRDHSCPTHTFCNYTSSTIFLSSTRDH SCPTHTSCNYTSSTIFLSSTRDHSCPTHTFCNYTSSTIFLSSTRDH CPTHTFCNYTSSTIFLSSTRDHSCPTHTFCNYTSSTIFLSSTRDH SCPHTHSCNYTSSTIFLSSTRDHSCPTHTSCNYTPSITLSSC CPABLQTEGSNGKKEVLSGFQVVLEDTVLPPEGGGQPDDRGTIN DISVLKWTRRGEQADHFTQTPLDPGSGQVLVRUDMERRPDHMQQH SCQHLITAVADHLFKLKTTSWELGFFRSALELDTPSMTAEQVAA IEGSVEKKIRDRLPVNTRELSLDDPEVEQVSGRGLPDDHAGFIR VVNIEGVDBNMCCGTHVSNLSDLQVVLKLIGTEKGKKNRTNLIFL SGMRVLKWMERSHGTEKALTALKCGAEDHVEAVKKLONSTKIL OKNNLMLLRCLAVH I HABLRNSPDWGGVVI LHRKEGDSEFMN I ANEIGSBETLLFLTVGDEKGGGLFILLAGPPASVETLGRVAEVL EKGGAKKGRPGCKATKMSRRMEAQALLQDVISTGSAKE 6375 1 1535 AIMAAATREVRLPEAGCEGRERCWNPSRSRSHSGEGGLAMSET CPGRPRRPGQQVVRGPTMLVTAYLAFVCLLASCULGPYVLYHY FLEGGIALLYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTY SLCCLTKLSQDYFVLLVGRALGGLSTALLFSAFRAWYHEHVENER HDFPREWIPATPARAAFNHVLLVVAGVAAEAVASWIGLGPVAP FVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDR RVLLLGTIQALFESVIFIFVELWTPVLLDPHAAPLGIITSSSPMAA SLLGSSLYRIATSKRYHLQPHLLSAVLJUVSLFBHLTFSTSP				LLKQYILEKESALFSTELSVLHNFFSPSPKTRRQGEVVORLTRM
EICTVPCHKFTWCLDACTRERPYDSKRARELQGFLDGVKKGQE QVLGDLSMILCDPFAINTLALSTVRHLQELVCQETLPRDSPDLL LLERLALGQSAMDMIDSQVFKEPKMEVELITRFLPMLMSPLVD DYTFNVTQKLPAEEKAPVSYPNTLPSSTKPLQGQRMACEVGLY YVLHITKQRNKNALLRLDPGLVETFGDLAFGDIFHLLTGNLAL LADEFALEDFCSSLFDGFFLTASPKKENVHRHALRLLHHLRV APSKLEALQKALEPFGQSGEAVKELYSQLGEKLEQLDHRKPSPA QAAETPALELPLSVPAPAPAPL BSRRARASPARLPAMVSWIISRLVVLIFGTLYPAYYSVKAVKSK DIKEYVKMMYWIIFALFTTAETFTDIFLCMPFPYYELKIAFVA WLLSPYTKGSSLLYRKFVHPTLSKKKEIDDCLUQAKDRSYDAL VHFGKRGLNVAATAAVMAASKQQGALSERLRSFSMQDLTTIRGD GAPAPSGPPPPGSGRASGKHQPKMSRSASESASSGTA 6374 535 2105 HKLFCSYISTSEFFSSTRHHSCPTHTFCNYTSSTIFLSSTRDHS CPTHTFCNYTSSTIFLSSTRDHSCPTHTSCNYTSSTIFLSSTRDHS CPTHTFCNYTSSTIFLSSTRDHSCPTHTFCNYPRPIIRLSSC CPAELQTEGSNGKKRVLSGTQVULEDTVLPPEGGGQPDDRGTIN DISVLRVTRRGQADHFTQTPLDPGSQVLVRVDMERRFDHMQQH SCQHLITAVADHLFKLKTTSWELGRFRSAIELDTPSMTAEQVAA IRQSVBKKIRDRLPVNVRELSLDDPYEQVSGRLPDDHAGFIR VVNIEGYDSMCCGTHVSNLSDLQVIKIGFEKGKKNRTNLIFL GKNNLMLLRCLAVHIAHSLENSPDWGGVULHRREGDSEFNNII ANEIGSETLIFTUTGDEKGGCFPLLAGPPASVETLGPRVABVL EGKGAGKKGRFQGKATKMSRMBAQALLQVISTGSAKE 6375 1 1535 AMAAATRPVRLEFAGGEGRERCMNPSRSSHSGEGGLAMSRT CPGRPRRPGQQVVRGPTMLVTAYLAFVGLLASCLGLELSRCRAK PPGRACSNPSFLERFQLDFTQVYYLALAADMLQAPYLYKLYQHYY FLEGGIAILYVCGLASTVLFGLVASSLVDMLGRKNSCVLFSLTY SLCCLTKLSQDYFVLLVGRALGGLSTALLFSAPAWYIHEVVER HDFPAEWIPATPARAAFWHVLAVVAGVAAAEAVASWIGLGFVAP FVAAIPILLALGALALRNMGENVDRQAFSRTCAGGLRCLLSDR RVLLLGTIQALFESVIFIFVFUDHGRAFUTJDFGIFSSFMAA SLLGSSLYRIATSKYRHLQPNHLLSLAVLJVVFSLEMITFSTSP]	1		VGKNVKLYDMVLQFLRTLFLRTRNVHYCTLRAELLMSLHDLDVG
OVLOBISMILCDPFAINTLAISTVRHLOELUGGTLPERS PDLL LLERLAIGGAMDMIDSQVFKBPKMEVELITRFLPMLMS PLVD DYTFNVDQKLPABEKARVSYPNTLDESTFKFLOEGRMACEVGLY YVLHITKQRNKNALLRLUPGLVETTGDLAFGDIFLHLLTGNLAL LADEFALEDFOSSLEDGFLTASPRKENVHRALRLLIHLHPRV APSKLEALQKALEPTGGSGEAVKELYSCIGEKLEGLDHRKPSPA QAAETPALEDLPSVPAPAPL 6373 67 711 PSRARASPARLPAMVSWIISRLVVLIPGTLYPAYYSYKAVKSK DIKEYVKWMMYWIIFALFTTABTFTDIFLCWPFFYYELKIAFVA WLLSPYTKGSSLLYKKFVHPTLSSKEKEIDDCLVQAKDRSYDAL VHFGKRGLINVAATAAVMAASKGQGALSERLRSFSMQDLTTIRGD GAPAPSGPPPPGGGRASGKHQPKMSRSASSASSGTA 6374 535 2105 HKLFCSYISTSEFPSSTRHHSCPTHTFCNYTSSTIFLSSTRDHS CPTHTFCNYTSSTIFLSSTROHSCPTHTCNYTSSTIFLSSTRDHS CPTHTFCNYTSSTIFLSSTROHSCPTHTCNYPRPIIRLSSC CPABLQTEGSNGKKBVLSGFQVVLEDTVLPPEGGGDPDRGTIN DISVLRVTRRGEQADHFTQTPLDPGSQVLVRVDWERRFDHMQQH SCGHLITAVADHLFKLKTTSWELGRFRSAIELDTPSMTAEQVAA IEGSVBKKIRDRLPVNVRELSLDDPEVEQVSGRGLPDDHAGFIR VWNIEGVDSNMCCGTHVSNLSDLQVIKILGTEKGKKNRTNLIFL GKNNLKWLERSHGTEKALTALLKCGAEDHVEAVKKLQNSTKIL OKNNLNLLRDLAVHIAHSLRNSPDWGGVVLLHREGDSEFMNII ANBIGSESTLLFLTVGDEKGGIFLLAGPPASVETLGPRVAEVL EGKGAKKGRFGCKATKMSRRMBAQALLOPYISTGSAKE 6375 1 1535 AIMAAATRPVRLPFAGGEGRERCMNSRSRSHSGEGGLAAMSRT CPGRPRRPGQVVVRGPTMLVTAYLAFVGLLASCLIGELSRCRAK PPGRACSNPSFLRFQLDFYQVYFLALADULQAFYLYKLYQHYY FLEGGIAILYVCGLASTVLPGLVASSLVDWLGRKNSCVLFSLTY SLCCLTKLSQDYFVLLVGRALGSTALLFSAFFAMYIHEHVER HPFPREWIPATFARAAFWHVLLAVVAGVAAAEAVASNIGLGFVAP FVAAIPLLLAGALA-RNWGENYDRQRAFSRTCAGGLRCLLSDR RVLLLGTIQALFESVIFIFVFFWTPVLDPRIGAFLGIIFSSFMAA SLLGSSLYNIATSKYRHLQPPHLLSLAVLIVVSSLMHITSTSSP	į l			EICTVDPCHKFTWCLDACIRERFVDSKRARELOGFLDGVKKGOE
LLLRILAGGGAMDMIDSQVFKBPKMEVELITRFLPMLMSPLVD DYTFNVDQKLPAEEKAPVSYPNTLPESFTKFLOEQRMACEVGLY YVLHITKQRNKNALLRLEGIVETFGGLAFGDI FLHLLITGNIAL LADEFALEDFCSSLFDGFFLTASPRKENVHHALRLLIHLHPRV APSKLEALQKALEPTGQSGEAVKELYSQLGEKLEQLDHKKFSPA QAAETPALELELPSVPAPAPL 6373 67 711 PSRAARASPARLDAMVSWIISRLVVLIFGTLYPAYYSYKAVKSK DIKEYVKWMMYWIIFALFTTAEFTDIFLCWFPFYYELKIAFVA WLLSPYTKGSSLLYKKFVHPTLSSKEKEIDDCLVQAKDRSYDAL VHFGKRGLNVAATAAVMAASKGQGALSERLRSFSMQDLTTIRGD GARAPSGPPPPGGGRASKKHGQPKMSRASESASSSGTA HKLFCSYIISTSEFPSSHHSCPTHTFCNYTSSTIFLSSTRDHS CPTHTFCNYTSSTIFLSSTRDHSCPTHTFCNYTSSTIFLSSTRDH HSCPTHTSCNYTSSTIFLSSTRDHSCPTHTFCNYTPSTIFLSSTRDH HSCPTHTSCNYTSSTIFLSSTRDHSCPTHTFCNYPRPIIRLSSC CPABLQTEGSNGKKEVLSGFQVVLEDTVLFPEGGGQPDDRGTIN DISVLRVTRRGEQADHFTQTPLDPGSQVLVRVDWERRFDHMQQH SGQHLITAVADHLFKLKTTSWELGRFRSAIELDTPSMTAEQVAA IEQGVNEKIRGRLPVNNVRELSLDDPEVEQVSGRGLPDDHAGFIR VVNIEGVJDSNMCCGTHVSNLSDLQVIKILGTERGKKNRTNLIFL SGRRVLKWMERSHGTEKALTALLKCGAEDHVEAVKKLQNSTKIL QKNNLNLLRCLAVHIAHSLRNSPDWGGVVIKHILGTERGKKNRTNLIFL SGRRVLKWMERSHGTEKALTALLKCGAEDHVEAVKKLQNSTKIL QKNNLNLLRCLAVHIAHSLRNSPDWGGVVIKHILGTERGKNRTNLIFL SGRRVLKWMERSHGTEKALTALLKCGAEDHVEAVKKLQNSTKIL QKSNLLNLLFLAVDHLEAVHIAHSLRNSPDWGGVVIKHKEGDSERMNII ANEIGSESTLLFLTVCDEKGGGLFLLIAGPPASVETLGPRVABVL EGKGAGKKGRFQGKATKMSRRMEAQALLQDYISTQSAKE 6375 1 1535 AIMAAATRFVILDEBGCGGGERERCWPSRSRSHSGEGGLAAMSRT CPGPRRRPGQQVVRGPTMLVTAYLAFVGLLASSLUDWLGRKNSCVLESLTY SLCCLTKLSQDYFVLLVGRALGGLSTALLFSAFEAWYIKLYCHYY FLEGGIAILVVCGLASTVLFGLLASSLUDWLGRKNSCVLESLTY SLCCLTKLSQDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVBR HDFPAEWIPATFARAAFWHNULAVAGVAAEAVASNIGLGPVAP FVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDR RVLLLGTIQALFESVIFIFVFLWFPLDPHGAPIGIIFSSFMAA SLLGSSLYRIATSKRYHLQPMHLLSLAVLIVVFSLFMLTFSTSP	i i			QVLGDLSMILCDPFAINTLALSTVRHLQELVGQETLPRDSPDLL
DYTFNVDQKLPAEEKAPVSYPNTLPESFTKFLQEQRMACEVGLY YVLHITKQRNKNALIRLLPGLVETFGDLAFGDIFLHLIGNLAL LADEFALEDFCSSLFPGFFLTASPRKENVHRHALRLLHHLHPRV APSKLEALQKALEPTGQSGEAVKELYSQLGEKLEQLDHRKPSPA QAAETPALELPLPSVPAPAPAPI BYRAARASPARLPAMVSWIISRLVVLIFGTLYPAYYSYKAVKSK DIKEYVKWMMYWIIFALFTTAETFTDIFLCWFPFYYSLKIAFVA WLLSPYTKGSSLLYRKFVHPTLSSKEKEIDDCLVQAKDRSYDAL VHFGKRGLNVAATAAVMAASKGQGALSERLRSFSMQDLTTIRGD GARAPSGPPPPGSGRASGKHGQPKMSRSASESASSSGTA 6374 535 2105 HKLFCSYISTSEFPSSTRHHSCPTHTFCNYTSSTIFLSSTRDHS CPHTHFCNYTSSTIFLSSTRDHSCPTHTSCNYTSSTIFLSSTRDH HSCPTHTSCNYTSSTIFLSSTRDHSCPTHTFCNYTSSTIFLSSTRDHS CPHREQNTHTSCNYTSSTIFLSSTRDHSCPTHTFCNYTSSTIFLSSTRDH HSCPTHTSCNYTSSTIFLSSTRDHSCPTHTFCNYTSSTIFLSSTR HSCPTHTSCNYTSSTIFLSSTRDHSCPTHTFCNYTSSTIFLSSTR HSCPTHTSCNYTSSTIFLSSTRDHSCPTHTFCNYTSSTIFLSSTR HSCPTHTSCNYTSSTIFLSSTRDHSCPTHTFCNYTSSTIFLSSTR HSCPTHTSCNYTSSTIFLSSTRDHSCPTHTFCNYTSSTIFLSSTR HSCPTHTSCNYTSSTIFLSSTRDHSCPTHTFCNYTSSTIFLSSTR HSCPTHTSCNYTSSTIFLSSTRDHSCPTHTFCNYTSSTIFLSSTR HSCPHRECONTSTIFLSSTRDHSCPTHTFCNYTSSTIFLSSTR HSCPTHTSCNYTSSTIFLSSTRDHSCPTHTFCNYTSSTIFLSSTR HSCPTHTSWELGRFRAIELDTPSMTAEQVAA IEGSVEKIRDRLPVNVELSLDDPEVEQVSGRGLPDDHAGFIR VWHIEGVDSMNCCGTHVSNLSDLQVIKIHGEGSEFMNII ANEIGSESTLLFLTVQBEKGGGLFLLAGPBASVETLGPRAEVL EGKGACKKGRFQGKATKMSRRMEQALLQDYISTQSAKE 6375 1 1535 AIMAAATRPVLPPEAGCEGRERCWNPSRSSHSGEGGLAAWSRT CPCRPRRPGQQVVRGPTMLVTAYLAFVGLLASCLUBLESKCRAK PPGRACSNPSFLRFQLDFYQVYFLALAADWLQAFYLYKLYQHYY FLEGQIAILVVCGLASTVLFGLUASSLUDWLGRKNSCVLFSLTY SLCCLFKLSQDYFVLLVGRALGGLSTALLFSAFEANY HEHVER HDFPAEWIPATFARAAFWNHVLNVAGVAAEAVASHIGLGPVAP FVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDR RVLLLGTIQALFESVIPIFVFLWFPLUPPLDPHGAPLGIIFSSFMAA SLLGSSLYRIATSKRYHLQPMHLLSLAVLIVVFSLFMLTFSTSP				LLLRLLALGQGAWDMIDSQVFKEPKMEVELITRFLPMLMSFLVD
YVLHITKQRNKNALKRILPGIVETFODLAFGDIFLHLITGNIAL LADEFALEDFCSSLFDGFFLTASPRKENVHRHALRLIHLHPRV APSKLEALQKALEPTGGSGEAVKELYSQLGEKLEQLDHRKPSPA QAAETPALELPLPSVPRAPAPL G373 67 711 PSRAARASPARLPAMVSWITSRLVVLIFGTLYPAYYSYKAVKSK DIKEYVKWMMYWI IFALFTTABETFDI PLCWPFYYELKIAFVA WLLSPYTKGSSLLYRKFVHPTLSSKEKEIDDCLVQAKDRSYDAL VHFGKRGLNVAATAAVMAASKGQALSERLRSFSMODLTTIRGD GAPAPSGPPPPGGRASGKHQQPMSRSASESASSGTA G374 535 2105 HKLFCSYISTSEFPSSTRHHSCPTHTFCNYTSSTIFLSSTRDHS CPTHTFCNYTSSTIFLSSTRDHSCPTHTFCNYTSSTIFLSSTRDHS CPTHTFCNYTSSTIFLSSTRDHSCPTHTFCNYPRPIIRLSSC CPABLQTEGSNOKKRVLSGFQVVLEDTULPPEGGGQDDDRGTIN DISULRVTRRGEQADHFTQTPLDPGSQVLVRVDWERRFDHMQQH SGQHLITAVADHLFKLKTTSWELGRFRSAIELDTPSMTAEQVAA IEGGSVNEKIRDRLPWRELSLDDPEVRQVSGREJPDDHAGPIR VVNIEGVDSNMCCGTHVSNLSDLQVIKLIGFEKGKKNRTNLIFL SGNRVLKWMERSHGTEKALTALKCGAEDHVEAVKKIQNSTKIL QKNNLNLILRLLAVHIAHSLRNSPDWGGVVILHRKEGDSEFMNII ANEIGSESTLIFLTVODEKGGGLFLLAGPPASVETLGPRVAEVL EGKGAGKKGRFOGKATKMSRRMEAQALLQDVISTOSAKE CPGFPRRPGQQVVROPFMLVTAVLAFVGLASCLGLELSRCRAK PPGRACSNPSFLRFQLDFYQVYFLALAADWLQAFYLYKLYQHYY FLEGGIALLVVCGLASTVLFGIVASSLVDWLGRKNSCVLFSLTY SLCCLTRLSQDFFVLVGRALGGLSTALLFSAFRAWYIHEHVBR HDFPAEWIPATFARAAFWNHVLAVVGGVAAEAVASWIGLGFVAP FVAAIPILLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDR RVLLLGTIQALFESV IFIVFIVETPVLDPHGDAPLGI IFSSFMAA SLLGSSLYRTATSKRYHLQPPHILLSLAVVLTVPSLFMLTFSTSP				DYTFNVDQKLPAEEKAPVSYPNTLPESFTKFLQEQRMACEVGLY
LADEFALEDFCSSLFDGFFLTASPRKENVHRHALRLLIHLHPRV APSKLEALQKALEPTGQSGEAVKELYSQLGEKLEQLDHRKFSPA QAAETPALEIPLPSVPAPAPL 6373 67 711 PSRAARASPARLPAMVSWITSRLVVLIFGTLYPAYYSYKAVKSK DIKEYVKMMYWIFALFTTABTFTDIFLCWPFFYYSLKIAFVA WLLSPYTKGSSLLYRKYHPTLSSKEKEIDDCLVQAKDRSYDAL VHFGKRGLNVAATAAAWAASKGQGALSERLRSFSMQDLTTIRGD GAPAPSGPPPPGGGRASGKHGQPKMSRSASESASSGTA 6374 535 2105 HKLFCSYLSTSEFPSSTRHHSCPTHTFCNYTSSTIFLSSTRDHS CPTHTFCNYTSSTIFLSSTRDHSCPTHTFCNYTSSTIFLSSTRDHS CPHTTSCNYTSSTIFLSSTRDHSCPTHTFCNYTPSTIFLSSTRDHS HSCPTHTSCNYTSSTIFLSSTRDHSCPTHTFCNYPRPIIRLSSC CPABLQTEGSNGKKEVLSGFQVVLEDTVLPPEGGQPDDRGTIN DISVLRVTRRGEQADHFTQTPLDPGSQVVLRVDWBERFDIMQQH SGQHLITAVADHLFKLKTTSWELGRFRSAIELDTPSMTAEQVAA IEQSVNEKIRDRLPVNVRELSLDDPEVEQVSGRGLPDDHAGPIR VVNIEGVDSNNCCGTHVSNLSDLQVIKILGTEKGKKNRTNLIFL SGRNVLKWMERSHGTEKALTALLKCGAEDHVEAVKKIQNSTKIL QKNNLNILLRILAVHIAHSLRNSPDWGCVVILHRKEGDSEFMNII ANEIGSESTLLFLTVUDEKGGGLFLLAGPPASVETLGPRVAEVL EGKGAGKKGRFQGKATKMSRRMBAQALLQDVISTGSAKE 6375 1 1535 AIMAAATRPVRLPEAGCEGRERCMPSRSRSHSEGGGLAAWSRT CPGRPRRPGQQVVRGPTMLVTAYLAFVGLLASCLGLELSRCRAK PPGRACSNPSFLRFQLDFYQVVFLALAADWLQAPYLYKLYQHYY FLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTY SLCCLTRLSQDYFVLLVGRALGGLSTALLFSAFRAWYHHEVBR HDFPAEWIPATFARAAFWNHVLAVVAGVAAEAVASWIGLGPVAP FVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDR RVLLLGTIQALFESV I PTVFVFLWFPVLDPHGAPLGI I FSSFMAA SLLGSSLYRIATSKRYHLQPFHLLLSLAVLTVVFSLFMLTFSTSP				YVLHITKQRNKNALLRLLPGLVETPGDLAFGDIFLHLLTGNLAL
APSKLEALQKALEPTGQSGEAVKELYSQLGEKLEQLDHRKPSPA QAAETPALELPLPSVPAPAPL 6373 67 711 PSRARASPARLPAMVSWIISRLVVLIFGTLYPAYYSYKAVKSK DIKEYVKWMYWIIFALFTTAETFTDIFLCAPPFYYELKIAFVA WLLSPYTKGSSLLYRKFVHPTLSSKEKEIDDCLVQAKDRSYDAL VHFGKRGLNVAATAAVMASKGQGALSERLRSFSMGDLTTIRGD GAPAPSGPPPFGSGRASGKHGQPKMSRSASESASSSGTA 6374 535 2105 HKLFCSYISTSEFPSSTRHHSCPTHTFCNYTSSTIFLSSTRDHS CPTHTFCNYTSSTIFLSSTRDHSCPTHTFCNYTSSTIFLSSTRDH SCPHHTSCNYTSSTIFLSSTRDHSCPTHTFCNYPRPIIRLSSC CPABLQTEGSNGKKBVLSGFQVVLEDTVLPPEGGGQPDDRGTIN DISVLRVTRRGEQADHFTQTFLDPGSQVLVRVDMERRFDHMQQH SCQHLITAVADHLFKLKTTSWELGRPRSAIELDTPSMTAEQVAA IEQSVNEKIRDRLPVNVNELSLDDDEVEQVSGRGLPDDHAGPIR VVNIEGVDSNMCCGTHVSNLSDLQVIKILGTEKGKKNRTNLIFL SGNRVLKWMERSHGTEKALTALLKCGAEDHVEAVKKIQNSTKIL QKNNINLLRGLAVHIAHSLRNSPDWGGVVILHRKEGDSEFMNII ANEIGSESTLLFLTVGDEKGGGLFLLAGPPASVETLGPRAVEVL EGKGAGKKGRFGCKATKMSRRMEAQALLQDYISTQSAKE CPGRPRPGQQVVRGPTMLVTAYLAFVGLLASCLGELLSRCRAK PPGRACSNPSFLRFQLDFYQVYFLALAADWLQAPYLYKLYQHYY FLEGOIALLYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTY SLCCLTKLSQDYFVLLVGRALGGLSTALLFSAFFAWYLHEHVER HDFPAEWIPATFARAAFWNHVLAVVAGVAAEAVASWIGLGPVAP FVAAIFLLALAGALALRNGGENYDRQRAFSRTCAGGLRCLLSDR RVLLLGTIQALFESVIFIFVFLWFPVLDPHGAPLGIIFSSFMAA SLLGSSLYRIATSKRYHLQPNHLLSLAVLIVVSSLFMLTFSTSP	1 .			LADEFALEDFCSSLFDGFFLTASPRKENVHRHALRLLIHLHPRV
GARTPALELPLSVPAPAPL GARTPALELPLSVPAPAPL GARTPALELPLSVPAPAPL DIKEYVKMMYMYIISRLVVLIFGTLYPAYYYSKAVKSK DIKEYVKMMYMYIIFALFTTAETFTDIFLCMPPFYYELKIAFVA WLLSPYTKGSSLLYRKFVHPTLSSKEKEIDDCLVQAKDRSYDAL VHFGKRGLNVAATAAVMAASKGGALSERLERSFSMQDLTTIRGD GAPAPSGPPPPGGGRASGKHGQPKMSRSASESASSGTA HKLFCSYISTSTEPSSTRHHSCPTHTFCNYTSSTIFLSSTRDHS CPTHTFCNYTSSTIFLSSTRDHSCPTHTFCNYTSSTIFLSSTRDHS CPTHTFCNYTSSTIFLSSTRDHSCPTHTFCNYPRPIIRLSSC CPABLQTEGSNGKKEVLIGFQVVLEDTVLFPEGGGQPDDRGTIN DISULRVTRRGEQADHFTOTPLDPGSQVLVRVDMERRFDHMQQH SCQHLITAVADHLFKLKTTSWELGRFRSAIELDTPSMTAEQVAA IEGSVNEKIRDRLPVNVRELSLDDPBVEQVSGRGLDDDHAGPIR VVNIEGVDSNMCCGTHVSNLSDLQVIKILGTEKGKKNRTNLIFL SGRRVLKKMERSHGTEKALTALLKCGAEDHVEAVKKIQNSTKIL QKNNLNLLRDLAVHIAHSLRNSPDWGGVVILHRKEGDSEFMNII ANEIGSESTLIFITUTODEKGGGLFLLAGPPASVETLGPRAVEVL EGKGAGKKGRFQGKATKMSRRMEAQALLQDYISTQSAKE PGGRASKKGFFQGKATKMSRRMEAQALLQDYISTQSAKE CPGRPRRPGQQVVRGPTMLVTAYLAFVGLLASCLGLELSRCRAK PPGRACSNPSFLRFQLDFYQVYFLALAADWLQAPYLYKLYQHYY FLEGQIALLYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTY SLCCLTKLSQDYFVLLVGRALGGLSTALLFSAFFAMYLHEHVBR HDFPAEWIPATFARAAFWNHVLAVVAGVAAEAVASWIGLGPVAP FVAAIPLLALAGALALRNMGENYDRQRAFSRTCAGGLRCLLSDR RVLLLGTIQALFSVIFIFVFLWFPVLDPGAPLGIIFSSFMAA SLLGSSLYRIATSKRYHLQPNHLLSLAVLIVVSSLFMLTFSTSP				APSKLEALQKALEPTGQSGEAVKELYSQLGEKLEQLDHRKPSPA
DIKEYVKWMYNIFALFTTABTFTDIFLCMPFFYYBLKIAFVA WLLSPYTKGSSLLYRKFVHPTLSSKEKEIDDCLVQAKDRSYDAL VHFGKRGLNVAATAAVMAASKGQGALSERLRSFSMQDLTTIRGD GAPAPSGPPPPGSGRASKHGQPKMSRSASESASSGTA HKLFCSYISTSEFPSSTRHHSCPTHTFCNYTSSTIFLSSTRDHS CPTHTFCNYTSSTIFLSSTRDHSCPTHTFCNYTSSTIFLSSTRDH HSCPTHTSCNYTSSTIFLSSTRDHSCPTHTFCNYPRPIIRLSSC CPABLQTEGSNGKKEVLSGFQVVLEDTVLPPEGGGQPDDRGTIN DISVLRVTRRGEQADHFTQTPLDPGSQVLVRVDWERRFDHMQQH SCGHLITAVADHLFKLKTTSWELGRFRSAIELDTPSMTAEQVAA IEQSVNEKIRDRLPVNVRELSLDDPEVEQVSGRGLPDDHAGFIR VVNIEGVDSNMCCGTHVSNLSDLQVIKILGTEKGKKNRTNLIFL SGNRVLKKMERSHGTEKALTALLKCGAEDHVEAVKKLQNSTKIL QKNNLNLLRDLAVHIAHSLRNSPDWGGVVILHRKEGDSEFMNII ANEIGSESTLLFTVGDEKGGGLFLLAGPPASVETLGPRVAEVL EGKGAGKKGRFQGKATKMSRRMEAQALLQDYISTQSAKE 1 1535 AIMAATRPVRLPEAGCEGRERCWNPSRSRSHSGEGGLAAWSRT CPGRPRRPGQQVVRGPTMLVTAYLAFVGLLASCLGLELSRCRAK PPGRACSNPSFLRFQLDFYQVYFLALAADWLQAPYLYKLYQHYY FLEGQIALLYVGGLASTVLFGLVASSLVDWLGRKNSCVLFSLTY SLCCLTKLSQDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVER HDFPAEWIPATFARAAFWNHVLAVVAGVAAEAVASWIGLGPVAP FVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDR RVLLLGTIQALFESVIFIFVFDWTPVLDPHGAFLGIIFSSFMAA SLLGSSLYRIATSKRYHLQPPHLLSLAVLIVVFSLEMLTFSSP				QAAETPALELPLPSVPAPAPL
WLLSPYTKGSSLLYRFVHPTLSSKEKEIDDCLVQAKDRSYDAL VHFGKKGLNVAATAAVMAASKGQGALSERLRSFSMQDLTTIRGD GAPAPSGPPPPGSGRASGKHGQPKMSRSASESASSGTA 6374 535 2105 HKLFCSYISTSEFPSSTRHHSCPTHTFCNYTSSTIFLSSTRDHS CPTHTFCNYTSSTIFLSSTRDHSCPTHTSCNYTSSTIFLSSTRDH HSCPTHTSCNYTSSTIFLSSTRDHSCPTHTFCNYPRPIIRLSSC CPABLQTEGSNGKKSVLSGFQVVLEDTVLPPEGGGQPDDRGTIN DISVLRVTRRGEQADHFTQTPLDPGSQVLVRVDWERRFDHMQQH SCQHLITAVADHLFKLKTTSWELGRFRSAIELDTPSMTAEQVAA IEQSVNEKIRDRLPVNVRELSLDDPEVEQVSGRGLPDDHAGFIR VVNIEGVDSNMCCGTHVSNLSDLQVIKILGTEKGKKNRTNLIFL SGNRVLKWMERSHGTEKALTALLKCGAEDHVEAVKKIQNSTKIL QKNNINLLRDLAVWIAHSLRNSPDWGGVVILHRKEGDSEFMNII ANEIGSESTLLFLTVGDEKGGGLFLLAGPPASVETLGFRVAEVL EGKGAGKKGRFQGKATKMSRRMEAQALLQDYISTQSAKE 1 1535 AMMAATRPVRLPFBAGCEGRERCWNPSRSRSHSGEGGLAAWSRT CPGRPRRPGQQVVRGPTMLVTAYLAFVGLLASCLGLELSRCRAK PPGRACSNPSFLRFQLDFYQVYFLALAADWLQAPYLYKLYQHYY FLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTY SLCCLTKLSQDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVER HDFPAEWIPATFARAFNNHVLAVVAGVAAEAVASWIGLGPVAP FVAAIPLLALAGALARNWGENYDRQRAFSRTCAGGLRCLLSDR RVLLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAA SLLGSSLYRIATSKRYHLQPNHLLSLAVLIVVFSLFMLTFSTSP	6373	67	711	PSRAARASPARL?AMVSWIISRLVVLIFGTLYPAYYSYKAVKSK
VHFGKRGLNVAATAAVMAASKGQGALSERLRSFSMQDLTTIRGD GAPAPSGPPPPGGBRASGKHGQPKMSRSASESGSTA 6374 535 2105 HKLFCSYISTSEFPSSTRHHSCPTHTFCNYTSSTIFLSSTRDHS CPTHTFCNYTSSTIFLSSTRDHSCPTHTSCNYTSSTIFLSSTRDH HSCPTHTSCNYTSSTIFLSSTRDHSCPTHTSCNYTSSTIFLSSTRD HSCPTHTSCNYTSSTIFLSSTRDHSCPTHTSCNYTSSTIFLSSTRD CPABLQTEGSNGKKBVLSGFQVVLEDTVLPPEGGGQPDDRGTIN DISVLRVTRRGEQADHFTQTPLDPGSQVLVRVDWERRFDHMQQH SGQHLITAVADHLFKLKTTSWELGRFRSAIELDTPSMTAEQVAA IEQSVNEKIRDLPVNVRELSLDDPEVEQVSGRGLPDDHAGFIR VVNIEGVDSMNCCGTHVSNLSDLQVIKILGTEKGKKNRTNLIFL SGNRVLKWMERSHGTEKALTALLKCGAEDHVEAVKKIQNSTKIL QKNNLNLLRDLAVHIAHSLRNSPDWGGVVILHRKEGDSEFMNII ANEIGSESTLLFLTVGDEKGGGLFLLAGPPASVETLGPRVAEVL EGKGAGKKGRFQGKATKMSRRMEAQALLQDYISTQSAKE CPGRPRREQQVVRGPTMLVTAYLAFVGLLASCLGLELSRCRAK PPGRACSNPSFLRFQLDFYQVYFLALAADWLQAPYLIKLYQHYY FLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTY SLCCLTKLSQDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVER HDFPAEWIPATFARAAFWNHVLAVVAGVAAEAVASWIGLGPVAP FVAAIPLLALAGAALALRNWGENYDRQRAFSRTCAGGRCCLLSDR RVULLGTLQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAA SLLGSSLYRIATSKRYHLQPNHLLSLAVVLIVVFSLFMLTFSTSP	1 1	ŀ		DIKEYVKWMMYWIIFALFTTAETFTDIFLCWPPFYYBLKIAFVA
GAPAPSGPPPPGGRASGKHGQPKMSRSASESASSGTA 6374 535 2105 HKLFCSYISTSEFPSSTRHHSCPTHTFCNYTSSTIFLSSTRDHS CPTHTFCNYTSSTIFLSSTRDHSCPTHTFCNYTSSTIFLSSTRDH HSCPTHTSCNYTSSTIFLSSTRDHSCPTHTFCNYPRPIIRLSSC CPABLQTEGSNGKKEVLSGFQVVLEDTVLPPEGGGQPDDRGTIN DISVLRVTRRGEQADHFTQTPLDPGSQVLVRVDWERRFDHMQQH SGGHLITAVADHLFKLKTTSWELGRFRSAIELDTPSMTAEQVAA IEQSVBKIRDRLPVNVRELSLDDPEVEGVGGRGLPDDHAGFIR VVNIEGVDSNMCCGTHVSNLSDLQVIKILGTEKGKKNKTNLIFL SGNRVLKWMERSHGTEKALTALLKCGAEDHVEAVKKIQNSTKIL QKNNLNLLRDLAVHIAHSLRNSPDWGGVVILHRKEGDSEFMNII ANEIGSESTLLFLTVGDEKGGGLFLLAGPPASVETLGPRVAEVL EGKGAGKKGRFQGKATKMSRRMEAQALLQDYISTGSAKE AIMAAATRPVRLPEAGCEGRERCWNPSRSRSHSGEGGLAAWSRT CPGRPRRPGQQVVRGPTMLVTAYLAFVGLLASCLGLELSRCRAK PPGRACSNPSFLRFQLDFYQVYFLALAADWLQAPYLYKLYQHYY FLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTY SLCCLTKLSQDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVER HDFPAEWIPATFARAAFWNHVLAVVAGVAAEAVASWIGLGPVAP FVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGRCCLLSDR RVULLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAA SLLGSSLYRIATSKRYHLQPNHLLSLAVVLIVVFSLFMLTFSTSP	1 1			WLLSPYTKGSSLLYRKFVHPTLSSKEKEIDDCLVOAKDRSYDAL
GAPAPSGPPPPGGRASGKHGQPKMSRSASESASSGTA 6374 535 2105 HKLFCSYISTSEFPSSTRHHSCPTHTFCNYTSSTIFLSSTRDHS CPTHTFCNYTSSTIFLSSTRDHSCPTHTFCNYTSSTIFLSSTRDH HSCPTHTSCNYTSSTIFLSSTRDHSCPTHTFCNYPRPIIRLSSC CPABLQTEGSNGKKEVLSGFQVVLEDTVLPPEGGGQPDDRGTIN DISVLRVTRRGEQADHFTQTPLDPGSQVLVRVDWERRFDHMQQH SGGHLITAVADHLFKLKTTSWELGRFRSAIELDTPSMTAEQVAA IEQSVBKIRDRLPVNVRELSLDDPEVEGVGGRGLPDDHAGFIR VVNIEGVDSNMCCGTHVSNLSDLQVIKILGTEKGKKNKTNLIFL SGNRVLKWMERSHGTEKALTALLKCGAEDHVEAVKKIQNSTKIL QKNNLNLLRDLAVHIAHSLRNSPDWGGVVILHRKEGDSEFMNII ANEIGSESTLLFLTVGDEKGGGLFLLAGPPASVETLGPRVAEVL EGKGAGKKGRFQGKATKMSRRMEAQALLQDYISTGSAKE AIMAAATRPVRLPEAGCEGRERCWNPSRSRSHSGEGGLAAWSRT CPGRPRRPGQQVVRGPTMLVTAYLAFVGLLASCLGLELSRCRAK PPGRACSNPSFLRFQLDFYQVYFLALAADWLQAPYLYKLYQHYY FLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTY SLCCLTKLSQDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVER HDFPAEWIPATFARAAFWNHVLAVVAGVAAEAVASWIGLGPVAP FVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGRCCLLSDR RVULLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAA SLLGSSLYRIATSKRYHLQPNHLLSLAVVLIVVFSLFMLTFSTSP] [VHFGKRGLNVAATAAVMAASKGQGALSERLRSFSMQDLTTIRGD
CPTHTFCNYTSSTIFLSSTRDHSCPTHTSCNYTSSTIFLSSTRDHS CPTHTFCNYTSSTIFLSSTRDHSCPTHTSCNYTSSTIFLSSTRD HSCPTHTSCNYTSSTIFLSSTRDHSCPTHTFCNYPRPIIRLSSC CPABLQTEGSNGKKEVLSGFQVVLEDTVLPPEGGGQPDDRGTIN DISVLRVTRRGEQADHFTQTPLDPGSQVLVRVDWERRFDHMQQH SGQHLITAVADHLFKLKTTSWELGRFRSAIELDTPSMTAEQVAA IEQSVNEKIRDRLPVNVRELSLDDPEVEQVSGRGLPDDHAGFIR VVNIEGVDSNMCCGTHVSNLSDLQVIKILGTEKGKKNRTNLIFL SGNRVLKWMERSHGTEKALTALLKCGAEDHVEAVKKIQNSTKIL QKNNLNLLRDLAVHIAHSLRNSPDWGGVVILHRKEGDSEFMNII ANEIGSESTLLFLTVGDEKGGGLFLLAGPPASVETLGPRVAEVL EGKGAGKKGRFQGKATKMSRRMEAQALLQDYISTQSAKE 1 1535 AIMAAATRPVRLPEAGCEGRERCWNPSRSRSHSGEGGLAAWSRT CPGRPRRPGQQVVRGPTMLVTAYLAFVGLLASCLGLELSRCRAK PPGRACSNPSFLRFQLDFYQVYFLALAADWLQAPYLIKLYQHYY FLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTY SLCCLTKLSQDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVER HDFPAEWIPATFARAAFWNHVLAVVAGVAAEAVASWIGLGPVAP FVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDR RVLLLGTLQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAA SLLGSSLYRIATSKRYHLQPMHLLSLAVVLIVVFSLFMLTFSTSP	1			GAPAPSGPPPPGSGRASGKHGQPKMSRSASESASSSGTA
HSCPTHTSCNYTSSTIFLSSTRDHSCPTHTFCNYPRPIIRLSSC CPABLQTEGSNGKKEVLSGFQVVLEDTVLPPEGGGQPDDRGTIN DISVLRVTRRGEQADHFTQTPLDPGSQVLVRVDWERFDHMQQH SGQHLITAVADHLFKLKTTSWELGRFRSAIELDTPSMTAEQVAA IEQSVNEKIRDRLPVNVRELSLDDPEVEQVSGRGLPDDHAGFIR VVNIEGVDSNMCCGTHVSNLSDLQVIKILGTEKGKKNRTNLIFIL SGNRVLKWMERSHGTEKALTALLKCGAEDHVEAVKKIQNSTKIL QKNNINLLRDLAVHIAHSLRNSPDWGGVVILHRKEGDSEFMNII ANEIGSEETLLFLTVGDEKGGGLFLLAGPPASVETLGPRVAEVL EGKGAGKKGRFQGKATKMSRRMEAQALLQDYISTQSAKE 1 1535 AIMAAATREVRLPEAGCEGRERCWNPSRSSSHSGEGGLAAWSRT CPGRPRRPGQQVVRGPTMLVTAYLAFVGLLASCLGLELSRCRAK PPGRACSNPSFLRFQLDFYQVYFLALAADWLQAPYLYKLYQHYY FLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTY SLCCLTKLSQDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVER HDFPAEWIPATFARAAFWNHVLAVVAGVAAEAVASWIGLGFVAP FVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGIRCLLSDR RVLLLGSTLQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAA SLLGSSLYRIATSKRYHLQPMHLLSLAVVLIVVFSLFMLTFSTSP	03/4	535	2105	HKLFCSYISTSEFPSSTRHHSCPTHTFCNYTSSTIFLSSTRDHS
CPABLQTEGSNGKKEVLSGFQVVLEDTVLPPEGGGQPDDRGTIN DISVLRVTRRGEQADHFTQTPLDPGSQVLVRVDWERRFDHMQQH SGQHLITAVADHLFKLKTTSWELGRFRSAIELDTFSMTAEQVAA IEQSVNEKIRDRLPVNVRELSLDDPEVEQVSGRGLPDDHAGFIR VVNIEGVDSNMCCGTHVSNLSDLQVIKILGTEKGKKNRTNLIFL SGNRVLKWMERSHGTEKALTALLKCGAEDHVEAVKKIQNSTKIL QKNNLNLLRDLAVHIAHSLRNSPDWGGVVILHRKEGDSEFMNII ANEIGSESTLLFLTVGDEKGGGLFLLAGPPASVETLGPRVAEVL EGKGAGKKGRFQGKATKMSRRMEAQALLQDYISTQSAKE 1 1535 AIMAAATRPVRLPEAGCEGRERCWNPSRSRSHSGEGGLAAWSRT CPGRPRRFGQQVVRGPTMLVTAYLAFVGLLASCLGLELSRCRAK PPGRACSNPSFLRFQLDFYQVYFLALAADWLQAPYLIYKLYQHYY FLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTY SLCCLTKLSQDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVER HDFPAEWIPATFARAAFWNHVLAVVAGVAAEAVASWIGLGFVAP FVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGIRCLLSDR RVLLLGTLQAFFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAA SLLGSSLYRIATSKRYHLQPMHLLSLAVVLIVVFSLFMLTFSTSP		i	İ	CPTHTFCNYTSSTIFLSSTRDHSCPTHTSCNYTSSTIFLSSTRD
DISULRVTRRGEQADHFTQTPLDPGSQVLVRVDWERRFDHMQQH SCQHLITAVADHLFKLKTTSWELGRFRSATELDTPSMTAEQVAA IEQSVNEKIRDRLPVNVRELSLDDPEVEQVSGRGLPDDHAGFIR VVNIEGVDSMCCGTHVSNLSDLQVIKILGTEKGKKNRTNLIFL SGNRVLKWMERSHGTEKALTALLKCGAEDHVEAVKKIQNSTKIL QKNNLNLLRDLAVHIAHSLRNSPDWGGVVILHRKEGDSEFMNII ANEIGSESTLLFLTVGDEKGGGLFLLAGPPASVETLGPRVAEVL EGKGAGKKGRFQGKATKMSRRMEAQALLQDYISTQSAKE 6375 1 1535 AIMAAATRPVRLPEAGCEGRERCWNPSRSRSHSGEGGLAAWSRT CPGRPRRPGQQVVRGPTMLVTAYLAFVGLLASCLGLELSRCRAK PPGRACSNPSFLRFQLDFYQVYFLALAADWLQAPYLIKLYQHYY FLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTY SLCCLTKLSQDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVER HDFPAEWIPATFARAAFWNHVLAVVAGVAAEAVASWIGLGPVAP FVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDR RVULLGTLQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAA SLLGSSLYRIATSKRYHLQPNHLLSLAVVLIVVFSLFMLTFSTSP		1		HSCPTHTSCNYTSSTIFLSSTRDHSCPTHTFCNYPRPIIRLSSC
SGGHLITAVADHLFKLKTTSWELGRFRSAIELDTPSMTAEQVAA IEQSVNEKIRDRLPWAVRELSLDDPEVEQVSGRGLPDDHAGPIR VVNIEGVDSMCCGTHVSNLSDLQVIKILGTEKGKKNRTNLIPL SGNRVLKWBERSHGTEKALTALLKCGAEDHVEAVKKIQNSTKIL QKNNLNLLRDLAVHIAHSLRNSPDWGGVVILHRKEGDSEFMNII ANEIGSESTLLFLTVGDEKGGGLFLLAGPPASVETLGPRVABVL ECKGAGKKGRFQGKATKMSRRMEAQALLQDYISTQSAKE 6375 1 1535 AIMAAATRPVRLPEAGCEGRERCWNPSRSRSHSGEGGLAAWSRT CPGRPRPQQVVRGPTMLVTAYLAFVGLLASCLGLELSRCRAK PPGRACSNPSFLRFQLDFYQVYFLALAADWLQAPYLJKLYQHYY FLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTY SLCCLTKLSQDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVER HDFPAEWIPATFARAAFWNHVLAVVAGVAAEAVASWIGLGPVAP FVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDR RVULLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAA SLLGSSLYRIATSKRYHLQPWHLLSLAVLIVVFSLFMLTFSTSP	1 1	ł		CPAKLQTEGSNGKKBVLSGFQVVLEDTVLFPEGGGQPDDRGTIN
IEGSVNEKIRDRLPVNVRELSLDDPEVEQVSGRGLPDDHAGPIR VVNIEGVDSNMCCGTHVSNLSDLQVIKILGTEKGKKNRTNLIFI SGNRVLKWMERSHGTEKALTALLKCGAEDHVEAVKKIQNSTKIL QKNNLNLLRDLAVHIAHSLRNSPDWGGVVILHRKEGDSEFMNII ANEIGSEETLLFLTVGDEKGGGLFLLAGPPASVETLGPRVAEVI EGKGAGKKGRFQGKATKMSRRMEAQALLQDYISTQSAKE 1 1535 AIMAAATRFVRLPEAGCEGRERCWNPSRSRSHSGEGLAAMSRT CPGRPRRPGQQVVRGPTMLVTAYLAFVGLLASCLGLELSRCRAK PPGRACSNFSFLRFQLDFYQVYFLALAADWLQAPYLYKLYQHYY FLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTY SLCCLTKLSQDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVER HDFPAEWIPATFARAAFWNHVLAVVAGVAAEAVASWIGLGPVAP FVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDR RVLLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAA SLLGSSLYRIATSKRYHLQPWHLLSLAVLIVVFSLFMLTFSTSP			1	DISVLRVTRRGEQADHFTQTPLDPGSQVLVRVDWERRFDHMQQH
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ODLITALGEMELSPRISTINGPLEKEPATSOLTSLUTRATIKE NEOIPTYER HINFKHITERGEPHENGYCARPHAGIJAGGWCCADC GLAWHRQCSKWYNDCKPDLKHYKKVYSCDLTTLVKAHTTKEPH VVDMCTREIESGRIJNSGLTVRYGGSDLIEDWAPDROGEKJA LSVMWEDINITGALKLYPROLPIPLITDAYPKPI ESAKIMD PDEOLETHERLELLIPPAHGETLRYLMALLKRYTHERVEN PDEOLETHERLELLIPPAHGETLRYLMALLKRYTHERVEN REGISTERESSREPREPFORSRERREREPPETRYBESKYTHKKYBEN RIGITYGPTHISSPELDAWAALNDIRYGVUVELLIKNEDILF QRYGDVRLIREORPYKLFVIISERSKYRKGKQLYPULKTKKTKIVPDHY NMSELIKIIRRRIGUNNAQAFFLLWNGHSWUSVSTPISEVYESB RDEOGLYMWYASQOTYGMLSY GAGPWEAFFDGGIGRESRRARHPOYKRPFGRVGGGDSGRRNMAVA DLALIFDVDIDSGVFKVVILIWHSAPSGADAASKSIVKGVK WASYHADIYDKVSGDMQKQCCDCCLGGRISHGSQDKKHIVVG YSAAVDAQAAISTEKKKARYDPDEVVWANDOY LENSVNNGGGAPERVLITGUHAVADIVCENCKTICHOW WASYHADIYDKVSGDMQKQCCDCCLGGRISHGSQDKKHIVVG YSAAVDAQAAISTEKKKARYDPDEVVWANDOY LENSVNNGGAPERVLITGUHAVADIVCENCKTICHOW PESSQKYKEGKYIIELAHMIKUNGMO 6380 1414 462 PRVGGGGGABPPURGGSGMARRALTUVKRGETPRNEKIIQGQ GVDEPLSETGFKQAAAAGITANVKFTHAFSDLMSTKOTMHGI LERSKFCCDMTVKYDSBLARKKYGVVEGGALSELRAMAKAAREB CFVFTPPGGSTLDQVKRGGIDPFFFLQCILLKEVGROFGOSGAS PSNCLETSLABIFFLGKNISSKNSDSGIFGLAASVLLVVSHGAY MRSLEVHFLIJUKKSLDJAVSSLLSUKTPFSHKKIIQGQ GVDEPLSETGFKQAAAANNFSEVYKLSSLLSUKTPSHVSHGAY MRSLEVHFLIJUKCSLDATLSSELLSUKTPTNOSLFFINFEKIIQGD LALFTSLLC AMYKRGUVQWBLEQDBHICKIDGGSGALVASGGBDGBHILINT TEPHHRITWSLCTISVSVIKYRALGAUTTPURSMALSLELCAMYSAGGA RCKOVYGIFVGSOMGLHHOTDTODLIGTEMAPNICVILAVB CTCLEVKLLIVSLUGGLISTICHTSCANVYLREAEKSPQLAG SYDGKVRILINHVTWIMITEFGHPAAINDRKUVYRAEKSPQLAG SYDGKVRILINHVTWIMITEFGHPAAINDRKUVYRAEKSPQLAG SYDGKVRILINHVTWIMITEFGHPAAINDRKUVYRAEKSPQLAG SYDGKVRILINHVTWIMITEFGHPAAINDRKUVYRAEKSPQLAG SYDGKVRILINHVTWIMITEFGHPAARINDRKUVYRAEKSPQLAG SYDGKVRILINHVTWIMITERGHPAANDRACKYLAROPGEPTAANDR KGIOMAASPSDSTFTATTRINNININAVWHOIDKRIPAVLEQL SVRARQWDQQDPSLAICTGGSGRKYLMBSPAGCMSVQUPGGOPA VALCOWLUCHLOSDBANLISKOHRCCOLTRARAVINGCOLARAS SYDRARGWDQQDPRIAICTGGSRIVINBSCEPKSKLLERTTINK KHILLERININGSVERVCULLDWATTGODAGNIFRAANDIRKCQCASTS AUTGVRCCMQVVQAGSGGADPANKYHGRUSGAGADVAKK PPPAPQOPPPPPAPAPARAGSSSGGGADAFSKKGHRASSPSEK GAHPSAARPLAAAPTAAPACRSSSGGGADAFSKKGHGAASPSEK G	6376	380	1437	ISSTOIDHYRESEL/MSKMPSKESBEGDVTMD NIIIVOKORGO
REQIPYERINDENHITEROPHICSYCANFHMIGLIAQGYCACC GLNYHQCSKNYPNOKYPDIKHYKVYSGEDLTDVKANFTKERP VVDMCIREIESGGLISEGLYRVSGESDLEDVKANEDRGEKAD ISVIMMEDINITIGALKIYPHOLPIPITYDAPKET ESAKIMI PDEGLETHREALKILPPHOCETT.RYLAMALKRYTLHEKENIMNA ENGLYVGFUTHISPELDAMAALKITTIBKENIMNA ENGLYVGFUTHISPELDAMAALKITTIBKENIMNA ENGLYVGFUTHISPELDAMAALKITTIBKYGEKOLPYLLKKENIMNA ENGLYVGFUTHISPELDAMAALKITTIBKYGEKOLPYLLKKENIMNA ENGLYGFUTHISPELDAMAALKITTIBKYGEKOLPYLLKKENIMNA ENGLYGFUTHISPELDAMAALKITTIBKYGEKOLPYLLKKENIMNA ENGLYGFUTHISPELDAMAALKITTIBKYGEKOLPYLLKKENIMNA MESELIKIIKRRIQLINNAQFITLINNGKONIMPTISEVYESE KDEOGLYMYVASQETYGMKLSV WARYHADIYDVSGMOKQGCOCCELGGGGITAGOKKITHVYG VSANAYADANAISTEKIKAKYPDYSTYMANDOY VSANAYADANAISTEKIKAKYPDYSTYMANDOY VSANAYADANAISTEKIKAKYPDYSTYMANDOY VSANAYADANAISTEKIKAKYPDYSTYMANDOY VSANAYADANAISTEKIKAKYPDYSTYMANDOY VSANAYADANAISTEKIKAKYPDYSTYMANDOY VSANAYADANAISTEKIKAKYPDYSTYMANDOY VSANAYADANAISTEKIKAKYPDYSTYMANDOY VSANAYADANAISTEKIKAKYPDYSTYMANDOY VSANAYADANAISTEKIKAKYPDYSTYMANDOY VSANAYADANAISTEKIKAKYPDYSTYMANDOY VSANAYADANAISTEKIKAKYPDYSTYMANDOY VSANAYADANAISTEKIKAKYPDYSTYMANDOY VSANAYADANAISTEKIKAKYPDYSTYMANDOY VSANAYADANAISTEKIKAKYPDYSTYMANDOY VSANAYADANAISTEKIKAKYPDYSTYMANDOY VSANAYADANAISTEKIKAKYPDYSTYMANDOY VSANAYADANAISTEKIKAKYPDYSTYMANDOY VSANAYADGORABERVILITGHAVADIYCKNOKYTILGKYPIL EERSKYCKOMYVKYDSALERKYVOVEKAKSIAVUVSHGAY MERIEDYFILDUKKYDSAAAISTEKIVOVEKOKASSOLAKSIAVOSAGOS PSACLETIJABIFPIGINISSYKSINSOSEIPIGAINKASAREBE CPYFTPPOGSTILOVKANGIDPFPPILOJILIKENDOKKOPSOOS PSACLETIJABIFPIGINISSYKSINSOSEIPIGAINKASAARELAVOKANAI MERIEDYFILDUKKYDSAANISSELINGANIPSEVYRILSENOPHANIA ARABARDANFAKVANOSAANIANSEVYRILISSELINGANAISSELINGANAISPERGAA MERIEDYFILDUKKYDIKATIGANAISSELINGANAISPERGAADANAIN TEHHAITTINAI TEHHAITTINAINAITAMAITEFGHAAINAIPSEVYRILISSELINGANAINAINAINAINAINAINAINAINAINAINAINAINAI	l			ODILITAALGMKI.GSPKSGVTTWODI VI RAVGOT MOTUMOS WA
GLANHAÇOSKAYENDCKPÜLKHYKKVYSCÜLTÜLVKAHTTKERN VVDMCIREISERGLASEGLIVKSGESÜLEÜLEÜKPERDEGKAL ISVAMYEDINIITGALKUYRÜLEIKENDEMAA. ENGIVYGPTIMSEPELDAMAALDDIBYOKLUVELLIKNEDILFA BORGELTÜLEALKLÜPPAHCETIKYLMALKKYKUTLEIKEKDIMMA. ENGIVYGPTIMSEPELDAMAALDDIBYOKLUVELLIKNEDILFA GRYEDVELIREGEPERTKERERDERTMYSEKTEKEKUNDELIF ORVEDVELIREGEPETKIPVIIERYKGEKQLEVLEKKEKUPUTEK ORVEDVELIREGEPETKIPVIIERYKGEKQLEVLEKKEKUPUTEK MASELIKIIREGEPTKIPVIIERYKGEKQLEVLEKKEKUPUTEK KDEDGELIMVYASQETTÖMKEN MASELIKIIREGEPTKIPVIIERYKGEKQLEVLEKKEKUPUTE MASELIKIIREGEPTKIPVIIERYKGEKQLEVLEKKEKUPUTE KDEDGELIMVYASQETTÖMKELY GAFFMERFPEGETGERSKRAREPÖRRVÖGGDSGRINMAVA DLALIFDVOLIBBOKYYKVUL HINSAPSGADABASKEIVKGVK WASYHADIYDKVASGOMOKOCCDCECLGGGISHGSODKKHIVVG YSANCHAQHAISTEKKIKARYDEVETVANDOL LENSVNINGGOPAERVILTIGHAVADIVCENCKTICHKYEHA FESSOKYKEGKYIIRLAHMIKUNGMO GYNEPLISTOF KOMANAGIFLINVKTHAFSSOLMHIKKOTMED FANCGGGGAGPPERVILTIGHAVADIVCENCKTICHKYEHA FESSOKYKEGKYIIRLAHMIKUNGMO GVOEPLISTOF KOMANAGIFLINVKTHAFSSOLMHIKKOTMED LESSKEKCHOMYVKTOSILERKYGVVEGGALSELRAMAKAAREB CPVFTPEGGFTILDOVKRIGTIPFSFILGILIKENGENGFOSGOGRAY MRSILDOVKRIGTURFSFILGINLESKINSHOSDIROKTOMSLEFI INFEGG REVEPTVQCICHNIQDILKGELTERSLINLESKINLESKINSHOSPI FILAGELIKA MASHADIVATUKASSALIKUKUNGAND 6381 1668 218 AVVRAGSRGFSGAGRAFROMARKSELMSVIPTRIOMELPET INFEGG REVEPTVQCICHNIQDILKGELTERSLINLESKINLESKINLEST TEPHILRITVASLICTISTOLUTTOLOJOHENSADSI-FILC AMYKGILVYVSIFVCSDWOLUTTOLOJOHTISHAPNOCVLAVND TCLEVKLLIYSLUGRILSTYSENSILGIKSVANGSSGFILANG SYDGKVILLAHTTISHATTEPHDAININDKWIVYKALEKSPOLIA SYDGKVILLAHTTISHATUKANDHOLUTILINATUKANDIOKIRLAFAVLEOL SVRARYODPOQPELALCTGGSENJINSKORSVOVPOGEOPPA VALCOMILOSDARLASKHINCHCETTETRAVVALCOJURANPALOGURAN VALCOMITANA VALCOMILOSDARLASKHINCHCETTETRAVVALCOJURANPALOGURAN ILDENHITYTINK KHINLETEKT POUNVORIHKEEKEKKILLEEPESGOPPA VALCOMILOSDARLASKHINCHCETTETRAVVALCOJURANPALOGURAN ILDENHITYTINK KHINLETEKT POUNVORIHKEEKEKKILLEEPESGOPPA VALCOMILOSDARLASKHINCHCOJURAKERANINIKKOOJURAK PHYLETELT POUNVORIHKEEKEKKILLEEPESGEPERILATOP HINGSYLEPEVULDIMOTTOROHONAHKOKIGHONAHKOKOOJURAKS PPAPAOOPPOPPAPARAGOPPONAHKOKHORI	1			NEOIPKYEKIHNEKWHTEPGPUNGEYGANEWIGI TAGUWGARA
VVDMCTRETESRGINSEGLYRYSGFSDLIEDVKMAPDRGEKAD ISVMMYEDINITITALKLYFDDLPIPLTYPKPYETESALIMD PDEOLETTHEALKLLEPAHCETTRYTMAHLKRYTHEKENLMGA ENGISVEDTHIMS PELDAMALINDITYORUVELLIKNEDILP ENGISVEDTHIMS PELDAMALINDITYORUVELLIKNEDILP GRYADVALIREQHPYKIPVITERY KOEKQLPYLDKTKRIPPDLW NMSELIKI IRRIQINANQAF FILLWIGKNUPVIDKTKRIPPDLW NMSELIKI IRRIQINANQAF FILLWIGKNUPVIDKTKRIPPDLW NMSELIKI IRRIQINANQAF FILLWIGKNUPVIDKTKRIPPDLW STERRIF ROMENTI IRRIQUENTANGAF FILLWIGKNUPVIDKTKRIPPDLW STERRIF ROMENTI IRRIQUENTANGAF FILWIGKNUPVIDKTKRIPPDLW STERRIF ROMENTI IRRIQUENTANGAF FILWIGKNUPVIDKT STERRIF ROMENTI IRRIGUENTANGAF FILWIGKNUPVIDKT STERRIF ROMENTI IRRIGUENTANGAF STERRIF ROMENTI IRRIG	1			GLNVHKOCSKMVPNDCKPDLKHVKVVVSCDI TOT VKANTONA
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6377 2311 1845 SIKRRISSERPREPGÖRERRERREPGYENTYSEKTYÖRETTE ORVEDVELIREOHPTKIPVITERYKGEKOLPVLDKTKYLVPDHY NMSELIKII KERKULANANQAFYLLVNGKSWYSYTI ISEVYESE KDEDGYMYVASQETFGMKLSV 6378 686 191 GAGPWAPPDGIGRERRERRERPGYENTYSEKTYÖREK KDEDGYMYVASQETFGMKLSV 6379 35 JAMES ERAGSESERALBERGYKAPPGEVGGSDSGERMANA 6379 35 ATRESSERVALRECAPOSQAPREPGRAGADSKERIMAVA LEASVANVQCADLECLIGGETISHQSQDKKHVYG WASYHADIYDKVSGOMOKQCCCCCGCGGSISHQSQDKKHVYG YSANAVDAJANISTEKI KAKYPDYEVTANDOY ERAGSESERALBRICAPOSQAPREPGRAACRESFQGSQRAY LENSVANVQCOPABERVLITGLHAVADIYCENCKTICMYZHA FESSQXYKEGKYI IELAMIKOMGMD 6380 1414 462 PAVGGRGADPFURSSGNMARFALTVVRIGETERNKEKIGOQ GVDELSSTIGKQAAAAGITINNVKTHAFSSDLARTKQTMHGI LERSKFCKDMTVKYDSRLRERKYGVVECKALSELBANAKAARBE CPYFTPPGETILOQVMRGIOTPFEHICQLIKANOKLPSSOLASVALVYSHGAY MRSLEDYBLTDLKCSLDATLSRSELMSVTNOSLPI INFEEG REVKPTVQCI OMNLQDHLNGLTENSLGINLPSKSNHEFELKGVP LALFTSLLC ANYKRGLVYWBUNTLQ ILQLTYCLDQIOMI ENSABLIFILC ANYKRGLVYWBUNTLQ ILQLTYCLDQIOMI ENSABLIFILC ANYKRGLVYWBUNTLQ ILQLTYCLDQIOMI ENSABLIFILC ANYKRGLVYWBUNTLQ ILQLTYCLDQIOMI ENSABLIFILC ANYKRGLVYWBUNTLQ ILQLTYCLDQIOMI ENSABLIFILC ANYKRGLVYWBUNTLQ ILQLTYCLDQIOMI ENSABLIFILC ANYKRGLVYWBUNTLQ ILQLTYCLDQIOMI ENSABLIFILC ANYKRGLVYWBUNTLQ ILQLTYCLDQIOMI ENSABLIFILC ANYKRGLVYWBUNTLQ ILQLTYCLDQIOMI ENSABLIFILC ANYKRGLVYWBUNTLQ ILQLTYCLDQIOMI ENSABLIFILC ANYKRGLVYWBUNTLQ ILQLTYCLDQIOMI ENSABLIFILC ANYKRGLVYWBUNTLQ ILQLTYCLDQIOMI ENSABLIFILC ANYKRGLVYWBUNTLQ ILQLTYCLDQIOMI ENSABLIFILC ANYKRGLVYWBUNTLQ ILQLTYCLDQIOMI ENSABLIFILL ANYKRGLVYWBUNTLQ ILQLTYCLDQIOMI ENSABLIFILL ANYKRGLVYWBUNTLQ ILQLTYCLDQIOMI ENSABLIFILLOF LALFTSLIC ANYKRGLVYBOQDELGENGTOTON ENSABLIFILLOF ANYKRGLVYBALERGENGTON ENSABLIFILLOF ANYKRGLVYBALERGENGTARANCOLLAND TCLEKKILLYSLOGELLSTYSAYBRIGIKSVAWSPSSQFLAVG SVDGKYTILLHANTWMI TEFGGIPAA INDRKITVYK FILLARIAND LGCLSFPPPRAGAGPLESSESKYBI ASVEYSGOTLGHTTNK KHHULETEKTPROWYRCHREKKKSEKULGEFFENLKKSEVLYY TVEKKGH ISSOLKHYMPSKKKHOQUQUANCHONGKNIKALERGERG BECONTAL TYPHADA INDRKHYMBOLADA INDRKHYMFILLANANATE LENLISTYEVPCVLDLMMTRQBERGARGANAYKFICASSUVYM LIPAHTTCALLAND ENSABLIFICATION E	ł			PDEOLETLHEALKLLPPAHCETI.RVI.MAHI.KRVIT.HEVENT.MAKA
SRIERRSSERPREPOGEREREREREPDETMINESETTFKORRTFE ORVEDVILLERGHPETKEPVI IERVIGUPULUKKEKTUVDHV NMSELIKIIRRRLOLINANQAFFLLVNGHSMVSVSTPISEVYESE KDEGGILVHVYASQETFGMKLSV GAGPMEAFPDGIGERSERARELPOYKRPFGRVGGGDSGRRNMAVA DLALIPUVDIDSDGVFKYVLIRVHSAPRSGAPAASKEIVRGYK MASYHADIJDKVSGGMOKGCCCCECLGGSISHOSODKKHHVYG YSMAYGPAQHAISTEKIKAKYPDYEVTWANDGY ERAGSEPSFRALBERGAPGSQAPRWEDRAACRSFGGSGRAY LFNSVVNVGCGPAEERVLITCHHAVADIYCENCKTTIGMKYEHA FESSQKYKEGKYIIELARMIKONGMD 6380 1414 462 PAVGGGGAGFPTHGRSGSMARFALTVVKHGETRPNKEKIIGGQ GVDEPLSTGFKQAAPAGIFLNVKFTHAFSSDLMFTKOTMHGI LERSKFCKOMTVKYDSREBERKYGVVENSDESGIFGLARAARBE CFVFTPPGGETLOVKMRGIDPFPPLODILLKEADQKEQFSQGS PSNCLETELASIFPLGKKHISKVNSDSGIFGLARAARBE CFVFTPPGGETLOVKMRGIDPFPPLODILLKEADQKEQFSQGS PSNCLETELASIFPLGKKHISKVNSDSGIFGLARAARBE CFVFTPPGGETLOVKMRGIDPFPPLODILLKEADQKEQFSQGS PSNCLETELASIFPLGKKHISKVNSDSGIFGLARAARBE CFVFTPPGGETLOVKMRGIDPFPPLODILLKEADQKEQFSQGS PSNCLETELASIFPLGKHISKVNSDSGIFGLARAARBE CFVFTPPGGETLOVKMRGIDPFPPLODILLKEADQKEQFSQGS PSNCLETELASIFPLGKHISKVNSDSGIFGLARABABE CFVFTPPGGETLOVKMRGIDPFPPLODILLKEADQKEQFSQGS PSNCLETELASIFPLGKHISKVNSDSGIFGLARABEB CFVFTPPFPGGETLOVKMRGIDPFPPLODILLKEADQKEQFSQGS PSNCLETELASIFPLGKHISKVNSDSGIFGLARABABE CFVFTPPFPFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	<u> </u>			ENLGIVFGPTLMRSPELDAMAALNDIRYORLUVELLIVNEDILE
GRVEDVRLIREGHETKIPVIIERWIGEKQLPVLIKTKFLUPDHU MSELIKII RIRRIGLINNOAFFILLVNGEKWYSTPISEVYBSE KDEDGFLYMVYASQETFGMILSY GAGPWEAFPDGIGRESKRARIPGYKRPPGRVGGGDSGREMMAVA DLALIPDVDIDSDGVFKYVLIRVISAPSGAPAAESKEIVRGYK WASYHADIYDKVSGDMKKGCCDCCLGGGRISHGSQDKKHHVYG YSMAYGPAQHAISTEKIK KKYPDVEVYMDOY 6379 35 378 ERAGSFSFSKALBRCAPQRSQAPRWDRAACRRSFQGSOGRAY LFMSVVNVGCGPAEERVLITCHHAVADIYCEKCKTITGMKYEHA FSSKKYKEGKYIIELAHMIKDNKOM GOVDEPLISTGFKQAAAAGIFILNVKFHAFSSDLMRYRKGYMGI LERSKECKDMTVKYDGRIBERKYGVVEGKALEELRAMAKAAREB CPVFTPDFGGTLOQVKMRGIDFFFLOQLITCHSKENHIGKO GVDEPLISTGFKQAAAAGIFILNVKFHAFSSDLMRYRKGYMGHI LERSKECKDMTVKYDGRIBERKYGVVEGKALEELRAMAKAAREB CPVFTPDFGGTLOQVKMRGIDFFFLOQLITCHSKSNHHFPLKGUP LALFTSLLC AMYKRGLVQWSLEDFBHICKIDBGSAGLVASCWSPOGHILINT TEPHLRITUNSLCTKSVSYINFYRACLQGIFTFTBGRYNGLAF RDCKDYVSIFVCSDMQLLRHEDTDTQDLIGIBMAPNGCVLAVM TCHBYKILLYSLGRUSTYSYARWSLGVSVASPGSRGHLINT TEPHLRITUNSLCTKSVSYINFYRACLQGIFTFTBGRYNALARE RDCKDYVSIFVCSDMQLLRHEDTDTQDLIGIBMAPNGCVLAVM TCLBYKILLYSLDGRILLSTYSARWSLGVSVASPGSGLUS SVDGKVRILNHVYMKNITEFGHPAAINDPKIVVYKRAEKSPOLG LGCLSFPPPRAGAGPLPSSESKFTASVPVSLGTIKRVTDRANB XGGIGMLAFSPDSYFLARRINNIPNAWWONICKLEFRYLEQU SSVRAFQWDQQPRLAICTGGSBLYLWSPASCMSVQVPGEGDFA YLSLCWHLSGDSMALLSKDHFCLCFLTEWAVTAGCQLGGHT TVEKKGRISGOKHYNNYMONICKLEFRYLEQU SSVRAFQWDQQPRLAICTGGSBLYLWSPASCMSVLYPGY TVEKKGRISGOKHYNNYMONICKRAFTRYLEQU SVLSLCWHLSGDSMALLSKDHFCLCFLTEWAVTAGCQLGGHT TVEKKGRISGOKHYNNYMONICKRAFTRYLEQU SVLSLCWHLSGDSMALLSKUHYCLGCHTAKVTORGCQLGGHT NYKHGRAARPLAAPTDAADACRSSVGGMFANNYRGKNACHGOCGGGGG SKRSPEVULDSDAADELDLSESADBSAGAVANYRIGASSVDVRM IDFAHTTCRLYGCDTVVHRGQDASTFICISSLDTVTSISEGG B GAHESAARPLAAPTDAAPSAKQRGSKGGHGAASFSEK GAHESAARPLAAPTDAAPSAKQRGSKGGHGGAASFSEK GAHESAARPLAAAPTBAAPSAKQRGSKGGHGGAASFSEK GAHESAARPLAAAPTBAAPSAKQRGSKGGHGGASFSEKGAHFGGGGGGGGIS SSSSSASAAAAAAAASSSAGCSRKGGRAASFSEKGAHFGGGGGGGGIS SSSSSASAAAAAAAASSSAGCSRKGGRAASFSEKGAHFGGGGGGGGIS SSSSSASAAAAAAAASSSAGCSRKGGRAAFRFFYLAUVAAAAGS GWCHHVLEGQVYRSHDDFSROEELGGGGGGGGGIS	6377	2311	1845	SRIRRRSSRRPREPPGPSRRRRRRRRPPPPTMPSEKTEVOPPTPF
6378 686 191 GAGPWEAFPDG IGERSKRARLPOYKERPEGVEGGDSGRRMAVA DLALIPUVIASQETFGKLSV WASYHADIYDKVSGDWYKYVLIRVHSAPRSGAGASKKILHYG WASYHADIYDKVSGDWKKGCDCECLGGGRISHGSQDKKHHYG YSMAYGPAQHAISTEKIKAKYPDEVTWANDDY LENSVNNYGCGPABERVLITGLHAVADIYCENCKTTLGWKYEHA FESSGKYKKEGKYITELAHMIKDNGMO 6380 1414 462 FAVGGGRGAGPPTURGSGMMARFALTVVRHGETRFNKEKIJGGG GVDEPLSETGFKGAARAGIFLINVKFTHAFSSDLMTKYGTMEGI LERSKFCKDWTKYYDSRLERKYKGVVEGKALSELRAWKARABE CPVFTPPGGETLQVKMRGIDPFFPLGOLILKEADQKEOPSQOS PSNCLETSLASIFFLGVKMISSKNINSGETGLASSQUKKYHGKY MRSLEPYFLTDLKCSLPATLSRSLMSVTFNTGMSLFIINFEC REVKPTVGCICMNLQDHLNGLTENSLGLINLPSKSNHFEPLKGVP LALFTSLLC AMYKRGLVQVMSLEDPEHICKIDEGSAGLVASGVSPGHHILMT TEPHLRITVMSLCTKSVSYIKYBCLQGIFTFRDGRYMALAER RDCKDYVSIFVCSDWQLLRHFDTDTDLTGISHAPMSCVLAVWD TCLEYKILLYSLGRLISTYSAYEMSLGIKSPANSPSSGFLAVG SVDGKVRILLHVTWKHITFGFHDAAINDFKLVVKREARESPQLG LCCLSFPPPPRAGAGPLPSSESKYEIASVVSUOTKREVTRYDTRANP XGIGIMLASPSDSYFLATRONNIPINAWWOIKKLEFAPVLEQL SPVRAFGWDOOPILAICTGGSRLYLWSPAGCMSVOVPGEGDFA TCHEYKILLYSLGRLISTYSAYEMSLGIKSVAWSDGVAFGVIGAV SVDGKVRILLHVTWKHITFGFHDAAINDFKLVVKREARESPQLG LCCLSFPPPRAGAGPLPSSESKYEIASVVSUOTKREVTRYDRANP XGIGIMLASPSDSYFLATRONNIPINAWWOIKKLEFAPVLEQL SPVRAFGWDOOPILAICTGGSRLYLWSPAGCMSVOVPGEGDFA VLSLCWHLSGDSMALLSKDHYCCLDLETEAVVTAGCRGLGGHT VLSLCWHLSGDSMALLSKDHYCCLDLETEAVVTAGCRGLGGHT VLSLCWHLSGDSMALLSKDHYCCLDLETEAVVTAGCRGLGGHT NICKGRYSPLEVULDIANGTROHGDASEEKAANGTRKCQGSTS AVIGGRYCCMOVYQAGSGOLMPNNYKYHGRKLSVGFKEALFOFF NIGHYLBRELLGPVLKKLTELKAVLERGESYRFYSSSLLVIYDG KERPEVVLDDIABEDLEDLSESSADSAGAYAYKPIGASSUUVRM IDFAHTTCRLYGEDTVVHEQOAGYIFTGASSUUVRM IDFAHTTCRLYGEDTVVHEQOAGYIFTGASSUUVRM IDFAHTTCRLYGEDTVHEQOAGYIFTGASSUUVRM IDFAHTTCRLYGEDTVHEQOAGYIFTGASSGUDVAK PPPAPQOPPPPPAPAPACRS PSPGGAPASFPGRAPSLASCP AARAAAAPAMPSAKQRGSKGGHGAASFPEKGAHGGAGGGGGGS SSSSSASAAAAAAAASSSAGCSRKGRAAASFPEKGAHGGAGGGGGGS SSSSSASAAAAAAAASSSAGCSRKGRAAASFPEKGAHGGGGGGGS SSSSSASAAAAAAAASSSAGCSRKGRAAAFFFLAUAAAAFS GCWCHWULEGQQAGYIFTGAGGGGGGGGGS				QRVEDVRLIREQHPTKIPVIIERYKGEKOLPVIDKTKELVPDHV
6378 686 191 GAGFWEAFFDGGGGRSRRARHOYKRPFGRVGGGGSGRRMANA DLALIPDVDIDSDGVFXVVLIRVHSAPRSGAPAAESKEIVRGYK WARYHADIYDKVSGDMQKOGCDCECLGGGRISHGGDKKIHVYG YSMAYGPAQHAISTEKIKAKYPPYFUTWANDGY SARAYGPAQHAISTEKIKAKYPPYFUTWANDGY FRAGSFSFSRAALRRCAPQRSQAPRAFBCRARCRSFGGSGGRAY LFNSVVNVGCGPAEGRVLITGHLANDIYCENCKTILGWKYEHA FESSQAYRKGKYITELAHMIKDMGWD LFNSVVNVGCGPAEGRVLITGHLANDIYCENCKTILGWKYEHA FESSQAYRKGKYITELAHMIKDMGWD GVDEPLSTTGFKQAAAAGIFLINVKYTHAFSSDLMTKKOTMGGI LERSKECKDMTVKYDSALRERKYGVVEKKALSELRAMAKAAEB CCPFTFPGGGTLDQVWKRGIDDFFGLLLKEADQKEOFSGGS PSNCLETSLABIFFLGKVVYKRGDFFGGSGGRAY LALFTSLLC AMYKRGLVQVKRGIDDFFGLLLKEADQKEOFSGGS PSNCLETSLABIFFLGKVVYKRGDFFGGS PSNCLETSLABIFFLGKVYVKRGDFSGNS PSNCLETSLABIFFLGKVYVKRGDFSGGS PSNCLETSLABIFFLGKVYVKRGDFSGGS PSNCLETSLABIFFLGKVYVKRGDFSGGS PSNCLETSLABIFFLGKVYVKRGDFSGGS PSNCLETSLABIFFLGKVYVKRGDFSGGS PSNCLETSLABIFFLGKVYVKRGDFSGGS PSNCLETSLABIFFLGKVYVKRGDFSGGS PSNCLETSLABIFFLGKVYVKRGDFSGGS PSNCLETSLABIFFLGKVYVKRGDFSGGS PSNCLETSLABIFFLGKVYVKRGDFSGGS PSNCLETSLABIFFLKGVY LALFTSLLC AMYKRGLVQVKRGDFFFTGGTAAMKAAEBE CCFFFFTDGGTLTGVKRGTAKTHOMSKRGLVGVKRGDFSGGS PSNCLETSLABIFFLKGVY LALFTSLLC AMYKRGLVQVKSLEQPBWHCKLDGGNAGLWSFDGRHILNT TEFHLRITVVSLCTKSVSVIKYFACLGGTFFTTDGTAMLAER RDCKDYVSIFVCSDWOLLBHFFTDTQDLTGIBMAPNGCVLAVWD TCLETKLLSTSAARKACLGGTFFTTDGTAMLAER RDCKDYVSIFVCSDWOLLBHFFTDTQDLTGIBMAPNGCVLAVWD TCLETKLLSTSAARKACLGGTFFTTDGTAMLAER RDCKDYVSIFVCSDWOLLBHFFTDTQDLTGIBMAPNGCVLAVWD TCLETKLLSTSAARKACLGGTFFTDGCTAMLAER RDCKDYVSIFVCSDWOLLBHFFTDTVQDLTGIBMAPNGCVLAVWD TCLETKLLSTSAARKACLGGTFFTDGCTAMLAER RDCKDYSIFVCSDWOLLBHFFTDTVQDLTGIBMAPNGCVLAVWD TCLETKLLSTSAARKACLGGTFFTDGCTAMLAER RDCKDYSIFVCSDWALLSTSAARKACLGGTFFTDGCTAMLAER RDCKDYSIFVCSDWALLSTSAARKACLGGTFFTDGCCAARAACAARAACAARAACAARAACAARAACAARAACAARAACAARAACAARAAAAAA				NMSELIKIIRRRLQLNANQAFFLLVNGHSMVSVSTPISEVVESE
6379 666 191 GAGFWEAFPDG GGRSRRARLFOYKRPFGRVGGGDSGRRMAVA DLALIPDVDIDSDVFKYVLIRVHSARPRSGPAAESKEIVRGYK WASYHADIYDKIVSGMCKQCCCCCGGGRISHGSOKKHOYG YSMAYGPAQHAISTEKIKAKYPDYEVTWANDOY 6379 35 378 BRAGSFSFSRALKRCAPGRSGAFDEBACKRSFGGSGRAY LFRSVAVNVGCGPAERRVLITGLHAVADIYCENCKTIGKKYEHA FESSQXYKEGKYIIELHHMIKDNGWD 6380 1414 462 PAVGGGRGAGPPITGRGSGNARAFATTVVRHGETFFNKEKIIGGO GVDEPLSTGFKQAAAAGIFINVKFTHAFSSDLMFTKGTMIGI LERSKEKDMTVKKDSLIRERKYGCKGALSELRAMAKAREB CPVFTPPGGETLDQVKMRGIDPFFLCQLILKEAQKRGFSGGS PSNCLETSLABIFPLGKNHSSKVNSDSGIPGLAASVLVVSHGAY MRSLFDYFLTDLKCSLDATLSRSELMSVTPNTGMSLFIINFEG REVKPTVQCICMNLQDHLNGLTENSLGINLPSKNHFEPLKGVP LALFTSLLC 6381 1668 218 AVVRAGGSRGFSGGWRFRQAAMNFSEVFKLSSLLCKFSPDGK YLASCVQYKLDEDPSHIKCTDEGSAGLVASCWSPDGRHILNT TEPHLRITVMSLCTKSVSYIKKPKACLGGTFFTRDGRYMALAER RDCKDYVSIFVCSDWQLLRHFDDTDQDLTHEWSADSLFILC AMYKRGLVQVWSLEQDPSHIKCKTDEGSAGLVASCWSPDGRHILNT TEPHLRITVMSLCTKSVSYIKKPKACLGGTFFTRDGRYMALAER RDCKDYVSIFVCSDWQLLRHFDDTDQDLTGIEWAPNGCVLAVWD TCLEYKILLYSLDGRLSTYSAYEMSLGIKSVAWSFSSQFLAVG SYDGKVRILNNVTWKHITEFGBPAAINDPKUVYKEAEKSPOLG LCCLSFFPPRRGAGPLPSSESKYETASVPVSLQTLKFVTDRANP XIGIGMLAFSSPGSYFLATRINDIPNAWWWDIQKLRLFAVLEQL SPVRAFOWDPQDPPLSSESKYETASVPVSLQTLKKFVTDRANP XIGIGMLAFSSPGSYFLATRINDIPNAWWWDIQKLRLFAVLEQL SPVRAFOWDPQDPLSSESKYETASVPVSLQTKKKSPVLYY TVEKKGNISSGLKHYMPMSMKCHQQQLQRMKENAKHRNQYKFIL LENLTSRYEVPCVJDLKMGTRQHGDDASEKKAANQIRKCQGSTS AVIGSVRVCGMQVVQAGSGGLMFMKKYGRKLSVQFKKSLLFGVFYNG KEHPLETTEKTPROWWONGHKEEKMKYRGKKLSVQFYKSALLFVTINK KHHVLETTKYTPDWGNKKEKEKMKYRGKKLSVQFYKSALLFVTINK KHHVLETTKYTPDWGNKKHEKMKYRGKKLSVQFYKSALFVTING KERPLEVVLOSHABLLSGESAGNAVKPIGASSPSK GAHPSAARPLAAPTPAAPACRSPSPGGAPASSPSKALVITYDG KERPSVVLOSHABLLSGESGAGRAYKPSSSLLVIYDG KERPSVVLOSHABLLSGESGAGRAYKPSSSLLVIYDG KERPSVVLOSHABLAARAPAMPSAKQRGKGGGGGGGKS SSSSSASAAAAAAAASSSSASCSRCEGALGRALNFLFYLALVAAAAFS GWCHHVLESVQQVRFSKODFSGRAGASFSGADDVAKK PPPAPQQPPPPPAPPQOPPQPPQNQAAGGGGGGGGGGS SSSSSAAAAAAAAASSSSASCSRCEGALGRALNFLFYLALVAAAAFS GWCHHVLESVQQVRFSKODFSGRAGAGGGGGGGGKS SSSSSAAAAAAAAASSSSASCSRCEGLOGLGGGGGGGGKS				KDEDGPLYMVYASQETFGMKLSV
DLLALIPOUDISDGYPKYULIRVHSAPRSGAPAESKEIVRGYK WASYHADIYDKYSGHOMKOKCCCGECGGGRISHGSQDKKHUVYG YSMAYGPAGHAISTEKIKAKYPDYEVTWANDGY ERAGSPSFSRAALRRCAPQBSQAPRWPDRAACRSFCGSGGRY LFMSVVNVQCGPAEGRVLITGHAVADIYCENCKTTLGWKYEHA FESSQKYKEGKYIIELAHMIKDMGWD 6380 1414 462 PAVGGGRAGPPYTGRGSGNARPALTUVUHGETTPMKEKIIQGQ GVDEPLSETGFKQAAAAGIFLNNVKFTHAFSSDLMTKQTMGGI LERSKPCKDWTWKYDSRLERRKYGVVECKALSELRAMAKAAREB CVPYTPPGGETLQVWKRGDDFPELQLILKKEAQKEGPSGGS PSNCLETSLABIFPLGKNHGSKVNSDSGIFGLAASULVVSHGAY MRSLFDYFLTDLKCSLDATLSRSELVJTNTGMSLFIINFEEG REWKPTVQCICMNLQDHLNGLTENSLGIINLPSKSNNFFPELKGVP LALFTSLLC AMYKRGLOVSLDDATLSRSELMSVTPNTGMSLFIINFEEG REWKPTVQCICMNLQDHLNGLTENSLGIINLPSKSNNFFPELKGVP LALFTSLLC AMYKRGLOVSLSDOPBWHCKTDGSAUASCWSPDGRHILNT TEPHLRITVMSLCTKSVSYIKYPKACLQGITFTRGRYMALAER RDCKDYVSIFVCSBWCLLHAFFOTDODLTGLBAPNGCVLAVWD TCLBYKILLYSLDGRLESTSAYBWSLGIINSAWSFSSOFLAVG SYDGKVRILNNVTWKMITEFGBPAAINDPKLVYKEAEKSPOLG LCCLSFPPPRAGAGPLPSSESKYEITASPPVSLQTLKPVTDRAND XIGIGMLAFSBDSYFLATRNDNIPNAVWVWDIQKLRLPAVLEGL SPVRAFQWDPQQPRLAICTGGSRLYLMSPAGGNSVUVGBGDFA VLSICWHLSGDSMALLSKDHFCLCFLETEAVVGTACRQLGGHT FEEDEDRINLCIIAYPLKGDHGIVDIVONSDCEPKSKLLRWTTNK KHHVLETEKYPKDWVGDHKEKEKKRENEVSVQFKSALPOFP HNGRYLRRELLGPVLKKITELKAVLERGESYRFYSSSLLVIYDG KERPEVVLOGAMOTHEKEKEKKRESUGOFTARAFOKYFIIL LENLTSRYEUPCVLDLMMTTRQHGDDASEKRAMQIRKCQOSTS AVIGUVCGGQVVQAGGGGLMFMKKYGRKLSUQGFKSALPOFP HNGRYLRRELLGPVLKKLTELKAVLERGESYRFYSSSLLVIYDG KERPEVVLOGAMOTHAGAAAAAAAAASSASCSGLMFMYKGRKLSUQGFKGALFOSEK GAHPSAARPLAAPTPAAPACRSPSPEGGAPASPFRGAPSLASQP AARAAAAPAMPSAKQRGCHGAASPSEKGHGRAASPSEK GAHPSAARPLAAPTPAAPACRSPSPEGGAPASPFRGAPSLASQP AARAAAAPAMPSAKQRGCHGGAASPSEKGAHBSGGADDVAKK PPPAPQQPPPPPAPAPQCHPQNQAMIGKGGKGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	6378	686	191	GAGPWEAFPDGIGRRSRRARLPOYKRPPGRVGGGDSGRRNMAVA
######################################				DLALIPDVDIDSDGVFKYVLIRVHSAPRSGAPAAESKEIVRGVK
6389 378 BRAGSPEGRALHERGAPQRSQAPMPDRAACRSFQGSQRAY LFNSVANVGCGPAERVLITCHHAVADIYCENCKTIGMKYEHA FESSQKYKEGKYI IBLAHMIKDNOMD 6380 1414 462 PAPOGGRGAGPPIGRGSGMRAFALTVURHGETRPNKEKIIQGO GVDEPLSETGFKQDAAAGIFLNNVKFTHAFSSDLMRTKQTMHGI LERSKFCKDMTVKYDSRIRERKYGVVEGKALSELRAMAKAREB CPVFTPPGGETLDQVKMGIDFFFLCQLILKERDQKEGFSQGS PSNCLETSLABIFPLGNKHSSKVMSDGSIFGLAASVLWYSHGAY MRSLEPYFLTDLKKSLPATLGSSELMSVTPNTGMSLFIINFEG REVKPTVQCICMNLQDHLNGITERSLGLMLPSKSNHFEPLKGVP LALFTSLLC ANYKRGLVQVWSLEQPBWHCKIDEGSAGLWASCWSPDGRHILNT TEFHLRITVWSLCTKSVSYIKYPKACLQGITFTRGGRMALAER RDCKDYVSIFVCSWQLLRHFDTDTQDLTGIEWAPNGCVLAVWD TCLBYKILLYSLDGRLLSTYSALEWSLGVSWASPSGSFLAVG SUDGKVRILNHVTNKMTTEGHPAAINDFKIVVYKEAEKSQLE LCCLSFPPPRAGAGPLPSSESKYEIASVPSLQTLKEPVTDRANP KGIGMLAFSPDSYLATMADUTNAWWWDIQKLRLFAVLEQL SPVRAFQWDPQQPRLAICTGGSRLYLWSPAGCWGVVPGEGDFA VLSLCWHLSGDSMALLSKOHFCLCFLETEAVVGTACRGGHT TVEKKGNISSQLKHYNPWSMKCHQQOLQRMKENAKHNOVKFIL LENNLTSKYEVPCVLDLKMGTRGGDAESEKANGIRKCQGSTS AVIGVRVCGMQVYQAGSGGLMFMNXYHGRKLSVQGFKEALFQFF HNGRYLRRELLGPVLKKLTELKAVLEGESSTFYSSSLLVYDG KERPEVVLDSDAEDLEBLESADESAGAYAYKFIGASSVDVMM IDFAHTTCRLYGEDTVVHEQDAGYIFGLQSLIDIVTEISEESG E 6383 3159 1061 SPAPGRFSPHGSQFAARAAAPAMPSAKQRGSKGGIGAASPSEK GAHPSAARPLAAPTPAAPACRS PSIGGABASPGEKGAHPSGGADDVAKK PPPAPQQPPPPPAPHQQHPQQHPQQHPQQHPQQARAKGGGGGGGKS SSSSASAAAAAAAASSSASCSRRLGRALHFEVLALVAAAAFS GGCHMHVLEEVQCVGRRSHOGFRGGGGGGGKS SSSSSASAAAAAAAAASSSASCSRRLGRALHFEVLALVAAAAFS	1			WAEYHADIYDKVSGDMQKQGCDCECLGGGRISHOSODKKIHVYG
6380 1414 462 PAVQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ				YSMAYGPAQHAISTEKIKAKYPDYEVTWANDGY
LFMSVVNVGGGPAERKYLITGLHAVADIYCENCKTTLGWKYEHA FESSQYXKEGKYKI IBLAMH KUNGWD PAVQGQRGAGPPTGRGSGNMARFALTVVRHGETRFNKEKI IQGQ GVDEPLSETGFKQAAAAGI FLNNVKFTHAFSSDLMRTKQTMHGI LERSKPCKDMTVKYDGRLRERKYGVVBCKALSELRAMAKAAREB CPVFTPPGGETLDQVKRRGIDPFEPLCQLILKEADQKEQFSQGS PSNCLETSLAEIFPLGKNHSSKVNDSDGIPCLAASVLVVSKGAY MRSLFPYFLTDLKCSLPATLSKSELMSVTPNTGMSFITINFEEG REVKPTVQCICMNLQDHLNGLTENSLGINLPSKSNHFEPLKGVP LALFTSLLC AVYKRQGSRGFSGAGWRPRQAAMNFSEVFKLSSLLCKFSPDGK YLASCVQYRLVVRDVNTLQILQLYTCLDQIGHIEWSADSLFILC AMYKRGLUQVWBLOPBWHCKIDDGSAGUVASCWSPDGRHILNT TEFHLRITVWSLCTKSVSYIKYPKACLQGITFTRDGRYMALAER RDCKDYVSIFVCSDMQLLHFFDTDTQDLTGIEWAPNGCVLAVWD TCLBKYKLLYSLDGRLLSTYSAYEWSLGIKSVAWSPSSQFLAVG SYDGKVRILNHVTWMMITEFGHPAAINDPKIVVYKRAEKSPQLG LCCLSFPPPRAGAGPLPSSESKYEIASVPVSLQTLKEVTDRANP KIGIGMLAFSPDSYFLATRNDIYNAVWNDIOKIRLFAVLEQL SPVRAFQNDPQOPRLAICTGGSRLYLWSPAGCMSVQVPGEGDFA VLSLCWHLSGDSMALLSKCHFCLCFIETERAVGTACRGLGGHT AVISLCWHLSGDSMALLSKCHFCLCFIETERAVGTACRGLGGHT KHHVLETSKTPKDWVGGHKEEKMKSHKLEEEFEWLKKSEVLYY TVEKKGNISSQLKHYNPWSMKCHQOLGMKERAKHRINGYKFIL LENLTSRYEVPCVLDLKMGTRQHGDDASEKKANQIRKCQGSTS AVIGYRVCGMQVYQAGSGQLMFMMKYHGRKLSVQGFKEALFQOFF HNGRYLRRELLIGPULKKLTELKAVLERQESYRFYSSSLLVIYDG KERPEVVLDSDAEDLEILSESADESAGAYAYKFIGASSVDVRM IDFAHTTCRLYGEDTVVHEGQDAGYIFGLQSLIDIVTEISEESG E 6383 3159 1061 SPAPGRPSPHGSQPAARAAAAPAMPSAKQRGSKGGHGAASPSEK GAHESAARPLAAPTPAAPACRSPSPEGGAAPSGGAGHASPSEK GAHESAARPLAAPTPAAPACRSPSPEGGAAPSGGABGNOKK ARAAAPAMPSAKQRGSKGGHGAASPSEKGAHPSGGADVAKK PPPAPQQPPPPPAPQUPQHPQNPQNARKGGHKGGGGGGKS SSSSASAAAAAAAAAAASASSASCSRCHGRAASPSGGADVAKK PPPAPQQPPPPPAPQUPPQNPQNARKEGGHKGGGGGGKS SSSSSASAAAAAAAAAASASSASCSRCHGGAASPSGGADVAKK PPPAPQQPPPPPAPQUPPQNPQNARHKGGHKGGGGGGKS SSSSSASAAAAAAAAAAASASSASCSRCLGGAGASPSGGGGKS SSSSSASAAAAAAAAAAASASSASCSRCEGGGAGASPSGGGGKS SSSSSASAAAAAAAAAASASSASCSRCEGGGGGKS SSSSSASAAAAAAAAAASASSASCSRCEGGGGGKS	6.3 /9	35	378	BRAGSPSPSRAALRRCAPQRSQAPRWPDRAACRRSFQGSQGRAY
FESSOKYKGGKYIIBLAHMIKONGMU PAVGORGAGPPYGRGGGMARFALTUVRHGETRPNKEKIIQGQ GVDEPLSETGFKQAAAAGIFLNNVKFTHAFSSDLMRTKQTHHGI LERSKEKKMTUKYDSRLRERKYGVVEGKALSELRAMAKAAREB CPVFTPPGGETLDQVMKRGIDPFPLCQLILKEADQKEQFSQGS PSNCLETSLAEIFPLGNWINSSKVNSDSGIPGLAASVLVVSHGAY MRSLFDYFLTDLKCSLPATLSRSELMSYTPNTGMSLFIINFEEG REVKPTVQCICUNLQDHLMGLTENSIGLNLPSKSNHFBPLKGVP LALFTSLLC AVVRAGGSRGFSGAGWRPRQAAAMNFSEVFKLSSLLCKFSPDGK YLASCVQYRLVVRDWTLQILQLYTCLDQIQHIENSABSLFILC AMYKRGLVQVWSLEQPEWHCKIDEGSAGLWSCWSPDGRHILNT TEPHLRITUWSLCTKSVSYIKYPKACLGGTFTEDGRYMALAER RDCKDYVSIFVCSDMOLLMFDTDQLLTGIEMAPNGCVLAVWD TCLEYKILLYSLDGRLLSTYSAYEWSLGIKSVAWSPSSQFLAVG SYDGKVRILNHVTWMMITEFGHPAAINDPKLVVYKEREKSPQLG LCCLSFPPPRAGGGPLPSSESKYEIASVPVSLQTIKEPKTDRANP KIGIGMLAFSPDSYPLATRNDNIPNKLVVYKEREKSPQLS SPVRAFQWDPQOPRLAICTGGSRLYLWSPAGCMSVQVPGEBDPA VLSLCWHLSGDSMALLSKDHFCLCFLETEAVCHTACRQLGGHT TVEKKGNISSQLKHYNPWSMKCHQOQLORMKENAKHNOVKFIL LENLTSRYEVPCVLDLKMGTRQHGDDASEEKAANQIRKCQGSTS AVIGVRVCGMQVYQAGSGQLMFMNKYHRGRLSVQGFKEALFQFF HNGRYLRRELLGPVLKHTELKAVLERGESTPYSSSLLVIYDO KERPEVVLDSDAEDLEDLSEESADESAGAYAYKPIGASSVDVRM IDFAHTTCRLYGEDTVVHEGQDAGYIFGLQSLIDIVTEISEESG E 6383 3159 1061 SPAPGRPSPHGSQPAARAAAPAARAPAAMPSAKQRGSKGGHGAASPSEK GAHPSAARPLAAPTPAAPACRSSPSGGGAASFSRKGGHGAASPSEK AARAAAAPAAMPSAKQRGSKGGHAASFSKKGHRGGGGGGGKS SSSSASAAAAAAAAAASASSASCSRLGRAANFLFYLALVAAAAFS GWCWHHVLEEVQQVRRSHQDPSRQFBELGGGLGGWGNSA				LFNSVVNVGCGPAEERVLLTGLHAVADIYCENCKTTLGWKYEHA
GUDEPISETOR KOADARGI FILMVIKTHER SEDILMRIKOTIMIGI LERSKE KUMTVKYDSKLREKKYGVVEGKALSELRAMAKAAREB CPVFTPPGGETLDQVKMRGIDFFEFLOQLILKENDGKEQFSQGS PSNCLETSLAEIFPLGKMHSKVMSDSGI FOLAASVLIVSHGAY MRSLEPJYFITDLKCSLPATLSRSELMSVTINTGMSLFI INFEEG REVKPTVQCICMNLQDHLNGLTENSLGINLPSKSNHFEPLKGVP LALFTSLLC 6381 1668 218 AVVRAGGSRGFSGGWRPRQAAAMNFSEVFKLSSLLCKFSPDGK YLASCUQVRLVVRDVNTLQILQLYTCLDQIQHIEWSADSLFI LC AMYKRGLVQVWSLEQPEWHCKIDEGSAGLVASCWSPDGRHILNT TEPHLRITWSLCTKSVSYIKVPKACLQGTFTRDGRYMALAER RDCKDYVSTFVCSDWQLLRHFDTDTQDLTGIEWAPMGCVLAVVD TCLEYKILLYSLDGRLLSTYSAVEWSLGIKSVAWSPSSOFLAVG SYDGKVRILNHTWKNITEFGHPAALNDPKIVVYKREKESPQLG LCCLSFPPPRAGGPLPSSESKVEIASVPVSLQTLKPVTDRANP XIGIGMLAFSPDSYFLATRNDNIPNAVWWDIQKRLFAVLEQL SPVRAFQWDPQOPRLAICTGGSRLYLWSPAGCMSVQVPGEGDPA VLSLCWHLSGDSMALLSKOMFCLQOLDRWKENAKHRNQYKFIL LENLTSRYEVPCVLDLKMGTRQHGDDASEKAANQIRKCQGSTS AVIGVRVCGMOVYAGSGQLMFMNKYHGRKLSVQGFKEALFOPF HNGRYLRRELLGPVLKKLTEAVLERGESYFYSSSLLYIYDG KERPEVVLDSDAEDLEDLSEESADESAGAYAYKPIGASSVDVRM IDFAHTTCRLYGCDTVVHEGQDASTFRGRSLDIVTEISEESG E GAHESAARPLAAPTPAAPACRSPSSGGAPASFPGRSPSLASQP ARRAAAPAMAPSAKQGGSKGGHGAASFSEK GAHESAARPLAAPTPAAPACRSPSSGGAPASFPGRAPRSLASQP AARAAAAAAAAASSASGCGGGAASSFSKGGHGAASFSEK GHCCHHVLEEVQQVPSCHOA	6390			FESSQKYKEGKYIIELAHMIKDNGWD
LERSKFCKOMTVKYDSRLRERKYGVVEGKALSELRAMAKAARRE CPYFTPPGGTLDQVKRRG1DPFEPLCQLILKEADQKEQFSQGS PSNCLETSLAE1FPLGKHHSSKVNDSGIPGLAASVLVVSHGAY MRSLFDYFLTDLKCSLPATLSRSELMSVTPNTGMSLF11NFEEG REVKPTVQCICMNLQDHLNGLTRSLGLNLPSKSNHFEPLKGVP LALFTSLLC AVVRAGGSRGFSGAGMRPRQAAAMNFSEVFKLSSLLCKFSPDGK YLASCVQYRLVVRDNTTLQILQLYTCLDQIGHIEMSADSLFILC AMYKRGLVQVMSLEQPBWHCKIDEGSAGLWASCWSPDGRHILNT TEPHLRITVWSLCTKSVSY1KYPKACLQGITFTRDGRYMALABER RDCKDYVSIFVCSDWQLLRHBDTDTQDLTGIEMAPNGCVLAVND TCLBYKILLYSLDGRLLSYSAYEMSLGIKSVAWSPSSQFLAVG SYDGKVRILNHVTWKMITEFGHPAAINDPKIVVYKEAEKSPQLG LGCLSFPPPRAGAGPLPSSESKYEIASVPVSLQTLKPVTDRAMP XIGIGMLAFSPDSYFLATRONIPNAVWWDIQKLRLFAVLEQL SPVRAFQWDPQQPRLAICTGGSRLYLWSPACCMSVQVPGEGDFA VLSLCWHLSGDSMALLSKDHFCLCFLETEAVVGTACRQLGGHT TVEKKGNISSQLKHYNFWSMKCHQQLQRMKENAKHRQYKFIL LENLTSRYEVPCVLDLKMGTRGKLSVQSFKSALLFQFF HNGRYLRELLGPVLKKLTELKAVLERGESYRFYSSSLLVIYDG KERPEVVLDSDAEDLEDLSEESADESAGAYAYKPIGASSVDVRM IDFAHTTCRLYGEDTVVHEQQDAGY1FGLQSLIDIVTEISBESG E 6383 3159 1061 SPAFGRPSPHGSQPAARAAAPAMPSAKQRGSKGGHGAASPSEK GAHPSAARPLAAPTPAAPACRSPSPGGAPASFPGRAPRSLASQP AARAAAPAMPSAKQRGSKGGHAASFSEKGAHPSGGADDVAKK PPPAPQQPPPPPAPPQQPPQQHPQNQAHGKGGRGGGGGGKS SSSSSAAAAAAAAASSSASCSRLGRALNFLEYLALVAAAAFS GWCWHHVLEEVQQVRRSHODFSRORELEGGLGOLVGVKOVSLOA	6360	1414	462	PAVQGQRGAGPPIGRGSGNMARFALTVVRHGETRFNKEKIIQGQ
CPVFTPFGGETLOQVKMGGIDFFELOQLILKEADQKEQFSQGS PSNCLETSLABIFPLGKNNSSKVNSDSGIFGLAASVLVVSHGAY MRSLFDYFLTDLKCSLPATLSRSELMSVTFNTGMSLF1 INFEEC REVKPTVQCICMNLQDHLNGLTENSLGLNLPSKSNHFEPLKGVP LALFTSLLC AVVRAGSRGFSGAGWRFRQAAAMNFSEVFKLSSLLCKFSPDGK YLASCVQYRLVVRDVNTLQILQLYTCLOQIGHIEWSADSLFILC ANYKRGLVQVWSLEQPBWHCKIDEGSAGLVASCWSPDGRHILNT TEFHLRITVWSLCTKSVSYIKYPKACLQGITFTRDGRYMALAER RDCKDYVSIFVCSDWQLLRHFDTDTQDLTGIBWAPNGCVLAVND TCLBYKILLYSLDGRLLSTYSAYEWSLGIKSVAWSPSSQFLAVG SYDGKVRILNNTWKMTIEFGHPAAINDPKLVYKEAEKSPQLG LGCLSFPPPRAGAGPLPSSESKYBIASVPVSLQTLKPVTDRANP KIGIGMLAFSPDSYFLATRNDNIPNAVWWDIQKLRLFAVLEQL SPVRAFQWDPQQPRLAICTGGSRIYLWSPAGCMSVQVPGEGDFA VLSLCWHLSGDSMALLSKDHFCLCFLETEAVVGTACRQLGGHT FEEDEDRNLCLIAYPLKGDIGIVDIVDNSDCEPFKSKLLRWTTNK KHHVLETEKTPKDWVRQHRKEEKMKSHKLEEFFEWLKKSEVLYY TVEKKGNISSQLKHYNPWSNKCHQOLQRMKENAKHRNQYKFIL LENLTSRYEVPCVLDLKMGTRQHGDDASEEKAANQIRKCQQSTS AVIGVRVCGMQVYQAGSGQLMFMNKYHGRKLSVGGFKEALFQFF HNGRYLRRELLGPVLKKLTELKAVLERGESYRFYSSSLLVIYDG KERPEVVLDSDAEDLEDLSESSADESAGAYAYKPIGASSUDVRM IDFAHTTCRLYGEDTVVHEGQDAGYIFGLQSLIDIVTEISEESG E 6383 3159 1061 SPAFGRPSPHGSQPAARAAAAAAPANPSAKQRGSKGHGAASPSEK GAHPSAAAPLAAPTAAPAPARPSAKQRGSKGHGAASPSEK GAHPSAARPLAAPTAAPAPARPSAKQRGSKGHGAASPSEK SSSSASAAAAAAAASSSASSERGAHPSGGADDVAKK PPPAPQQPPPPPAPHQQDPPPPAPHQOQPQQAPARGGGRGGGGGGKS SSSSSASAAAAAAAASSSASSERGRAANFELGRALHFLEVILALVAAAAFS GWCWHHVLEEVQQVRRSHQDFSROREELGGGLGOGVGVOVSLOA	1 1			GVDEPLSETGFKQAAAAGIFLNNVKFTHAFSSDLMRTKOTMHGI
PSNCLETSLABIFPLGKNISSKVNSDSGIPGLAASULVVSHGAY MRSLFDYFLTDLKCSLPATLSRSELMSVTPNTGMSLFIINFEEG REVKPTVQCICMILQDHLMGLTENSLGINLPSKSNHFEPLKGVP LALFTSLLC AVVRAGGSRGFSGAGWRPRQAAMNFSEVPKLSSLLCKFSPDEK YLASCVQYRLVVRDVNTLQILQUYTCLDQIQHIEWSADSLFILC AMYKRGLVQVWSLEQPEWHCKIDEGSAGLVASCWSPDGRHILNT TEFHLRITUWSLCTKSVSYIKYRACLQGTTFTRDGRYMALAER RDCKDVVSIFVCSDWQLLRHFDTDTQDLTGIEWAPNGCVLAVWD TCLEYKILLYSLDGRLLSTYSAYEWSLGIKSVAWSPSSQFLAVG SYDGKVRILNHVTWKMITEFGHDAAINDPKLVVYKEAEKSPQLG LGCLSFPPPRAGAGPLPSSSESKYEIASVPVSLQTLKFVTDRANP XIGIGMLAFSPDSYFLATRNDNIPNAVWWDIOKLRLFAVLEQL SPVRAFQWDDQQPRLAICTGGSRLYLWSPAGCMSVQVPGEGDFA VLSLCWHLSGDSMALLSKUPFLCFLETEAVVGTACRGLGGHT FEEDEDRNLCLIAYPLKGDHGTVDIVDNSDCEPKSKLLWTTNK KHHVLETEKTPKDWVRQHRKEEKMKSHKLEEFEWLKKSSVLYY TVEKKGNISSQLKHYNDPWSMKCHQQQLQRMKENAKHRNQYKFIL LENLTSRYEVPCVLDLKWGTRQHGDDASEEKAANQIRKCQQSTS AVIGVRVCGMQVYQAGSGQLMFMNKYHGRKLSVQGFKEALFQFF HNGRYLRRELLGPVLKKLTELKAVLERQESYRFYSSSLLVIYDG KERPEVVLDSDAEDLEDLSESADESAGAYAYKPIGASSVDVRM IDFAHTTCRLYGEDTVVHEGQDAGYIFGLQSLDIVTEISEESG E 6383 3159 1061 SPAPGRPSPHGSQPAARAAAAPMFSAKQRGSKGGHGAASPSEK GAHPSAARPLAAPTPAAPACRSPSPGGAPASPRSLASQP AARAAAAPAMPSAKQRGSKGGHGAASPSEKGAHPSGGADDVAKK PPPAPQQPPPPPAPHQQHPQNPQNQAHGKGGHRGGGGGGGKS SSSSSASAAAAAAASSSACSRRIGRALNFLFYLALVAAAAFS GWCHHVUEEVQQVRRSHQDPSRQRGSKGGHGAASPSEKGAHPSGGADDVAKK PPPAPQQPPPPPAPHQQHPQQNPQNQAHGKGGHRGGGGGGGKS SSSSSASAAAAAAAASASSCSRLIGRALNFLFYLALVAAAAFS GWCHHVUEEVQQVRRSHQDPSRGGELGGGLGGVKOKYOSLOA	i i			LERSKFCKDMTVKYDSRLRERKYGVVEGKALSELRAMAKAAREE
MRSLFDYFLTDLKCSLPATLSRSELMSUTPNTGMSLF1INFEEG REVKPTVQCICMNLQDHLNGLTENSLGLNLPSKSNHFEPLKGVP LALFTSLLC AVVRAGGSRGFSGAGWRPRQAAMNFSEVFKLSSLLCKFSPDGK YLASCVQYRLVVRDVNTLQILQLYTCLDQIGHIEWSADSLFILC AMYKRGLVQWSLEQPEWHCKIDEGSAGLVASCWSPDGRHILNT TEFHLRITWSLCTKSVSYIKYPKACLQGTIFTRDGRYMALAER RDCKDVVSIFVCSDWQLLRHFDTDTQDLTGIEWAPNGCVLAVWD TCLEYKILLYSLDGRLLSTYSAYEWSLGIKSVAWSPSSQFLAVG SYDGKVRILNHVTWKMITEFGHPAAINDPKIVVYKEAEKSPQLG LGCLSFPPPRAGAGPLPSSESKYEIASVPVSLQTLKFVTDRANP KIGIGMLAFSPDSYFLATRNDNIPNAVWWDIQKLRLFAVLEQL SPVRAFQWDPQQPRLAICTGGSRLYIWSPAGCMSVQVYGEGOFFA VLSLCWHLSGDSMALLSKDHFCLCFLETEAVVGTACRQLGGHT KHHVLETEKTPKDWVRQHRKEEKMSHKLEEFFWLKKSEVLYY TVEKKGNISSQLKHYNPWSMKCHQQQLQRMKENAKHRNQYKFIL LENLTSRYEVPCVLDLKMGTRQHGDDASEEKAANQIRKCQQSTS AVIGTVCCMQVYQAGSGQLMFMNKYHGRKLSVQGFKEALFQFF HNGRYLRRELLGPVLKKLTELKAVLERQESYRFYSSSLLVIYDG KERPEVVLDSDABDLEDLSEESADESAGAYAYKPIGASSVDVRM IDFAHTTCRLYGEDTVVHEGQDAGYIFGLQSLIDIVTEISEESG E 6383 3159 1061 SPAPGRPSPHGSQPAARAAAAPAMPSAKQRGSKGGHGAASPSEK GAHPSAARPLAAPTPAAPACRSPSPGGAPSFGRAFRSLASQP AARAAAPAMPSAKQRGSKGGHGAASPSEKGAHPSGGADDVAKK PPPAPQQPPPPPAPHQQHQQHPQNQAHGKGGHRGGGGGGGKS SSSSASAAAAAAAASSSASCSRRLGRALNFLFYLALVAAAAFS GWCHHVLEEVQQVRRSHQDPFSRQREELGGGLGGVKOKONSLOA	:	. i		CPVFTPPGGETLDQVKMRGIDFFEFLCQLILKEADQKEQFSQGS
REVKPTYQCICMNLQDHLNGLTENSLGLNLPSKSNHFEPLKGUP LALFTSLLC AVVRAGGSRGFSGAGWRPRQAAMMFSEVPKLSSLLCKFSPDGK YLASCVQYRLVVRDVNTLQILQLYTCLDQIQHIEWSADSLFILC AMYKRGLVQWWSLEQPEWHCKIDEGSAGLVASCWSPDGRHILNT TEFHLRITVWSLCTKSVSYIKYPKRCLQGITFTRDGRYMALAER RDCKDVVSIFVCSDWQLLRHFDTDTQDLTGIEWAPNGCVLAVWD TCLEYKILLYSLDGRLLSTYSAYEWSLGIKSVAWSPSSQFLAVG SYDGKVRILNNVTWKNITEFGHPAAINDPKIVVYKEAEKSPQLG LGCLSFPPPRAGAGPLPSSESKYEIASVPVSLQTLKFVTDRANP KIGIGMLAFSPDSYFLATRNDNIPNAVWWDIQKLRLFAVLEQL SPVRAFQWDPQQPRLAICTGGSRLYLWSPAGCMSVQVPGEGDFA VLSLCWHLSGDSMALLSKDHFCLCFLETEAVVGTACRQLGGHT 6382 2 1062 FEEDEDRNLCLIAYPLKGDHGIVDIVONSDCEPKSKLLRWTTNK KHHVLETEKTPKDWWQCHKKEEKMKSHKLEEFFWLKKSBVLYY TVEKKGNISSQLKHYNPWSMKCHQQQLQRMKENAKHRNQYKFIL LENLTSRYEVPCVLDLKMGTRQHGDDASEEKAANQIRKCQQSTS AVIGVRVCGMQVYQAGSGQLMFNNKYHGRKLSVQGFKEALFOFF HNGRYLRRELLGPVLKKLTELKAVLERQESYRFYSSSLLVIYDG KERPEVVLDSDAEDLEDLSESADESAGAYAYKPIGASSVDVRM IDFAHTTCRLYGEDTVVHEGQDAGYIFGLQSLIDIVTEISEESG E 6383 3159 1061 SPAPGRPSPHGSQPAARAAAPAMPSAKQRGSKGGHGAASPSEK GAHPSAARPLAAPTPAAPACRSFSPGGAPASFPGRAPRSLASQP AARAAAPMPSAKQRGSKGGHGAASPSEKGAHPSGGADDVAKK PPPAPQQPPPPPPAPHPQQHPQQHPQNQAHGKGGHRGGGGGGKS SSSSASAAAAAAAAASSSSSSCSRRLGRALNFLFYLALVAAAAFS GWCVHHVLEEVQQVRRSHQDFSRQREELGGGLOGVGOKVOSLOA]	1		PSNCLETSLAEIFPLGKNHSSKVNSDSGIPGLAASVLVVSHGAY
ALFTSLLC AVVRAGSRGFSGAGWRFRQAAAMNFSEVFKLSSLLCKFSPDGK YLASCVQYRLVVRDUNTLQILQLYTCLDQIQHIEWSADSLFILC AMYKRGLVQVWSLEQPEWHCKIDEGSAGLVASCWSPDGRHILNT TEFHLRITUWSLCTKSVSYIKYPKACLQGITFTRDGRYMALAER RDCKDYVSIFVCSDWQLLRHFDTDTQDLTGIEWAPNGCULAVWD TCLBYKILLYSLDGRLLSTYSAYEWSLGIKSVAWSPSSGFLAVG SYDGKVRILNYUWMITEFGHPAAINDPKIVVYKEAEKSPQLG LGCLSFPPPRRAGGEIPSSESKYSIASVPVSLQTLKPVTDRANP KIGIGMLAFSPDSYFLATRNDNIPNAVWWDIQKLRLFAVLEQL SPVRAFQWDPQQPRLAICTGGSRLYLWSPAGCMSVQVVGEGDFAA VLSLCWHLSGDSMALLSKDHFCLCFLETEAVVGTACRQLGGHT TVEKKGNISSQLKHYNPWSMKCHQQQLQRMKENAKHRNQYKFIL LENLTSRYEVPCVLDLKMGTRQHGDDASEEKAANQIRKCQQSTS AVIGVRVCGMQVYQAGSGQLMFNNKYHGRKLSVQGFKEALFQFF HNGRYLRELLGPVLKKLTELKAVLERQESYRFYSSSLVIYDG KERPEVVLDSDAEDLEDLSEESADESAGAYAYKPIGASSVDVRM IDFAHTTCRLYGEDTVVHEGQDAGYIFGLQSLIDIVTEISEESG E GAHPSAARPLAAFTPAAPACRSFSPGGAPASFPGRAPRSLASQP AARAAAPMPSAKQRGSKGGHGAASPSEK GAHPSAARPLAAPTPAAPACRSFSPGGAPASFPGRAPRSLASQP AARAAAAPMPSAKQRGSKGGHGAASPSEKGAHPSGGADDVAKK PPPAPQQPPPPPPAPHPQQHPQQHPQNQAHGKGGHRGGGGGGGKS SSSSASAAAAAAAASSSSASCSRRLGRALNFLFYLALVAAAAFS GWCVHIVLEEVQQVRRSHQDFSRQREELGGGLOGVGOKVOSLOA	1			PEUND DE CONTRE
AVVRAQGSRGFSGAGWRPRQAAMMFSEVFKLSSLLCKFSPDGK YLASCVQYRLVVRDVNTLQILQLYTCLDQIQHIEWSADSLFILC AMYKRGLVQVWSLEQDBWHCKLDEGSAGLVASCWSPDGRHILNT TEPHLRITUWSLCTKSVSYIKYPKACLQGIFFTRDGRYMALAER RDCKDYVSIFVCSDWQLLRHFDTDTQDLTGIEWAPNGCVLAVWD TCLBYKILLYSLDGRLLSTYSAYEWSLGIKSVAWSPSSQFLAVG SYDGKVRILNIVTWKMITEFGHPAAINDPKIVVYKEAEKSPQLG LGCLSFPPPRAGAGPLPSSESKYEIASVPVSLQTLKPVTDRANP KIGIGMLAFSPDSYFLATRNDNIPNAVWWDIQKLRLFAVLEQL SPVRAFQWDPQQPRLAICTGGSRLYLWSPAGCMSVQVPGEGDFA VLSLCWHLSGDSMALLSKDHFCLCFLETEAVVGTACRQLGGHT VLSLCWHLSGDSMALLSKDHFCLCFLETEAVVGTACRQLGGHT KHHVLETEKTPKDWVRQHRKEEKMKSHKLEEEFEWLKKSEVLYY TVEKKGNISSQLKHYNPWSMKCHQQQLQRMKENAKHRNQYKFIL LENLTSRYEVPCVLDLKMGTRQHGDDASEEKAANQIRKCQQSTS AVIGVRVCGMQVYQAGSQQLMFMNKYHGRKLSVQGFKEALFQFF HNGRYLRRELIGPVLKKLTELKAVLERQESYFFYSSSLLVIYDG KERPEVVLDSDAEDLEDLSEESADESAGAYAYKPIGASSVDVRM IDFAHTTCRLYGEDTVVHEGQDAGYIFGLQSLIDIVTEISEESG E GAHPSAARPLAAPTPAAPACRSPSPGGAPASFPGRAPRSLASQP AARAAAPAPAMPSAKQRGSKGGHGAASPSEKGAHPSGADDVAKK PPPAPQQPPPPPAPHPQQHPQNQAHGKGGHRGGGGGGKS SSSSASAAAAAAASSSASCSRRLGRALNFLPYLALVAAAAFS GWCVHHVLEEVQQVRRSHQDFSRQREBLGGGLGGVGNVOSLOA	1		•	LDLETSIAC
YIASCVQYRLVYRDVNTLQILQLYTCLDQIQHIEWSADSLFILC AMYKRGLVQVWSLEQPEWHCKIDEGSAGLVASCWSPDGRHILNT TEFHLRITVWSLCTKSVSYIKYPKACLQGITFTRDGRYMALAER RDCKDYVSIFVCSDWQLILRHFDTDTQDLTGIEWAPNGCVLAWWD TCLBYKILLYSLDGRLLSTYSAYEWSLGIKSVAWSPSSQFLAVG SYDGKVRILNIVTWKMITEFGHPAAINDPKIVVYKEAEKSPQLG LGCLSFPPPRAGAGPLPSSESKYEIASVPVSLQTLKPVTDRANP KIGIGMLAFSPDSYFLATRNDNIPNAWWWDIQKLRLFAVLEQL SPVRAFQWDPQQPRLAICTGGSRLYLWSPAGCMSVQVPGEGDFA VLSLCWHLSGDSMALLSKDHFCLCFLETEAVVGTACRQLGGHT FEEDEDRNLCLIAYPLKGDHGIVDIVDNSDCEPKSKLLRWTTNK KHYVLETEKTPKDWVRQHRKEEKMKSHKLEEFEWLKKSEVLYY TVEKKGNISSQLKHYNPWSMKCHQQQLQRMKENAKHRNQYKFIL LENLTSRYEVPCVLDLLKMGTRQHGDDASEEKAANQIRKCQQSTS AVIGVRVCGMQVYQAGSGQLMFMNKYHGRKLSVQGFKEALFQFF HNGRYLRRELLGPVLKKLTELKAVLERQESYRFYSSSLLVIYDG KERPEVVLDSDAEDLEDLSEESADESAGAYAYKPIGASSVDVRM IDFAHTTCRLYGEDTVVHEGQDAGYIFGLQSLIDIVTEISEESG E 6383 3159 1061 SPAPGRPSPHGSQPAARAAAAPAMPSAKQRGSKGGHGAASPSEK GAHPSAARPLAAPTPAAPACRSPSPGGAPASFPGRAPRSLASQP AARAAAAPMPSAKQRGSKGGHGAASPSEKGHPSGGADDVAKK PPPAPQQPPPPPAPHPQQPPQHPQNPQNQAHGKGGHRGGGGGGKS SSSSSAAAAAAAAASSSASCSRRLGRALNFLFYLALVAAAAFS GWCVHHVLEEVQQVRRSHODFSRQREBLGGGLOGVEOKYOSLOA	6381	1668	218	
AMYKGLVQVWSLEQPEWHCKIDEGSAGLVASCWSPDGRHILNT TEFHLRITVWSLCTKSVSYIKYPKACLQGITFTRDGRYMALAER RDCKDYVSIFVCSDWQLLRHFDTDTQDLTGIEWAPNGCVLAVWD TCLEYKILLYSLDGRLLSTYSAYEWSLGIKSVAWSPSSOFLAVG SYDGKVRILNHVTWKMITEFGHPAAINDPKIVVVYKEAEKSPQLG LGCLSFPPPRAGAGPLPSSESKYEIASVPVSLQTLKPVTDRANP KIGIGMLAFSPDSYFLATRNDNIPNAVWVWDIQKLRLFAVLEQL SPVRAFQWDPQQPRLAICTGGSRLYLWSPAGCMSVQVPGEGDFA VLSLCWHLSGDSMALLSKDHFCLCFLETEAVVGTACRQLGGHT VLSLCWHLSGDSMALLSKDHFCLCFLETEAVVGTACRQLGGHT KHHVLETEKTPKDWVRQNHRKEEKMSSHKLEEFFEWLKKSBVLYY TVEKKGNISSQLKHYNPWSMKCHQQQLQRMKENAKHRNQYKFIL LENLTSRYEVPCVLDLKMGTRQHGDDASEEKAANQIRKCQQSTS AVIGVRVCGMQVYQAGSQQLMFMNXYHGRKLSVQGFKEALFQFF HNGRYLRRELLGPVLKKLTELKAVLERQESYRFYSSSLLVIYDG KERPEVVLDSDAEDLEDLSEESADESAGAYAYKPIGASSVDVRM IDFAHTTCRLYGEDTVVHEGQDAGYIFGLQSLIDIVTEISEESG E 6383 3159 1061 SPAPGRPSPHGSQPAARAAAPAMPSAKQRGSKGGHGAASPSEK GAHPSAARPLAAPTPAAPACRSPSPGGAPASFPGRAPRSLASQP AARAAAPAMPSAKQRGSKGGHGAASPSEKGAHPSGGADDVAKK PPPAPQQPPPPPAPHQQHPQQHPQQNPQNQAHGKGGHRGGGGGGGKS SSSSSASAAAAAAAASSSSASCSRRLGRALNFLFYLALVAAAAFS GWCVHHVLEEVQQVRRSHQDFSRQREELGGGLOGVBOKVOSLOA	1 1		210	VIASCUOVELINDENIMITATION WAS PROTOURNESS OF THE PRO
TEFHLRITVWSLCTKSVSYIKYPKACLQGITFTRDGRYMALAER RDCKDYVSIFVCSDWQLLRHFDTDTQDLTGIBWAPNGCVLAVWD TCLBYKILLYSLDGRLLSTYSAYEWSLGIKSVAWSPSSQFLAVG SYDGKVRILNHVTWKMITEFGHPAAINDPKIVVYKEAEKSPQLG LGCLSFPPPRAGAGPLPSSESKYEIASVPVSLQTLKPVTDRANP KIGIGMLAFSPDSYFLATRNDNIPNAVWWDIQKLRLFAVLEQL SPVRAFQWDPQQPRLAICTGGSRLYLWSPAGCMSVQVPGEGDFA VLSLCWHLSGDSMALLSKDHFCLCFLETEAVVGTACRQLGGHT VLSLCWHLSGDSMALLSKDHFCLCFLETEAVVGTACRQLGGHT FEEDEDENRLCLIAYPLKGDHGIVDIVDNSDCEPKSKLLRWTTNK KHHVLETEKTPKDWVRQHRKEEKMKSHKLEEEFEWLKKSEVLYY TVEKKGNISSQLKHYNPWSMKCHQQQLQRMKENAKHNQYKFIL LENLTSRYEVPCVLDLKMGTRQHGDDASEEKAANQIRKCQQSTS AVIGVRVCGMQVYQAGSGQLMFMNKYHGRKLSVQGFKEALFQPF HNGRYLRELLGPVLKKLTELKAVLERQESYRFYSSSLLVIYDG KERPEVVLDSDAEDLEDLSEESADESAGAYAYKPIGASSVDVRM IDFAHTTCRLYGEDTVVHEGQDAGYIFGLQSLIDIVTEISBESG E 6383 3159 1061 SPAPGRPSPHGSQPAARAAAPAMPSAKQRGSKGGHGAASPSEK GAHPSAARPLAAPTPAAPACRSPSPGGAPASFPGRAPRSLASQP AARAAAAPAMPSAKQRGSKGGHGAASPSEKGAHPSGGADDVAKK PPPAPQQPPPPPAPPQQHPQQHPQQAHGKGGHRGGGGGGGKS SSSSASAAAAAAAASSSSASCSRLGRALNFLFYLALVAAAAFS GWCVHHVLEEVQQVRRSHQDFSRQREELGGGLOGVBOKVOSLOA	1	i		AMAKAGI MOAMGI EODEMIGALEAGUS CAMB COMBERTIC
RDCKDYVSIFVCSDWQLLRHFOTDTQDLTGIEWAPNGCVLAVWD TCLEYKILLYSLDGRLLSTYSAYEWSLGIKSVAWSPSSQFLAVG SYDGKVRILNHVTWKMITEFGHPAAINDPKIVVYKEAEKSPQLG LGCLSFPPPRAGAGPLPSSESKYEIASVPVSLQTLKPVTDRANP KIGIGMLAFSPDSYFLATRNDNIPNAVWWDIQKLRLFAVLEQL SPVRAFQWDPQQPRLAICTGGSRLYLWSPAGCMSVQVPGEGDFA VLSLCWHLSGDSMALLSKDHFCLCFLETEAVVGTACRQLGGHT FEEDEDRNLCLIAYPLKGDHGIVDIVDNSDCEPKSKLLRWTTNK KHHVLETEKTPKDWVRQHRKEEKMKSHKLEEFEWLKKSEVLYY TVEKKONISSQLKHYNPWSMKCHQQQLQRMKENAXHRNQYKFIL LENLTSRYEVPCVLDLKMGTRQHGDDASEEKAANQIRKCQQSTS AVIGVRVCGMQVYQAGSGQLMFMNKYHGRKLSVQGFKEALFQPF HNGRYLRRELLGPVLKKLTELKAVLERQESYRFYSSSLLVIYDG KERPEVVLDSDAEDLEDLSEESADESAGAYAYKPIGASSVDVMM IDFAHTTCRLYGEDTVVHEGQDAGYIFGLQSLIDIVTEISEESG E 6383 3159 1061 SPAPGRPSPHGSQPAARAAAAPAMPSAKQRGKGGHGAASPSEK GAHPSAARPLAAPTPAAPACRSPSPGGAPASFPGRAPRSLASQP AARAAAAPAMPSAKQRGSKGGHGAASPSEKGAHPSGGADDVAKK PPPPAPQQPPPPPAPHPQQHPQQHPQQAHGKGGHRGGGGGGKS SSSSSASAAAAAAAASSSASCSRRLGRALNFLFYLALVAAAAFS GWCVHHVLEEVQQVRRSHDDFSRQREELGGGLGGVKVOSLOA	1 1			TERHI.RITUWGI.CTVCVCVITVVDVD.C.CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
TCLBYKILLYSLDGRLLSTYSAYEWSLGIKSVAWSPSSQFLAVG SYDGKVRILNHVTWKNITEFGHPAAINDPKIVVYKEAEKSPQLG LGCLSFPPPRAGAGPLPSSESKYEIASVPVSLQTLKPVTDRANP KIGIGMLAFSPDSYFLATRNDNIPNAVWWDIQKLRLFAVLEQL SPVRAFQWDPQQPRLAICTGGSRLYLWSPAGCMSVQVPGEGDFA VLSLCWHLSGDSMALLSKDHFCLCFLETEAVVGTACRQLGGHT VLSLCWHLSGDSMALLSKDHFCLCFLETEAVVGTACRQLGGHT FEEDEDRNLCLIAYPLKGDHGIVDIVDNSDCEPKSKLLRWTTNK KHHVLETEKTPKDWVRQHRKEEKMKSHKLEEEFFEWLKKSEVLYY TVEKKGNISSQLKHYNPWSMKCHQQQLQRMKENAKHRNQYKFIL LENLTSRYEVPCVLDLKMGTRQHGDDASEEKAANQIKKCQQSTS AVIGVRVCGMQVYQAGSGQLMFMNKYHGRKLSVQGFKEALFQFF HNGRYLRRELLGPVLKKLTELKAVLERQESYRFYSSSLLVIYDG KERPEVVLDSDAEDLEDLSEESADESAGAYAYKPIGASSVDVRM IDFAHTTCRLYGEDTVVHEGQDAGYIFGLQSLIDIVTEISEESG E 6383 3159 1061 SPAPGRPSPHGSQPAARAAAAPAMPSAKQRGKGGHGAASPSEK GAHPSAARPLAAPTPAAPACRSPSPGGAPASFPGRAPRSLASQP AARAAAAPAMPSAKQRGKGGHGAASPSEKGHPSGGADDVAKK PPPAPQQPPPPPAPHQQHPQQHQQNQAHGKGGHRGGGGGGKS SSSSASAAAAAAAAASSSASCSRLGRALNFLFYLALVAAAAFS GWCVHHVLEEVQQVRRSHDDFSRQREELGOGLOGVEOKVOSLOA]]			RDCKDYVSTEVCSDWOLLDHEDTDTODI TCLTUR DVCCCT
SYDGKVRILNHVTWKMITEFGHPAAINDPKIVVYKEAEKSPQLG LGCLSFPPPRAGAGPLPSSESKYEIASVPVSLQTLKPVTDRANP KIGIGMLAFSPDSYFLATRNDNIPNAVWVDIQKLRLFFAVLEQL SPVRAFQWDPQQPRLAICTGGSRLYLWSPAGCMSVQVPGEGDFA VLSLCWHLSGDSMALLSKDHFCLCFLETEAVVGTACRQLGGHT VLSLCWHLSGDSMALLSKDHFCLCFLETEAVVGTACRQLGGHT FEEDEDRNLCLIAYPLKGDHGTVDIVDNSDCEPKSKLLRWTTNK KHHVLETEKTPKDWVRQHRKEEKMKSHKLEEEFEWLKKSEVLYY TVEKKGNISSQLKHYNPWSMKCHQQQLQRMKENAKHRNQYKFIL LENLTSRYEVPCVLDLKMGTRQHGDDASEEKAANQIRKCQQSTS AVIGVRVCGMQVVQAGSGQLMFMNKYHGRKLSVQGFKEALFQFF HNGRYLRELLGPVLKKLTELKAVLERQESYRFYSSSLLVIYDG KERPEVVLDSDAEDLEDLSEESADESAGAYAYKPIGASSVDVRM IDFAHTTCRLYGEDTVVHEGQDAGYIFGLQSLIDIVTEISEESG E 6383 3159 1061 SPAPGRPSPHGSQPAARAAAAPAMPSAKQRGKGGHGAASPSEK GAHPSAARPLAAPTPAAPACRSPSPGGAPASFPGRAPRSLASQP AARAAAAPAMPSAKQRGSKGGHGAASPSEKGAHPSGGGGGKS PPPPAPQQPPPPPAPHPQQHPQQHPQQAHGKGGHRGGGGGKS SSSSSASAAAAAAAASSSASCSRLGRALNFLFYLALVAAAAFS GWCVHHVLEEVQQVRRSHDDFSRQREELGGGLGGVGOVYOSLOA	1 1			TCLBYKILLYSIDGRILSTYSAVEWSLGIVSVAWSDSCOW AVE
GSCLSFPPRAGAGPLPSSESKYEIASVPVSLQTLKPVTDRANP KIGIGMLAFSPDSYFLATRNDNIPNAVWWDIQKLRLFAVLEQL SPVRAFQWDPQQPRLAICTGGSRLYLWSPAGCMSVQVPGEGDFA VLSLCWHLSGDSMALLSKDHFCLCFLETEAVVGTACRQLGGHT VLSLCWHLSGDSMALLSKDHFCLCFLETEAVVGTACRQLGGHT FEEDEDRNLCLIAYPLKGDHGTUDIVDNSDCEPKSKLLRWTTNK KHHVLETEKTPKDWVRQHRKEEKMKSHKLEEFFEWLKKSEVLYY TVEKKGNISSQLKHYNPWSMKCHQQQLQRMKENAKHRNQYKFIL LENLTSRYEVPCVLDLKMGTRQHGDDASEEKAANQIRKCQQSTS AVIGVRVCGMQVYQAGSGQLMFMNKYHGRKLSVQGFKEALFQFF HNGRYLRRELLGPVLKKLTELKAVLERQESYRFYSSSLLVIYDG KERPEVVLDSDAEDLEDLSEESADESAGAYAYKPIGASSVDVRM IDFAHTTCRLYGEDTVVHEGQDAGYIFGLQSLIDIVTEISEESG E 6383 3159 1061 SPAPGRPSPHGSQPAARAAAAPAMPSAKQRGKGGHGAASPSEK GAHESAARPLAAPTPAAPACRSPSPGGAPASFPGRAPRSLASQP AARAAAAPAMPSAKQRGSKGGHGAASPSEKGAHPSGGADDVAKK PPPPAPQQPPPPPAPHPQQHPQQHPQQAPGAHGKGGHRGGGGGKS SSSSSASAAAAAAAASSSASCSRRLGRALNFLFYLALVAAAAFS GWCVHHVLEEVQQVRRSHDDFSRQREELGGGLGGVEOKVOSLOA] [J	SYDGKVRILNHVTWKMITEFGHDAAINDOKINIVYEAEVODOLO
KIGIGMLAFSPDSYFLATRNDNIPNAVWVMDIQKLRLFAVLEQL SPVRAFQMDPQQPRLAICTGGSRLYLWSPAGCMSVQVPGEGDFA VLSLCWHLSGDSMALLSKDHFCLCFLETEAVVGTACRQLGGHT VLSLCWHLSGDSMALLSKDHFCLCFLETEAVVGTACRQLGGHT FEEDEDRNLCLIAYPLKGDHGIVDIVDNSDCEPKSKLLRWTTNK KHHVLETEKTPKDWVRQHRKEEKMKSHKLEEFEWLKKSEVLYY TVEKKGNISSQLKHYNPWSMKCHQQQLQRMKENAKHRNQYKFIL LENLTSRYEVPCVLDLKMGTRQHGDDASEEKAANQIRKCQQSTS AVIGVRVCGMQVYQAGSGQLMFMNKYHGRKLSVQGFKEALFQFF HNGRYLRRELLGPVLKKLTELKAVLERQESYRFYSSSLLVIYDG KERPEVVLDSDAEDLEDLSEESADESAGAYAYKPIGASSVDYRM IDFAHTTCRLYGEDTVVHEGQDAGYIFGLQSLIDIVTEISEESG E 6383 3159 1061 SPAPGRPSPHGSQPAARAAAAPAMPSAKQRGKGGHGAASPSEK GAHESAARPLAAPTPAAPACRSPSPGGAPASFPGRAPRSLASQP AARAAAAPAMPSAKQRGSKGGHGAASFSEKGAHPSGGADDVAKK PPPPAPQQPPPPPAPPQQHPQQHPQQAHGKGGHRGGGGGGKS SSSSSASAAAAAAAASSSASCSRRLGRALNFLFYLALVAAAAFS GWCVHHVLEEVQQVRRSHDDFSRQREELGOGLOGVEOKVOSLOA	1 1	1		LGCLSFPPPRAGAGPLPSSESKYETASVPVSLOTIKBUTTDPAND
SPVRAFQMDPQQPRLAICTGGSRLYLWSPAGCMSVQVPGEGDFA VLSLCWHLSGDSMALLSKDHFCLCFLETEAVVGTACRQLGGHT FEEDEDRILCLIAYPLKGDHGIVDIVDNSDCEPKSKLLRWTTNK KHHVLETEKTPKDWVRQHRKEEKMKSHKLEEFFEWLKKSEVLYY TVEKKGNISSQLKHYNPWSMKCHQQQLQRMKENAXHRNQYKFIL LENLTSRYEVPCVLDLKMGTRQHGDDASEEKAANQIRKCQQSTS AVIGVRVCGMQVYQAGSGQLMFMNKYHGRKLSVQGFKEALFQPF HNGRYLRRELLGPVLKKLTELKAVLERQESYRFYSSSLLVIYDG KERPEVVLDSDAEDLEDLSESADESAGAYAYKPIGASSVDVRM IDFAHTTCRLYGEDTVVHEGQDAGYIFGLQSLIDIVTEISEESG E 6383 3159 1061 SPAPGRPSPHGSQPAARAAAPAMPSAKQRGSKGGHGAASPSEK GAHPSAARPLAAPTPAAPACRSPSPGGAPASFPGRAPRSLASQP AARAAAAPAMPSAKQRGSKGGHGAASPSEKGAHPSGGADDVAKK PPPPAPQQPPPPPAPHPQQHPQQHPQQAHGKGGHRGGGGGGKS SSSSSASAAAAAAAAASSSASCSRRLGRALNFLFYLALVAAAAFS GWCVHHVLEEVQQVRRSHDDFSRQREELGOGLOGVEOKVOSLOA	1 1	1		KIGIGMLAFSPDSYFLATRNDNIPNAVWVWDTOKLPLEAVIEOL
6382 2 1062 FEEDEDRILCLIAYPLKGDHGIVDIVDISDCEPKSKLLRWTTIK KHHVLETEKTPKDWVRQHRKEEKMKSHKLEEFEWLKKSEVLYY TVEKKGNISSQLKHYNPWSMKCHQQQLQRMKENAXHRNQYKFIL LENLTSRYEVPCVLDLKMGTRQHGDDASEEKAANQIRKCQQSTS AVIGVRVCGMQVYQAGSQQLMFMNKYHGRKLSVQGFKEALFQFF HNGRYLRRELLGPVLKKLTELKAVLERQESYRFYSSSLLVIYDG KERPEVVLDSDAEDLEDLSEESADESAGAYAYKPIGASSVDVRM IDFAHTTCRLYGEDTVVHEGQDAGYIFGLQSLIDIVTEISEESG E 6383 3159 1061 SPAPGRPSPHGSQPAARAAAAPAMPSAKQRGSKGGHGAASPSEK GAHPSAARPLAAPTPAAPACRSPSPGGAPASFPGRAPRSLASQP AARAAAAPAMPSAKQRGSKGGHGAASPSEKGAHPSGGADDVAKK PPPAPQQPPPPPAPPQPPQQHPQQHQQNQAHGKGGHRGGGGGGKS SSSSSASAAAAAAAASSSASCSRLGRALNFLFYLALVAAAAFS GWCVHHVLEEVQQVRRSHDDFSRQREELGOGLOGVEOKYOSLOA	1 1			SPVRAFQWDPQQPRLAICTGGSRLYLWSPAGCMSVOVPGEGDFA
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TVEKKGNISSQLKHYNPWSMKCHQQQLQRMKENAKHRNQYKFIL LENLTSRYEVPCVLDLKKMGTRQHGDDASEEKAANQIRKCQQSTS AVIGVRVCGMQVYQAGSGQLMFMNKYHGRKLSVQGFKEALFQFF HNGRYLRELLGPVLKKLTELKAVLERQESYRFYSSSLLVIYDG KERPEVVLDSDAEDLEDLSEESADESAGAYAYKPIGASSVDVRM IDFAHTTCRLYGEDTVVHEGQDAGYIFGLQSLIDIVTEISEESG E 6383 3159 1061 SPAPGRPSPHGSQPAARAAAAPAMPSAKQRGSKGGHGAASPSEK GAHPSAARPLAAPTPAAPACRSPSPGGAPASFPGRAPRSLASQP AARAAAAPAMPSAKQRGSKGGHGAASFSEKGAHPSGGADDVAKK PPPPAPQQPPPPPAPHPQQHPQQAPGKGGHGGGGGGKS SSSSSASAAAAAAAASSSASCSRLGRALNFLFYLALVAAAAFS GWCVHHVLEEVQQVRRSHDDFSRQREELGOGLOGVEOKVOSLOA	1 1			KHHVLETEKTPKDWVRQHRKEEKMKSHKLEEEFEWLKKSEVLVV
LENLTSRYEVPCVLDLKMGTRQHGDDASEEKAANQIRKCQQSTS AVIGTRVCGMQVYQAGSGQLMFMNKYHGRKLSVQGFKEALFQFF HNGRYLRRELLGPVLKKLTELKAVLERQESYRFYSSSLLVIYDG KERPEVVLDSDAEDLEDLSEESADESAGAYAYKPIGASSVDVRM IDFAHTTCRLYGEDTVVHEGQDAGYIFGLQSLIDIVTEISEESG E 6383 3159 1061 SPAPGRPSPHGSQPAARAAAAPAMPSAKQRGKGGHGAASPSEK GAHESAARPLAAPTPAAPACRSPSPGGAPASFPGRAPRSLASQP AARAAAAAAAAAAAAAAAAAASSASCSRGHGAASFSEKGAHESGGADDVAKK PPPPAPQQPPPPPAPHQQHPQQHPQQAHGKGGHRGGGGGGKS SSSSSASAAAAAAAASSSASCSRLGRALNFLFYLALVAAAAFS GWCVHHVLEEVQQVRRSHDDFSRQREELGOGLOGVEOKYOSLOA	f 1	j	1	TVEKKGNISSQLKHYNPWSMKCHOOOLORMKENAKHRNOYKFII.
AVIGNVCGMQVYQAGSGQLMFMNKYHGRKLSVQGFKEALFQFF HNGRYLRRELLGPVLKKLTELKAVLERQESYRFYSSSLLVIYDG KERPEVVLDSDAEDLEDLSEESADESAGAYAYKPIGASSVDVRM IDFAHTTCRLYGEDTVVHEGQDAGYIFGLQSLIDIVTEISEESG E 6383 3159 1061 SPAPGRPSPHGSQPAARAAAAPAMPSAKQRGKGGHGAASPSEK GAHPSAARPLAAPTPAAPACRSPSPGGAPASFPGRAPRSLASQP AARAAAAPAMPSAKQRGSKGGHGAASPSEKGAHPSGGADDVAKK PPPPAPQQPPPPPAPHPQQHPQQHPQQAHGKGGHRGGGGGGKS SSSSASAAAAAAAASSSASCSRLGRALNFLFYLALVAAAAFS GWCVHHVLEEVQQVRRSHDDFSRQREELGOGLOGVEOKYOSLOA]	Ì	İ	LENLTSRYEVPCVLDLKMGTRQHGDDASEEKAANOIRKCOOSTS
HNGRYLRRELLGPVLKKLTELKAVLERQESYRFYSSSLLVIYDG KERPEVVLDSDAEDLEDLSEESADESAGAYAYKPIGASSVDVRM IDFAHTTCRLYGEDTVVHEGQDAGYIFGLQSLIDIVTEISEESG E 6383 3159 1061 SPAPGRPSPHGSQPAARAAAAPAMPSAKQRGSKGGHGAASPSEK GAHPSAARPLAAPTPAAPACRSPSPGGAPASFPGRAPRSLASQP AARAAAAAAAAAAAAAAAAASSAGSRGGGGGGKS PPPAPQQPPPPPAPQQPPQQHPQNQAHGKGGHRGGGGGGKS SSSSSASAAAAAAAAASSASCSRLGRALNFLFYLALVAAAAFS GWCVHHVLEEVQQVRRSHDDFSRQREELGOGLOGVEOKYOSLOA		Í	ľ	AVIGVRVCGMQVYQAGSGQLMFMNKYHGRKLSVQGFKEALFOFF
KERPEVVLDSDAEDLEDLSEESADESAGAYAYKPIGASSVDVRM IDFAHTTCRLYGEDTVVHEGQDAGYIFGLQSLIDIVTEISEESG E SPAPGRPSPHGSQPAARAAAPAMPSAKQRGSKGGHGAASPSEK GAHPSAARPLAAPTPAAPACRSPSPGGABASFGRAPRSLASQP AARAAAPAMPSAKQRGSKGGHGAASPSEKGAHPSGGADDVAKK PPPAPQQPPPPPAPHPQQHPQQHPQNQAHGKGGHRGGGGGGKS SSSSSASAAAAAAAAASSSASCSRLGRALNFLFYLALVAAAAFS GWCVHHVLEEVQQVRRSHQDFSRQREGGGGGLOGVEOKYOSLOA	{.	ļ		HNGRYLRRELLGPVLKKLTELKAVLEROESYRFYSSSLLVIYDG
IDFAHTTCRLYGEDTVVHEGQDAGYIFGLQSLIDIVTEISEESG E SPAPGRPSPHGSQPAARAAAPAMPSAKQRGSKGGHGAASPSEK GAHPSAARPLAAPTPAAPACRSPSPGGAPASFARAFSLASQP AARAAAPAMPSAKQRGSKGGHGAASPSEKGAHPSGGADVAKK PPPAPQQPPPPPAPHPQQHPQQHPQNQAHGKGGHRGGGGGGKS SSSSSASAAAAAAAAASSSASCSRLGRALNFLFYLALVAAAAFS GWCVHHVLEEVQQVRRSHQDFSRQREELGOGLOGVEOKYOSLOA				KERPEVVLDSDAEDLEDLSEESADESAGAYAYKPIGASSVDVRM
6383 3159 1061 SPAPGRPSPHGSQPAARAAAPAMPSAKQRGSKGGHGAASPSEK GAHPSAARPLAAPTAAPACRS PSPGGAPAS FPGRAPRSLASQP AARAAAPAMPSAKQRGSKGGHGAASPSEKGAHPSGGADDVAKK PPPAPQQPPPPPAPHPQQHPQQHPQNQAHGKGGHRGGGGGGKS SSSSASAAAAAAAAASSSASCSRLGRALNFLFYLALVAAAAFS GWCVHHVLEEVQQVRRSHDDFSRQREELGOGLOGVEOKYOSLOA				IDFAHTTCRLYGEDTVVHEGQDAGYIFGLQSLIDIVTEISEESG
GAHPSARPLAPTPAAPACRSPSEGAPASAASPSEK GAHPSAARPLAAPTPAAPACRSPSEGAPASFPGAPRSLASQP AARAAAPAMPSAKQRGSKGGHGAASPSEKGAHPSGADDVAKK PPPAPQQPPPPPAPHPQQHPQQNPQNQAHGKGGHRGGGGGGKS SSSSSASAAAAAAAASSSASCSRLGRALNFLFYLALVAAAAFS GWCVHHVLEEVQQVRRSHQDFSRQREELGOGLOGVEOKYOSLOA	6303			E
GAHPSAARPLAAPTPAAPACRSPSPGGAPASFPGRAPRSLASQP AARAAAPAMPSAKQRGSKGGHGAASFSEKGAHPSGGADDVAKK PPPAPQQPPPPPAPHPQQHPQQHPQQAHGKGGHRGGGGGGKS SSSSASAAAAAAAASSSASCSRRLGRALNFLFYLALVAAAAFS GWCVHHVLEEVQQVRRSHDDFSRQREELGOGLOGVEOKVOSLOA	0303	3159		SPAPGRPSPHGSQPAARAAAPAMPSAKQRGSKGGHGAASPSEK
AARAAAPAMPSAKQRGSKGGHGAASPSEKGAHPSGGADDVAKK PPPAPQQPPPPPAPHPQQHPQQHPQNQAHGKGGHRGGGGGGGKS SSSSSASAAAAAAASSSASCSRRLGRALNFLFYLALVAAAAFS GWCVHHVLEEVQQVRRSHQDFSROREELGOGLOGVEOKVOSLOA		Ţ	1	GAHPSAARPLAAPTPAAPACRSPSPGGAPASFPGRAPRSLASOP
PPPAPQQPPPPPAPHPQQHPQQHPQNQAHGKGGHRGGGGGGGKS SSSSSASAAAAAAASSSSCSRRLGRALNFLFYLALVAAAAFS GWCVHHVLEEVQQVRRSHQDFSROREELGOGLOGVEOKVOSLOA		1	+	AARAAAAPAMPSAKQRGSKGGHGAASPSEKGAHPSGGADDVAKK
SSSSSASAAAAAAASSSASCSRRLGRALNFLFYLALVAAAAFS GWCVHHVLEEVQQVRRSHQDFSRQREELGGGLGGVEOKVOSLQA	1		i	PPPAPQQPPPPPAPHPQQHPQQHPONOAHGKGGHRGGGGGGKS
GWCVHHVLEEVQQVRRSHQDFSRQREELGGGLGGVEOKVOSLQA	i i	ļ	1	SSSSSASAAAAAAASSSASCSRRLGRALNFLFYLALVAAAAFS
TFGTFESILRSSQHKQDLTEKAVKQGESEVSRISEVLQKLQNEI		-	ŀ	GWCVHHVLEEVQQVRRSHQDFSRQREELGOGLOGVEOKVOSLOA
				TEGTESTLRSSQHKQDLTEKAVKQGESEVSRISEVLQKLQNEI

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine
ŀ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ł	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ł	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
1			LKDLSDGIHVVKDARERDFTSLENTVEERLTELTKSINDNIAIF
İ			TEVQKRSQKEINDMKAKVASLEESEGNKQDLKALKEAVKEIQTS
i	ĺ		AKSREWDMEALRSTLQTMESDIYTEVRELVSLKQEQQAFKEAAD TERLALQALTEKLLRSEESVSRLPEEIRRLEEELRQLKSDSHGP
			KEDGGFRHSEAFEALQQKSQGLDSRLQHVEDGVLSMQVASARQT
	•		ESLESLLSKSQEHEQRLAALQGRLEGIGSSEADQDGLASTVRSL
			GETQLVLYGDVEELKRSVGELPSTVESLQKVQEQVHTLLSQDQA
ł			QAARLPPQDFLDRLSSLDNLKASVSQVEADLKMLRTAVDSLVAY
<u></u>			SVKIETNENNLESAKGLLDDLRNDLDRLFVKVEKIHEKV
6384	738	1904	IWEVPVCLTHLLHLQQANQPLPPPSSSINEEDADEANRAIGEKR
]			AAPDSGKKPKTPKTKQQKDPNEPQKPVSAYALFFRDTQAAIKGQ
			NPNATFGEVSQIVASMWDSLGEEQKQVYKRKTEAAKKEYLKALA
			AYRASLVSKAAAESAEAQTIRSVQQTLASTNLTSSLLLNTPLSQ
i i			HGTVSASPQTLQQSLPRSIAPKPLTMRLPMNQIVTSVTIAANMP
			SNIGAPLISSMGTTMVGSAPSTQVSPSVQTQQHQMQLQQQQQQQ
1			QQQMQQMQQQLQQHQMHQQIQQQHFQHHMQQHLQQQQQH LQQQINQQQLQQQLQQRLQLQHQHQHQSQPSPRQHSPVASQI
1			TSPIPAIGSPQPASQQHQSQIQSQTQTQVLSQVSIP
6385	2	1584	PRVRANDVAAGAQAVVSAGMAKSNGENGPRAPAAGESLSGTRES
			LAQGPDAATTDELSSLGSDSEANGFAERRIDKFGFIVGSQGAEG
			ALEEVPLEVLRQRESKWLDMLNNWDKWMAKKHKKIRLRCQKGIP
			PSLRGRAWQYLSGGKVKLQQNPGKFDELDMSPGDPKWLDVIERD
j l			LHRQFPFHEMFVSRGGHGQQDLFRVLKAYTLYRPEEGYCQAOAP
i l			IAAVLLMHMPAEQAFWCLVQICEKYLPGYYSEKLEAIQLDGEIL
			FSLLQKVSPVAHKHLSRQKIDPLLYMTEWFMCAFSRTLPWSSVL
1 1			RVWDMFFCEGVKIIFRVGLVLLKHALGSPEKVKACQGQYETIER
1			LRSLSPKIMQEAFLVQEVVELPVTERQIEREHLIQLRRWQETRG
			ELQCRSPPRLHGAKAILDAEPGPRPALQPSPSIRLPLDAPLPGS
]	•		KAKPKPPKQAQKEQRKQMKGRGQLEKPPAPNQAMVVAAAGDACP PQHVPPKDSAPKDSAPQDLAPQVSAHHRSQESLTSQESEDTYL
6386	819	195	TVCGSFYLGIMQRASRLKRELHMLATEPPPGITCWQDKDQMDDL
	1		RAQILGGANTPYEKGVFKLEVIIPERYPFEPPQIRFLTPIYHPN
! !			IDSAGRICLDVLKLPPKGAWRPSLNIATVLTSIQLLMSEPNPDD
	:	•	PLMADISSEFKYNKPAFLKNARQWTEKHARQKQKADEEEMLDNL
			PEAGDSRVHNSTQKRKASQLVGIEKKFHPDV
6387	1	662	PGPTHASADAWADAWAQPNMAMHNKAAPPQIPDTRRELAELVKR
	}	•	KQELAETLANLERQIYAFEGSYLEDTQMYGNIIRGWDRYLTNOK
			NSNSKNDRRNRKFKEAERLFSKSSVTSAAAVSALAGVQDQLIEK
			REPGSGTESDTSPDFHNQENEPSQEDPEDLDGSVQGVKPQKAAS
6388	1	660	STSSGSHHSSHKKRKNKNRHSPSGMFDYDFEIDLKLNKKPRADY
""	+	662	PGPTHASADAWADAWAQPNMAMHNKAAPPQIPDTRRELAELVKR
	ļ		KQELAETLANLERQIYAFEGSYLEDTQMYGNIIRGWDRYLTNQK
	1		NSNSKNDRRNRKFKEAERLFSKSSVTSAAAVSALAGVQDQLIEK REPGSGTESDTSPDFHNQENEPSQEDPEDLDGSVQGVKPQKAAS
			STSSGSHHSSHKKRKNKNRHSPSGMFDYDFEIDLKLNKKPRADY
6389	1074	497	AEPGDRMAGHRLVLVLGDLHIPHRCNSLPAKFKKLLVPGKIQHI
		, -	LCTGNLCTKESYDYLKTLAGDVHIVRGDFDENLNYPEQKVVTVG
	·]		QFKIGLIHGHQVIPWGDMASLALLQRQFDVDILISGHTHKFEAF
			EHENKFYINPGSATGAYNALETNIIPSFVLMDIQASTVVTYVYQ
			LIGDDVKVERIEYKKP
6390	158	535	GEERKEGRAPGKAFAPERNPAKMEKEETTRELLLPNWQGSGSHG
		ļ	LTIAQRDDGVFVQEVTQNSPAARTGVVKEGDQIVGATIYFDNLQ
L			SGEVTQLLNTMGHHTVGLKLHRKGDRFFPSLGQTWDP
6391	5386	2897	VRWNSKTECYLSIQTQENFPANLNELVNCIVISSLVTTQRKLKA
			MSLLGSRNQLARAVLNPNPMDFCTKDLLTTTSERIIAYLRDFNE
<u> </u>			DOKKAIETAYAMVKHSPSVAKICLIHGPPGTGKSKTIVGLLYRL

SEQ	Predicted	Predicted end	Amino acid segment cost-
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ио:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
i	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
- (corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
[amino acid	sequence	Codon, /=possible nucleotide deletion,
ł	sequence	1	\=possible nucleotide insertion)
			LTENQRKGHSDENSNAKIKQNRVLVCAPSNAAVDELMKKIILEF
			KEKCKDKKNPLGNCGDINLVRLGPEKSINSEVLKFSLDSQVNHR
			MKKELPSHVQAMHKRKEFLDYQLDELSRQRALCRGGREIQRQEL
	ļ	ĺ	DENTSKUSVEDORI ACVIVENCADROVEDORI STATEMENT
			DENISKVSKERQELASKIKEVQGRPQKTQSIIILESHIICCTLS TSGGLLLESAFRGQGGVPPSCVIVDEAGQSCEIETLTPLIHRCN
ĺ			KIJI JEDDVOI DDWLY CHYZODYGUDOGOGO ZEIETLTPLIHRCN
1			KLILVGDPKQLPPTVISMKAQEYGYDQSMMARFCRLLEENVEHN
1			MISRLPILQLTVQYRMHPDICLFPSNYVYNRNLKTNRQTEAIRC
[SSDWPFQPYLVFDVGDGSERRDNDSYINVQEIKLVMEIIKLIKD
	İ .		KRKDVSFRNIGIITHYKAQKTMIQKDLDKEFDRKGPAEVDTVDA
ł	1		FQGRQKDCVIVTCVRANSIQGSIGFLASLQRLNVTITRAKYSLF
1	· .		ILGHLRTLMENQHWNQLIQDAQKRGAIIKTCDKNYRHDAVKILK
İ			LKPVLQRSLTHPPTIAPEGSRPQGGLPSSKLDSGPAKTSVAASL
			YHTPSDSKEITLTVTSKDPERPPVHDQLQDPRLLKRMGIEVKGG
1	1		IFLWDPQPSSPQHPGATPPTGEPGFPVVHQDLSHVQQPAAVVAA
			LSSHKPPVRGEPPAASPEASTCQSKCDDPEEELCHRREARAFSE
6392	972	186	GEQEKCGSETHHTRRNSRWDKRTLEQEDSSKKRKLL
		100	GRTGVDLASSMAHRLQIRLLTWDVKDTLLRLRHPLGEAYATKAR
			AHGLEVEPSALEQGFRQAYRAQSHSFPNYGLSHGLTSRQWWLDV
1 .			VLQTFHLAGVQDAQAVAPIAEQLYXDFSHPCTWQVLDGAEDTLR
i i		•	ECRTRGLRLAVISNFDRRLEGILGGLGLREHFDFVLTSEAAGWP
'			KPDPRIFQEALRLAHMEPVVAAHVGDNYLCDYQGPRAVGMHSFL VVGPQALDPVVRDSVPKEHILPSLAHLLPALDCLEGSTPGL
6393	2017	730	TGGSKMAAVATCGSVAASTGSAVATASKSNVTSFQRRGPRASVT
1 .		, 50	NDSGPRLVSIAGTRPSVRNGQLLVSTGLPALDQLLGGGLAVGTV
i i			LLIEFDYVNIVCDI FRYDR ADGINGUDLUSTGLPALDQLLGGGLAVGTV
1 1			LLIEEDKYNIYSPLLFKYFLAEGIVNGHTLLVASAKEDPANILQ ELPAPLLDDKCKKEFDEDVYNHKTPESNIKMKIAWRYQLLPKME
1 1			IGPVSSSRFGHYYDASKRMPQELIEASNWHGFFLPEKISSTLKV
1 1	ĺ		EPCSLTPGYTKLLQFIQNIIYEEGFDGSNPQKKQRNILRIGIQN
1 1			LGSPLWGDDICCAENGGNSHSLTKFLYVLRGLLRTSLSACIITM
			PTHLIQNKAIIARVTTLSDVVVGLESFIGSERETNPLYKDYHGL
1 1	i i		IHIRQIPRLNNLICDESDVKDLAFKLKRKLFTIERLHLPPDLSD
1 1			TVSRSSKMDLAESAKRLGPGCGMMAGGKKHLDF
6394	1418	511	GAAAGGEGARRPAAMATVMAATAAERAVLEEEFRWLLHDEVHA
1.			VLKQLQDILKEASLRFTLPGSGTEGPAKQENFILGSCGTDQVKG
i I	ŀ		VLTLQGDALSQADVNLKMPRNNQLLHFAFREDKQWKLQQIQDAR
]			NHVSQAIYLLTSRDQSYQFKTGAEVLKLMDAVMLQLTRARNRLT
[]	[TPATLTLPEIAASGLTRMFAPALPSDLLVNVYINLNKLCLTVYQ
} {			LHALQPNSTKNFRPAGGAVLHSPGAMFEWGSQRLEVSHVHKVEC
L			VIPWLNDALVYFTVSLQLCQQLKDKISVFSSYWSYRPF
6395	13	658	PSGRPTRPLCCAARGAARHGGSVSGWPAGRTPTETSNPGSSVM
			ESVTFEDVAVEFIQEWALLDSARRSLCKYRMLDQCRTLASRGTP
}	1	· .	PCKPSCVSQLGQRAEPKATERGILRATGVAWESQLKPEELPSMQ
1	ł	ı	DLLEEASSRDMQMGPGLFLRMQLVPSIEERETPLTREDRPALQE
			PPWSLGCTGLKAAMQIQRVVIPVPTLGHRNPWVARDSGE
6396	1	1221	ANILSSPSKRGQKGTLIGYSPEGTPLYNFMGDAFQHSSQSIPRF
1 1	1	·- }	IKESLKQILEESDSRQIFYFLCLNLLFTFVELFYGVLTNSLGLI
ļ [i		SDGFHMLFDCSALVMGLFAALMSRWKATRIFSYGYGRIEILSGF
	1		INGLFLIVIAFFVFMESVARLIDPPELDTHMLTPVSVGGLIVNL
1 1			IGICAFSHAUSHAUGAGOGGGUGGGUGGGGGGGGGGGGGGGGGGGGGGGGG
[]		Ĭ	IGICAFSHAHSHAHGASQGSCHSSDHSHSHHMHGHSDHGHGHSH
, J	}	ļ	GSAGGGMNANMRGVFLHVLADTLGSIGVIVSTVLIEQFGWFIAD
	'	Ì	PLCSLFIAILIFLSVVPLIKDACQVLLLRLPPEYEKELHIALEK
		ŀ	IQKIEGLISYRDPHFWRHSASIVAGTIHIQVTSDVLEQRIVQQV
			TGILKDAGVNNLTIQVEKEAYFQHMSGLSTGFHDVLAMTKQMES MKYCKDGTYIM
6397	391	122	
			GAGGVGRFEAIRAPARMIEVVCNDRLGKKVRVKCNTDDTIGDLK KLIAAQTGTRWNKIVLKKWYTIFKDHVSLGDYEIHDGMNLELYY
	···		

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
İ	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
ļ	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first	amino acid	L-Leucine, M-Methionine, N-Asparagine, P-Proline, Q-Glutamine, R-Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
l .	sequence	} -	\=possible nucleotide insertion)
		<u> </u>	0
6398	353	1306	HKQMGPLINRCKKILLPTTVPPATMRIWLLGGLLPFLLLLSGLQ
]	1		RPTEGSEVAIKIDFDFAPGSFDDQYQGCSKQVMEKLTQGDYFTK
ł			DIEAQKNYPRMWQKAHLAWLNQGKVLPQNMTTTHAVAILFYTLN
J	ł		SNVHSDFTRAMASVARTPQQYERSFHFKYLHYYLTSAIQLLRKD
			SIMENGTLCYEVHYRTKDVHFNAYTGATIRFGQFLSTSLLKEEA
			QEFGNQTLFTIFTCLGAPVOYFSLKKEVLIPPYELFKVINMSYU
l			PRGDWLQLRSTGNLSTYNCQLLKASSKKCIPDPIAIASLSFLTS
6300			VIIFSKSRV
6399	75	1245	PNLETYFGRRCEKDSMNFTPTHTPVCRKRTVVSKRGVAVSGPTK
	[RRGMADSLESTPLPSPEDRLAKLHPSKELLEYYOKKMAECEAEN
ł			EDLLKKLELYKEACEGOHKLECDLOOREEFIAFLOKALSDMOVC
	1		LFQEREHVLRLYSENDRLRIRELEDKKKIONLLALVGTDAGEVT
1	1		YFCKEPPHKVTILQKTIQAVGECEQSESSAFKADPKISKRRPSR
1			ERKESSEHYQRDIQTLILQVEALQAQLGEQTKLSREQIEGLIED
	(RRIHLEEIQVQHQRNQNKIKELTKNLHHTQELLYESTKDFLQLR
1			SENONKEKSWMLEKDNLMSKI KQYRVQCKKKEDKIGKVLPVMHE
6400	2520	1053	SHHAQSEYIKVMSLCRNEVVYFSGRVEGIPKNLQFVM KTMKCDEVVYEVQSAILRHNCGYAMKTGKFFHNLMERKDFETWL
	!		DNISVTFLSLTDLQKNETLDILLISLSGAVQLRHLSNNLETLLKR
1	·		DFLKLLPLELSFYLLKWLDPQTLLTCCLVSKQWNKVISACTEVW
1			QTACKNLGWQIDDSVQDALHWKKVYLKAILRMKQLEDHEAFETS
1			SLIGHSARVYALYYKDGLLCTGSDDLSAKLWDVSTGQCVYGIQT
			HTCAAVKFDEQKLVTGSFDNTVACWEWSSGARTOHFRGHTCAUR
			SVDYNDELDILVSGSADFTVKVWALSAGTCLNTLTGHTEWVTKV
}			VLQKCKVKSLLHSPGDYILLSADKYEIKIWPIGREINCKCLKTL
			SVSEDRSICLQPRLHFDGKYIVCSSALGLYOWDFASYDTLRVIK
			TPEIANLALLGFGDIFALLFDNRYLYIMDLRTESI.TSRWDLDEV
]			RKSKRGSSFLAGEASWLNGLDGHNDTGLVFATSMPDHSIHLVLW
6401	109	755	KEHG
	109	765	PGAAWSRPDLRGCCTGPQPALRMLVLPSPCPQPLAFSSVETMEG
1 1			PPRRTCRSPEPGPSSSIGSPQASSPPRPNHYLLIDTQGVPYTVL
1			VDEESQREPGASGAPGQKKCYSCPVCSRVFEYMSYLQRHSITHS
] .]		1	EVKPFECDICGKAFKRASHLARHHSIHLAGGGRPHGCPLCPRRF
6402	1196	279	RDAGELAQHSRVHSGERPFQCPHCPRRFMEQNTLQKHTRWKHP TTSQCGGIRQSSAIPVASMEFAAICLRNALLLLPEEQQDPKQEN
]			GAKNSNQLGGNTESSESSETCSSKSHDGDKFIPAPPSSPLRKQE
			LENLKCSILACSAYVALALGDNLMALNHADKLLQQPKLSGSLKF
j j		ł	LGHLYAAEALISLDRISDAITHLNPENVTDVSLGISSNEQDQGS
			DKGENEAMESSGKRAPQCYPSSVNSARTVMLFNLGSAYCLRSEY
į l			DKARKCLHQAASMIHPKEVPPEAILLAVYLELONGNTOLALOTT
			KRNQLLPAVKTHSEVRKKPVFQPVHPIQPIOMPAFTTVORK
6403	2	1690	RGIHTSVLQGNLQNQMYSHNVVIMNLNNLNLTOVOORNI.TTNLO
	į.	,	RSVDDTSQAIQRIKNDFQNLQQVFLQAKKDTDWLKEKVOSLOTI.
		}	AANNSALAKANNDTLEDMNSQLNSFTGOMENITTISOANEONI.K
			DLQDLHKDAENRTAIKFNQLEERFQLFETDIVNIISNISYTAHH
			LRTLTSNLNEVRTTCTDTLTKHTDDLTSLNNTLANIRLDSVSLD
		,	MQQDLMRSRLDTEVANLSVIMEEMKLVDSKHGOLIKNFTILOGD
	ļ	į	PGPRGPRGDRGSQGPPGPTGNKGQKGEKGEPGPPGPAGRRGDTG
- 1	1	1	PAGPPGERGGKGSKGSQGPKGSRGSPGKPGPOGPSGDPGPDGDD
	İ		GKEGLPGPQGPPGFQGLQGTVGEPGVPGPRGLPGLPGVPGMPGP
-	}		KGPPGPPGPSGAVVPLALQNEPTPAPEDNSCPPHWKNFTDKCYY
	1	1	FSVEKEIFEDAKLFCEDKSSHLVFINTREEQQWIKKQMVGRESH
]	ľ	WIGLTDSERENEWKWLDGTSPDYKNWKAGQPDNWGHGHGPGEDC
6404	1070		AGLIYAGQWNDFQCEDVNNFICEKDRETVLSSAL
	1012	222	AAALAMAAPAPGLISVFSSSQELGAALAQLVAQRAACCLAGARA

SEQ	Predicted	Predicted end	l liming agid community
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
İ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ŀ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /-possible nucleotide deletion,
L	sequence		\=possible nucleotide insertion)
			RFALGLSGGSLVSMLARELPAAVAPAGPASLARWTLGFCDERLV
ł			PFDHAESTYGLYRTHLLSRLPIPESQVITINPELPVEEAAEDYA
ı			KKLRQAFQGDSIPVFDLLILGVGPDGHTCSLFPDHPLLQEREKI
	1		VAPISDSPKPPPQRVTLTLPVLNAARTVIFVATGEGKAAVLKRI
		<u></u>	LEDQEENPLPAALVQPHTGKLCWFLDEAAARLLTVPFEKHSPL
6405	1	1456	AALPRPTPRAPLGREGTGSDSEMAASMFYGRLVAVATLRNHRPR
			TAQRAAAQVLGSSGLFNNHGLQVQQQQQRNLSLHEYMSMELLQE
			AGVSVPKGYVAKSPDEAYAIAKKLGSKDVVIKAQVLAGGRGKGT
1	ĺ		FESGLKGGVKIVFSPEEAKAVSSQMIGKKLFTKQTGEKGRICNQ
	1		VLVCERKYPRREYYFAITMERSFQGPVLIGSSHGGVNIEDVAAE
			TPEAIIKEPIDIEEGIKKEQALQLAQKMGFPPNIVESAAENMVK
l			LYSLFLKYDATMIBINPMVEDSDGAVLCMDAKINFDSNSAYROK
			KIFDLQDWTQEDERDKDAAKANLNYIGLDGNIGCLVNGAGLAMA
1			TMDIIKLHGGTPANFLDVGGGATVHQVTEAFKLITSDKKVLAIL
			VNIFGGIMRCDVIAQGIVMAVKDLEIKIPVVVRLQGTRVDDAKA
			LIADSGLKILACDDLDEAARMVVKLSEIVTLAKQAHVDVKFQLP
6406			I
6406	1036	167	HPRQMRGEDTPEAPPYSSGRYDSIKTEVSGCPEDLTVGRAPTAD
İ			DDDDDDDDDHDDHEDNDKMNDSEGMDPERLKAFNMFVRLFVDENLDRM
1			VPISKQPKEKIQAIIESCSRQFPEFQERARKRIRTYLKSCRRMK
1 .			KNGMEMTRPTPPHLTSAMAENILAAACESETRKAAKRMRLEIYQ
			SSQDEPIALDXQHSRDSAAITHSTYSLPASSYSQDPVYANGGLN
1 1			YSYRGYGALSSNLQPPASLQTGNHSNGESGEARALASRPAPSWV
6407	492	150	CRAALGSGMGRGKQRPVMERGCLTA
0407	432	150	VGLCLAVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGV
			SWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNAC
6408	1458	903	VLTISPVQPEDDADYYCSVGYGFSP
0.90	1430	, 903	RGCITSSQAWRLFGGVTRGFNMRIEKCYFCSGPIYPGHGMMFVR
			NDCKVFRFCKSKCHKNFKKKRNPRKVRWTKAFRKAAGKELTVDN
1			SFEFEKRRNEPIKYQRELWNKTIDAMKRVEBIKQKRQAKFIMNR
1			LKKNKELQKVQDIKEVKQNIHLIRAPLAGKGKQLEEKMVQQLQE DVDMEDAP
6409	150	446	NTALANLLRCFTCDRLCGGCTAPAPPAHQGIVLQPVMPSCDPGP
			GPACLPTKTFRSYLPRCHRTYSCVHCRAHLAKHDELISKSFQGS
1 1		:	HGRAYLFNSV
6410	85	607	RGGTAGCVACLGCWGQSSSPKAAFPAGSACLPADSCPCLLFQAC
] [AISGLFNCITIHPLNIAAGVWMIMNAFILLLCEAPFCCQFIEFA
	ł		NTVAEKVDRLRSWQKAVFYCGMAVVPIVISLTLTTLLGNAIAFA
	ŀ	ĺ	TGVLYGLSALGKKGDAISYARIQQQRQQADEEKLAETLEGEL
6411	302	772	RLSIMASSINEDPEGSRITYVKGDLFACPKTDSLAHCISEDCRM
	ļ	-	GAGIAVLFKKKFGGVQELLNQQKKSGEVAVLKRDGRYIYYLITK
		ł	KRASHKPTYENLQKSLEAMKSHCLKNGVTDLSMPRIGCGLDRLO
<u> </u>			WENVSAMIEEVFEATDIKITVYTL
6412	61	1709	RPVTSFSPLPGSCGGRLGTRTMLGRSLREVSAALKQGQITPTEL
ļ	ľ		CQKCLSLIKKTKFLNAYITVSEEVALKQAEESEKRYKNGQSLGD
			LDGIPIAVKDNFSTSGIETTCASNMLKGYIPPYNATVVQKLLDO
		į	GALLMGKTNLDEFAMGSGSTDGVFGPVKNPWSYSKQYREKRKQN
	1		PHSENEDSDWLITGGSSGGSAAAVSAFTCYAALGSDTGGSTRNP
	1	` ,	AAHCGLVGFKPSYGLVSRHGLIPLVNSMDVPGILTRCVDDAAIV
1			LGALAGPDPRDSTTVHEPINKPFMLPSLADVSKLCIGIPKEYLV
İ	J	1	PELSSEVQSLWSKAADLFESEGAKVIEVSLPHTSYSIVCYHVLC
	1	İ	TSEVASNMARFDGLQYGHRCDIDVSTEAMYAATRREGFNDVVRG
	ļ		RILSGNFFLLKENYENYFVKAQKVRRLIANDFVNAFNSGVDVLL
	1	ł	TPTTLSEAVPYLEFIKEDNRTRSAQDDIFTQAVNMAGLPAVSIP
	ļ	}	VALSNOGLPIGLQFIGRAFCDQQLLTVAKWFEKQVQFPVIQLQE
			LMDDCSAVLENEKLASVSLKQ

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ΩI	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	D=Proline, Q=Glutamine, R=Arginine,
İ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
6413	2	885	HEPRCAGMAASLWMGDLEPYMDENFISRAFATMGETVMSVKIIR
1			NRLTGIPAGYCFVEFADLATAEKCLHKINGKPLPGATPAKRFKL
1			NYATYGKQPDNSPEYSLFVGDLTPDVDDGMLYEFFVKVYPSCRG
}			GKVVLDQTGVSKGYGFVKFTDELEQKRALTECQGAVGLGSKPVR
]	J		LSVAIPKASRVKPVEYSQMYSYSYNQYYQQYQNYYAQWGYDQNT
Ì			GSYSYSYPQYGYTQSTMQTYEEVGDDALEDPMPQLDVTEANKEF
			MEQSEELYDALMDCHWQPLDTVSSEIPAMM
6414	1	538	RGGRAALLPWRRFPCCRPRPQPARPSSRATPGPRSPGMATSIGV
			SFSVGDGVPEAEKNAGEPENTYILRPVFQQRFRPSVVKDCIHAV
			LKEELANAEYSPEEMPQLTKHLSENIKDKLKEMGPDRYKMVVQV
1 .			VIGEORGEGVFMASRCFWDADTDNYTHDVFMNDSLFCVVAAFGC
			PYY
6415	2	1168	FVRQWQSSHRRACGLGCEARAGGGEEPRGRASSVAGWVGAFRAP
1	}		FIEAAVAGLGAGSGKRRRGWKMPVHSRGDKKETNHHDEMEVDYA
			ENEGSSSEDEDTESSSVSEDGDSSEMDDEDCERRRMECLDEMSN
ļ	,		LEKQFTDLKDQLYKERLSQVDAKLQEVIAGKAPEYLEPLATLOE
ſ			NMQIRTKVAGIYRELCLESVKNKYECEIQASRQHCESEKLLLYD
1			TVQSELBEKIRRLEEDRHSIDITSELWNDELOSRKKRKDPFWPD
	l		KKKPGVVSGPYIVYMLQDLDILEDWTTIRKAMATLGPHRVKTEP
			PVKLEKHLHSARSEEGRLYYDGEWYIRGQTICIDKKDECPTSAV
		- <u></u>	ITTINHDEVWFKRPDGSKSKLYISQLQKGKYSIKHS
6416	410	1519	EIAPADLEIPACAPVLLSRATSSTMSVTGGKMAPSLTQEILSHL
1 1	}		GLASKTAAWGTLGTLRTFLNFSVDKDAQRLLRAITGQGVDRSAI
1 1			VDVLTNRSREQRQLISRNFQERTQQDLMKSLQAALSGNLERIVM
1			ALLQPTAQFDAQELRTALKASDSAVDVAIEILATRTPPQLQECL
			AVYKHNFQVEAVDGITSETSGILQDLLLALAKGGRDSYSGIIDY
			NLAEQDVQALQRAEGPSREETWVPVFTQRNPEHLIRVFDQYQRS
1			TGQELEEAVQNRFHGDAQVALLGLASVIKNTPLYFADKLHQALQ
	İ		ETEPNYQVLIRILISRCETDLLSIRAEFRKKFGKSLYSSLQDAV
6417	1 -	845	KGDCQSALLALCRAEDM RGESRVLWSELEGEAGGAGGWASSLNARMDNRFATAFVIACVLS
	-	043	I.I.CTI YMAA CICEDEBUREN GOUGHIGGE WAS LINARMONR FATAFVIACVLS
1 1			LISTIYMAASIGTDFWYEYRSPVQENSSDLNKSIWDEFISDEAD EKTYNDALFRYNGTVGLWRRCITIPKNMHWYSPPERTESFDVVT
	İ		KCVSFTLTEQFMEKFVDPGNHNSGIDLLRTYLWRCQFLLPFVSL
1			GLMCFGALIGLCACICRSLYPTIATGILHLLAGLCTLGSVSCYV
1 +		į	AGIELLHQKLELPDNVSGEFGWSFCLACVSAPLQFMASALFIWA
			AHTNRKEYTLMKAYRVA
6418	2	662	TRTRPRRPPGLGAAVGKAGARSTSTPAGASPAAAYQADPPPPAH
]			TPAPPPPPPCGGIACHGEPAKFYGYDNLQRQPIFTTQQEAELVQ
]			YPDCKSSSGNIGEDPDHLNQSSSPSQMFPWMRPQAAPGRRRGRQ
]	ļ	ľ	TYSRFQTLELEKEFLFNPYLTRKRRIEVSHALALTERQVKIWFQ
		[NRRMKWKKENNKDKFPVSRQEVKDGETKKEAOELEEDRAEGLTN
6419	1	973	PGRPRVRNFDLNSKSILQEFFCTRSIQIPANRSKTAMSKCPIFP
! !		1	MARSISTSGPLDKEDTGRQKLISTGSLPATLQGATDSLGLEWHL
[]	1	ĺ	PSPDPVTVPYLSPLVVWKELESLLENEGDHAITVADFVDHHPIV
	1		FWNLVWYFRRLDLPSNLPGLILSSBHCNKYSKIPRHCMSEDSKY
.	. [J	VLIQMLWDNMKLHQDPGQPLYILWNAHTQKYPMVHLLOKSDNSF
] 1	Ì	1	NQELLKSMVKSIKMNDVYGPMSQILETLNKCPHFKRORSLYREI
		ļ	LFLSLVALGRENIDIDAFDKEYKMAYDRLTPSQVKSTHNCDRPP
		ļ	STGVMECRKTFGEPYL
6420	207	1187	RKMIDKNQTCGVGQDSVPYMICLIHILEEWFGVEQLEDYLNFAN
]	1	YLLWVFTPLILLILPYFTIFLLYLTIIFLHIYKRKNVLKEAYSH
			NLWDGARKTVATLWDGHAAVWHGYEVHGMEKIPEDGPALIIFYH
	• •		GAIPIDFYYFMAKIFIHKGRTCRVVADHFVFKIPGFSLLLDVFC
			ALHGPREKCVEILRSGHLLAISPGGVREALISDETYNIVWGHRR
<u> </u>	<u></u>		GFAQVAIDAKVPIIPMFTQNIREGFRSLGGTRLFRWLYEKFRYP

WO 01/53312

SEQ	Predicted	Predicted end	I have
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine.
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown +-Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion
ļ	sequence		\=possible nucleotide insertion)
1			FAPMYGGFPVKLRTYLGDPIPYDPQITAEBLAEKTKNAVQALID
6421	1844	3.53	KHQRIPGNIMSALLERFH
1 0421	. 1944	362	WALSLRROPERMSNKLLSPHPHSVVLRSEFKMASSPAVLRASRL
1			YQWSLKSSAQFLGSPQLRQVGQIIRVPARMAATLILEPAGRCCW
1			DEPVRIAVRGLAPEQPVTLRASLRDEKGALFQAHARYRADTLGE
1	1		LDLERAPALGGSFAGLEPMGLLWALEPEKPLVRLVKRDVRTPLA VELEVLDGHDPDPGRLLCQTRHERYFLPPGVRREPVRVGRVRGT
1			LFLPPEPGPFPGIVDMFGTGGGLLEYRASLLAGKGFAVMALAYY
			NYEDLPKTMETLHLEYFEEAMNYLLSHPEVKGPGVGLLGISKGG
		:	ELCLSMASFLKGITAAVVINGSVANVGGTLRYKGETLPPVGVNR
			NRIKVTKDGYADIVDVLNSPLEGPDQKSFIPVERAESTFLFLVG
1			QDDHNWKSEFYANBACKRLOAHGRRKPOIICYPETGHYIEPPYR
	,		PLCRASLHALVGSPIIWGGEPRAHAMAQVDAWKQLQTFFHKHLG
6400			GREGTIPSKV
6422	181	2133	EGENLSWFQEFWGDIAKEPYWKTPCPGPFLRYNFDVTKGKIFIE
1			WMKGATTNI CYNVLDRNVHEKKLGDKVAFYWEGNEPGETTOITY
	1		HQLLVQVCQFSNVLRKQGIHKGDRVAIYMPMIPELVVAMLACAR
			IGALHSIVFAGFSSESLCERILDSSCSLLITTDAFYRGEKLVNL
			KELADEALQKCQEKGFPVRCCIVVKHLGRAELGMGDSTSQSPPI
j			KRSCPDVQISWNQGIDLWWHELMQEAGDECEPEWCDAEDPLFIL
1 .			YTSGSTGKPKGVVHTVGGYMLYVATTFKYVFDFHAEDVFWCTAD IGWITGHSYVTYGPLANGATSVLFEGIPTYPDVNRLWSIVDKYK
!	'		VTKFYTAPTAIRLLMKFGDEPVTKHSRASLQVLGTVGEPINPEA
}			WLWYHRVVGAQRCPIVDTFWQTETGGHMLTPLPGATPMKPGSAT
ŀ			FPFFGVAPAILNESGEELEGEAEGYLVFKQPWPGIMRTVYGNHE
[RFETTYFKKFPGYYVTGDGCQRDQDGYYWITGRIDDMLNVSGHL
1			LSTAEVESALVEHEAVAEAAVVGHPHPVKGECLYCFVTLCDGHT
ľ	.		FSPKLTEELKKQIREKIGPIATPDYIONAPGLPKTRSGKIMRRV
6423			LRKIAQNDHDLGDMSTVADPSVISHLFSHRCLTIO
0423	614	1237	ANLKEIPRDLPPETVLLYLDSNQITSIPNEIFKDLHQLRVLNLS
1 1			KNGIEFIDEHAFKGVAETLOTLDLSDNRIQSVHKNAFNNLKARA
1 1	·		RIANNPWHCDCTLQQVLRSMASNHETAHNVICKTSVLDEHAGRP
1 i			FLNAANDADLCNLPKKTTDYAMLVTMFGWFTMVISYVVYYVRQN
6424	- i	1188	QEDARRHLEYLKSLPSRQKKADEPDDISTVV
l i		1100	KKVSWPVAAMVHCSCVLFRKYGNFIDKLRLFTRGGSGGMGYPRL
	1		GGEGGKGGDVWVVAHNRMTLKQLKDRYPRKRFVAGVGANSKISA LKGSKGKDWBIPVPVGISVTDENGKIIGELNKENDRILVAQGGL
ŀ			GGKLLTNFLPLKGQKRIIHLDLKLIADVGLVGFPNAGKSSLLSC
ł	i		VSHAKPAIADYAFTTLKPELGKIMYSDFKQISVADLPGLIEGAH
			MNKGMGHKFLKHIERTRQLLFVVDISGFQLSSHTQYRTAFETII
-	,		LLTKELELYKEELQTKPALLAVNKMDLPDAQDKFHELMSQLQNP
	l		KDFLHLFEKNMIPERTVEFQHIIPISAVTGEGIEELKNCIRKSI.
- CASE			DEQANQENDALHKKQLLNLWISDTMSSTEPPSKHAVTTSKMDII
6425	1850	1144	LAMEGGGGIPLETLKEESOSRHVLPASFEVNSLOKSNWGFLLTG
		j	LVGGTLVAVYAVATPFVTPALRKVCLPFVPATMKOIENVVKMLR
			CRRGSLVDIGSGDGRIVIAAAKKGFTAVGYELNPWI,VWYSPVPA
j		į	WREGVHGSAKFYISDLWKVTFSQYSNVVIFGVPOMMLOLRKKLE
[İ	RELEDDARVIACRFPFPHWTPDHVTGEGIDTVWAYDASTFRGRE
6426	30		KRPCTSMHFQLPIQA
	-	565	SRGAAVGGMSVAGGEIRGDTGGEDTAAPGRFSFSPEPTLEDIRR
-	İ	i	LHAEFAAERDWEQFHQPRNLLLALVGEVGELAELFQWKTDGEPG
İ		ļ	POGWSPRERAALQEELSDVLIYLVALAARCRVDLPLAVLSKMDI
			NRRRYPAHLARSSSRKYTELPHGAISEDQAVGPADIPCDSTGQT ST
6427	145		AASWGPPHVPKAGKMVSWMICRLVVLVFGMLCPAYASYKAVKTK
			NIREYVRWMMYWIVFALFMAAEIVTDIFISWFPFYYEIKMAFVL
			TOTAL TELEVISION OF THE PROPERTY OF THE PROPER

Dogdanning mucleotide location corresponding corresponding corresponding corresponding cofirst amino acid amino aci	SEO	Predicted	Predicted end	I have noted comment
No:				Amino acid segment containing signal peptide
location corresponding to first amino acid amino acid residue of amino acid possible nucleotide sinsertion) V-pyrosine, X-Unknown, *-Stop Coden, *-Joposible nucleotide deletion, V-possible nucleotide sinsertion) V-pyrosine, X-Unknown, *-Stop Coden, *-Joposible nucleotide sinsertion V-pyrosine, X-Unknown, *-Stop Coden, *-Joposible nucleotide sinsertion V-pyrosine, X-Unknown, *-Stop Coden, *-Joposible nucleotide sinsertion V-pyrosine, X-Unknown, *-Stop Coden, *-Joposible nucleotide sinsertion V-pyrosine, X-Unknown, *-Stop Coden, *-Joposible nucleotide sinsertion V-pyrosine, X-Unknown, V-	NO:			Glutamic Acid R-Phonulal price Collector
Leleucine, Memethionine, Neapsaragine, Proline, Gelutamine, Ranginine, Seridue of amino acid residue of amino acid sequence Proline, Gelutamine, Ranginine, Seridue, Verytopohan, Yeryt	i			Hawistiding Talgalousing Walled
amino acid residue of amino acid residue of amino acid amino acid sequence Sectine, Teffrenoine, V-Valine, W-Tryptophan, Y=Tyrosine, K-Unknown, *=Stop Codon, /=possible nuclectide deletion, Codon, /=possible nuclectide deletion, Codon, /=possible nuclectide deletion, Codon, /=possible nuclectide insertion) MLSPYTROSALIVERYWIPSISREKERIDATYCOAKERSYSTV LSPCKRGINIAASAAVQAATKSGGALAGKIRSTSMQDLRSISDA PAPAYMPBULLEDOVSKRPPJOYENSGLQDSDTEBECKWOTEA VPRAPAPREKPLIRSQSLRVVRKPPVPREGTSRSLKVRTRKK VPSDVDS	1	corresponding		LeLeucine MeMethionine NeAsparagine
amino acid residue of amino acid sequence Serine, T-Threonine, V-Valine, Sequence	İ			Paproline OaGlutamine Paradining
#### #################################		amino acid		S=Serine T=Threonine V=V=line
sequence Codon, /-possible nuclectide insertion NulspytKossllynkrynpsiskekeidayivoaksexyst Serkkoiniasaanvoantsocalaackekerystoodaksekrystoodaksekrystoodaksekrystoodaksekrystoodaksekrystoodaks		residue of	1	W=Tryptophan V-Tyrocine V-tipleness + 05-
Apposible nucleotide insertion]	amino acid	B .	Codon. /=nossible nucleotide deletion
MILLSPYTKASALLYRKFVIPSISRREKEIDAYIVQAKERSYETY LSPEKRGINIASAAPVOARTSGCALAGRIESTSCHESIORSICHE PRAPAYBIPLYLEDOVSHERPPIGYBAGGLQDSDTEDBEORSDTEA PRAPAYBIPLYLEDOVSHERPPIGYBAGGLQDSDTEDBEORSDTEA VERRAPRREKPILISQSLRVVKKRPPVREGTSRSLKVTKKKY VPSDVDS 444 SSEGGMÆBHOHVPIDTOTSKLLDMIJVERRICSLKWGSLVLTIR EKINAAIODMPESEIAQLLSGSYIHYPHCLRILDLIKGTEAST KNIFGRYSSGRMEDHGHVPIDTOTSKLLDMIJVERRICSLKWGSLVLTIR EKINAAIODMPESEIAQLLSGSYIHYPHCLRILDLIKGTEAST KNIFGRYSSGRMEDHGVPIDTOTSKLLDMIJVERSGLLVERVNYKS PSLKKOTAKCQIGDEVSKREEGCAGABREMEGPYFISCKOYGI TGENWGGSLLAUNDLPSGLAEIGAAAQGSLGSAIDVYQASVE VUSSPTEQUTJEMRIVOLGPSVKREEGCAGABREMEGPYFISCKOYGI TGENWGGSLLAUNDLPSGLAEIGAAAQGSLGSAIDVYQASVE PEGVAEDAIDWGDFGVEAVSGTOAFBOWARGPALTILLSE PEGVAEDAIDWGDFGVEAVSGTOAFBOWARGPALTILLSE TETRINGPLDELMELSIFLAQGRVELSERAUVYRFDALFLESF TETRINGPLDELMELSIFLAQGRVELSERAUVYRFDALFLESF TETRINGPLDELMELSIFLAQGRVELSERAUFYRFUNDT EFLQOKLKOSGLLALKKELMVQKQGSALEEGAALEPKIDLLIKE TKELQKILEADISKAYGEPYUNTVELSERAUVGBDRAAISFRSTIVVPANOL EFLQOKLKOSGLLALKKELMVQKQGSALEEGAALEPKIDLLIKE TKELQKILEADISKAYGEPYUNTVELSERAUVGBDRAAISFRSTIVVPANOL EFLQOKLKOSGLLALKKELMVQKQGSALEFGAALEPKIDLLIKE TKELQKILEADISKAYGEPYUNTVELSERAUVGBDRAAISFRSTIVVPANOL EFLQOKLKOSGLLALKKELMVQKQGSALEFGAALEPKIDLLIKE TKELQKILEADISKAYGEPYUNTVELSERAUGHDALSFRSTIVVPANOL EFLQOKLKOSGLLALKKELMVQKQGSALEFGAALEPKIDLLIKE TKELQKALEADISKAYGEPYUNTVELSERAUGHDALSFRSTIVVPANOL EFLQOKLKOSGLLALKKELMVQKQGSALEFFALDLIKE TKELQKALEADISKAYGEPYUNTVELSERAUGHDALSFRSTIVVPANOL EFLQOKLKOSGLLAUKHTYPEVAREBEGDTTCHANGFALKOR VVXVTADAITRNTCLLAVQFYGDVVTLACHAGAGEPKILVRANGFALSE TKELQKALEADISTATUSHANGTAL VVXVTADAITRNTCLLAVQFYGDVVTLACHAGAGEPKILVRANG TKALVSTOLAUKHTYPEVAREBEGDTTCHANGFALKOR PTWALAFSTOLAUKHTYPTAELAAGGSKALLIVOLTVLEBBEKPITTURAGGSKALLIVOLTVLEBBEKPITTURAGGSKALLIVOLTVLEBBEKPITTURAGGSKALLIVOLTVLEBBEKPITTURAGGSKALLIVOLTVLEBBEKPITTURAGGSKALLIVOLTVLEBBEKPITTURAGGSKALLIVOLTVLEBBEKPITTURAGGSKALLIVOLTSBATT TISEPTEVITTIFFANTYLINGTLOGGGGGGAGGGGGGG AMLEANABPSPEDPPTTURAFTYGOFTSTURAGGSSKAL TKYGGBAPVVLPTPPEAGAGGSTALTWGAGAFYKVANATURAGGSSKAL TKYGGBAPVVLPTPPEAGAGGSTALTWGAGAGGAGGGGGGGGGGGGGGGGGGGG	1	sequence		\=possible nucleotide insertion!
LSPGKRGLNIAASAAVQAATKSGGALAGKIRSTSMQLIKSTSMQTRA PAPAYHDPILIEDGVSKRPP1GERGAGIGLOSTGERGKODTEA VPRAPHPEKPLIRSGSLRVVKKKPPVREGTSRSLKVRTKKT VPSDVDS 444 SGSGGMEDHGHYPTDTGTSKLLDHIJDERHCSLKWGSLVLTIR EKINAAIODMPESEBIAQLLSGSYINYFHCLRILDLLKGTERST KNIFGRYSSGRMEDMGUTATIVENDRYTJVELGSLLVRVNYNET PSLKKQTAKCQGLOGUTSKREECQAGAARMREQFYISCKQVSLVTIR EKINAAIODMPESEBIAQLLSGSYINYFHCHRILDLLKGTRAFY KNIFGRYSSGRMEDMGUTATIVENDRYTJVELGLUDWINNET PSLKKQTAKCQGLOGUTSKREECQAGAARMREQFYISCKQVSL VCESPTEQVLPMRRVQKRGNSTYTSMRTGTESVVERHLEEG PEQVARDAINMGPOVASVSGTUSGIAGRAGIDHGIFPESDS KDRGGGIDMGDDAVALQITVLERGTOAPEGVARGEDAITLES PEQVARDAINMGPOVASVSGTUSGIAGRAGIDHGIPPESDS KDRGGGIDMGDDAVALQITVLERGTOAPEGVARGEDAITLES PEQVARDAINMGPOVASVSGTUSGIAGRAGIAPIL QGGTKEKWYTMYSVLEDLIGKLTSLQLGHLPMILASPRYVDRVT EFLQQKLKGSGLLAKKELMVQKOGSALECROALEPKIDLLEK TKELQKLIERDISKRYSGRPVKIMGTSL VVKSVTDKDAGDVLCVARRKVCDDYVVLKVDVWKPAKTEKEE PLOVALKSGTDLAKKELMVQKOGSALECROALEPKIDLLEK TKELQKLIERDISKRYSGRPVKIMGTSL TKELQKLIERDISKRYSGRPVKIMGTSL PERSWAAPREPLAAPDEDAAVGEDBERALSFORTIVVPAMGTI VVKSVTDKDAGDVLCVARRKVCDDYVVLKOVMVMRPAKTEKEE NDLKYVGGLAKVUVTNOGTLYFNEVGMEREGDTTCFARROYKKDEMVR VKVVTAPATTRIKTCLAVQVPYGDVVTVACEAKGEPMPKVTUS PTAKVIPTSSEKTYGTYQTOTLICHOAQGGGLORFUCKUSHING PTAKVIPTSSEKTYGTYQTOTLICHOAQGGGLORFUCKUSHING PTAKVIPTSSEKTYGLWFLORTIVUNGGGGLORFUCKUSHING PTAKVIPTSSEKTYGLWFLORTIVUNGGGGLORFUCKUSHING VSI INGETLIKLECPPPOAGGGRFSWTLIVNGHSGLORFUCKUSHING VSI INGETLIKLECPPPOAGGGRFSWTLIVNGHSGLORFUCKUSHING VSI INGETLIKLECPPPOAGGGRFSWTLIVNGHSGLORFUCKUSHING VSI INGETLIKLECPPPOAGGGRFSWTLINGHSINGLORFUCKUSHING VSI INGETLIKLECPPPOAGGGRFSWTLINGHSINGLORFUCKUSHING VSI INGETLIKLECPPPOAGGGRFSWTLINGHSINGHSPATTLORGUSHING VSI INGETLIKLECPPPOAGGGRFSWTLINGHSINGHSPATTLORGUSHINGHSINGH VSI INGETLIKLECPPPOAGGGRFSWTLINGHSPATTLORGUSHINGHSINGH VSI INGETLIKLECPPPOAGGGRFSWTLINGHSINGHSPATTLORGUSHINGH VSI INGETLIKLECPPPOAGGGRFSWTLINGHSINGHSINGH VSI INGETLIKLECPPPOAGGGRFSWTLINGHSPATTLORGUSHINGH VSI INGETLIKLECPPPOAGGGRFSWTLINGHSINGHSINGH VSI INGETLIKLECPPPOAGGGRFSWTLINGHSPATTLORGUSHINGH VSI INGETLIKLECPPPOAGGGRFSWTLINGHSPATTLORGUSHINGH VSI				WLLSPYTKGASLLYRKEVHDSLSPHEKETDAYTVOAKERGVERV
6428 1982 444 SGSGGKMEHOHVPIDIGTSKLIDMLVDRHCSLKROSIVLTIK EKINAAIODMPESETIAQLISGSYHYPHCLRILDLIKGTEAST KNITGRYSSGDKMEHOHVPIDIGTSKLIDMLVDRHCSLKROSIVLTIK EKINAAIODMPESETIAQLISGSYHYPHCLRILDLIKGTEAST KNITGRYSSGDKMORGIILIVKKNITYLUVEL PSILKKOLAKCOOLOGUSERKEBECQAGAAEMREQFYHSLKRYGKYT TGENVAGELLALUVADLPSQLAEIGAAAQSILGAIDVYQASUGF VCESPTEQVLPMLREVQXRONSTVIEMTGTEPSVVERPHLEEI PEQVARDAIDMOPFGVERVSEETDGGISAAAQSILGAIDVYQASUGF VCESPTEQVLPMLREVQXRONSTVIEMTGTSPSVVERPHLEEI PEQVARDAIDMOPFGVERVSEETDGGISAAAQSILGAIDVYQASUGF VCESPTEQVLPMLREVQXRONSTVIEMTGTSPSVVERPHLEEI PEQVARDAIDMOPFGVERVSEETDGGISAAAQGILGAIDVYGSGGAAALI QGGTKERVVITWSVEDLIIGKUTSLOQLHIPSDSVVERPHLEEI PETROPLDEIMELSIFIAQRAVELSEEADVLSVSGGGLAFAIL QGGTKERVVITWSVEDLIIGKUTSLOQLHIPSDSVERPVDRVV EFFLQOKILABIJSKRYSGRVVENSGDSVARGEPALTLLEK TETROPLDEIMELSIFIAQRAVELSEEADVLSVSGGGLAFAIL QGGTKERVVENSUMMGTSL EFFLQOKILABIJSKRYSGRVVENSGDSVARGEPALTLLEK TETROPLDEIMELSIFIAQRAVELSEEADVLSVSGGGAAAEIT VKSVTDLORDGDVLCVARNKVENGOPERLEGAALEPKLDLLEK TERLOQULCHARISTSLOPENSTUMMATSL UKSVTDLORDGDVLCVARNKVENGOPERLEGAALEPKLDLLEK NDHKVEYGGDLKVDCVARGLPREGDYTCARAKIELHKER NDHKVEYGGDLKVDCVARGLPREGDYTCARAKIELHKER NDHKVEYGGDLKVDCVARGLPREGDYTCARAKIELHKER NDHKVEYGGDLKVDCVARGLPREGDYTCARAKIELHKER NDHKVEYGGDLKVDCVARGLPREGDYTCARAKIELHKER NDHKVEYGGDLKVDCVARGLPREGDYTCARAKIELHKER NDHKVEYGGDLKVDCVARGLPREGDYTCARAKIELHKER NDHKVEYGGLKVDCVARGLPREGDYTCARAKIELHKER NDHKVEYGGLKVDCVARGLPREGDYTCARAKIELHKER NDHKVEYGGLKVDCVARGLPREGDYTCARAKIELHKAR QUCMARNEGERALIVOLTVLEPMERPTFHDF1SKKTAMAGH TISLASAAGTPTELMVALVCUTVLEPMERPTFHDF1SKKTAMAGH TISLASAAGTPTELLWSTDTDLSKOGGGRFKTLANGUMH ISCLSSVDAGAYECVARRAAGTTREDGGSKTLARKAGHTALKAG QUCMARNEGERALTARAVCARAGTTREDGGSKTAAKAGHTALKAG QUCMARNEGERALTARAVCARAGTTREDGGSKTAAKAGHTALKAG QUCMARNEGERALTARAVCARAGTTREDGGSKTAAKAGHTALKAG QUCMARNAGAAACAACAACAACAACAACAACAACAACAACAACAACA				LSFGKRGLNIAASAAVOAATKSOGALAGRIPSESMODI RETEDA
6428 1982 444 SGSGGWEDHOHVPIDIGTSKLLDHLUDREHGSLKWGSIJUTIR EKINAAIODMPESBEIJOLIGSGYHYPHTELDLKGTEAST KNIFGRYSGDRMEDHOEI IALYEKUNTYLVELSSLLVRRWYNEI PSLKKOIAKCOLOOBYSRKEBECQGAARBMREOPYHSKCKYGI TGENVRGELLALWICLFSQAARBMREOPYHSKCKYGI TGENVRGELLALWICLFSQAARBMREOPYHSKCKYGI TGENVRGELLALWICLFSQAARBMREOPYHSKCKYGI TGENVRGELLALWICLFSQAARBMREOPYHSKCKYGI TGENVRGELLALWICLFSQAARBMREOPYHSKCKYGI TGENVRGELLALWICLFSQAARBMREOPYHSKCKYGI TGENVRGELLALWICLFSGAARBMREOPYHSKCKYGI TGENVRGELLALWICLFSGAARBMREOPYHSKCKYGI VCESPTEQVLDMIRFVQKRGNSTVIEWRITTEPSVVERPHLEEL PEQVAEDAIDWGFOVEAVSEGTDGGISAARAILBY VCESPTEQVLDMIRFVQKRGNSTVIEWRITTEPSVVERPHLEEL PEQVAEDAIDWGFOVEAVSEGTDGGISAARAILBY TETROPLIDELBHEITLAGARGUISGAACHAUSSOGGIAPAILBY GGGTKKWTIMVSVLEDLIGKKITSLOLOHLPMILASERTVURVT EFLQQKLKOSGLALAKKELWYGKQGALEEGAALDWGSOGGAARAILGY GGGTKKWTIMVSVLEDLIGKKITSLOLOHLPMILASERTVURVT VKSVTÜRDAGADVLCVAANKVGGDALEGAASTGERTKVPANGTL TKELQALLEAUNGAABARAILGEAUNGAABARAILEKE TKELQALLEAUNGAABARAILEKE TKELQALLEAUNGAABARAILEKE TKELQALLEAUNGAABARAILEKE TKELQALLEAUNGAABARAILEKE TKELQALLEAUNGAABARAILEKE TKELQALLEAUNGAABARAILEKE TKELQALLEAUNGAABARAILEKE TKELQALLEAUNGAABARAILEKE TKELQALLEAUNGAABARAILEKE THINVIPTSEKYQIYQDAUNGAABARAILEKE TESTAVATARAILEKEAUNGAABARAILEKE	ı]	PAPAYHDPLYLEDOVSHRRPPIGYRAGGLODSDTEDECUSDTEA
6428 1982 444 SGSGGMEDHOHVPIDIGTSKLLDMLVDREHCSLKWGSLVLTIR ERINANIODMPESERIAQLISGSYIHVPHCLRILDLIKGTERST KNINGRYSGGMENGMET ILLYKENDTYLVLYGAVGE ERINANIODMPESERIAQLISGSYIHVPHCLRILDLIKGTERST KNINGRYSGGMENGMET ILLYKENDTYLVLYGAVGE VCESPTEQVILDMIRRYQGRENGTYLEWRITSPEVVERHEEL PSLKKQIARCQULODYSRKEBECQAGAAEMREQFYHSCKQYGI TGENVRGELLALWCHLSGILARGIANGIPESDS WERDGAUGHDAVALGITVLEAGTGAPEGYAFGAVGET TGENVRGELLALWCHLSGILARGIANGIPESDS KDROGGGINGDDAVALGITVLEAGTGAPEGYAFALL GGGTKERWITWSVEHDLIKGKTSJOLDHIHPSEDS KDROGGGINGDDAVALGITVLEAGTGAPEGYAFALT GGGTKERWITWSVEHDLIKGKTSJOLDHIHPSERTVORVT EFTQOKIKOSGLIALKKELWVQKQGEALEEQAALEPKLDLLER TETHNOFLDELMSLEIFLAQRAVELSEEADVLSVSGGGTARIL GGGTKERWITWSVEHDLIKKTSJOLDHIHPSERTVORVT EFTQOKIKOSGLIALKKELWVQKQGEALEEQAALEPKLDLLER TKEIQKLIEADISKKYSGGPVAIMATSL GGGTKERWITWSVEHDLIKKESTVORVT EFTQOKIKOSGLIALKKELWVQKQGEALEEQAALEPKLDLLER TKEIQKLIEADISKKYSGGPVAIMATSL GGGTKERVIVARNOTLIPHPETSISSEPDGILVSFANGSDS GGTKERVVERNOTLIPHPETSISSEPDGILVSFANGSDS GGTKERVVERNOTLIPHPETSISSEPDGILVSFANGSDS GGTKERVVERNOTLIPHPETSISSEPDGILVSFANGSDS GGTKERVVERNOTLIPHPETSISSEPDGILVSFANGSBORT GVKVAPATIKTSCLAVQVPYSTARVOTLIPKSAGE DRKTWHINVYOPPKINGNIPHITVRETAAGERPKVTWISAGE DRKTWHINVYOPPKINGNIPHITVRETAAGERPKVTWISAGE DRKTWHINVYOPPKINGTPHITVRETAAGERPKVTWISAGE GGATRAVOPPKINGTPHITVRETAAGERPKVTWISAGE DRKTWHINVYOPPKINGNIPHITVRETAAGERPKVTWISAGE GRATERVITTISLANGSAGTPTPSLWVLPPRGTULGSGGQLOFFYKADAMIH ISGLISSVDAGARSTYCCVARNASTERUVISKAGES SKETAMAGH TISLASSAAGTPTPSLWVLPPRGTULGPREGTFITVARPRE TISLASSAAGTPTPSLWVLPRGTULGPREGTFITVARPRE TISLASSAAGTPTPSLWVLPRGTULGPREGTFITVARPRE TISLASSAAGTTAGATTYPHITVARPRE TISLASSAAGTTAGATTYPHITVARPRE TISLASSAAGTTAGATTYPHITVARPRE TISLASSAAGTTAGATTYPHITVARPRE TISLASSAAGTTAGATTYPHITVARPRE TISLASSAAGTTAGATTYPHITVARPRE TISLASSAAGTTAGATTAGATTAGATTAGATTAGATTAGATT	ŀ	1		VPRAPARPREKPLIRSOSLRVVKRKPPVRRGTSPGLKTPTPVVT
EKINAJODWESSE IAQLISGSYIHTHELIDLIKGISHTIR EKINAJODWESSE IAQLISGSYIHTHELIDLIKGTEAST KNI I FGRYSSORMEDMOET IALVEKDNYTLVELSSLUVRNYNYET PSLKKIAKOLOOLOWSTRIEGECQAAGARBEYTISCKYGIG TGENVAGSLLALVKOLPSQLAST GAAAQGSLOEAIDVYQASVOG VCESPTEQUL MARFVQKERDSTYVERNOTEPSYVERPHLEEL PEQUAEDAIDMODPAULGITYLEAOTOAPEGYPHSCKYGIG KDPOGGDIDMODDAULGITYLEAOTOAPEGYPHSCKYGIG KDPOGGDIDMODDAULGITYLEAOTOAPEGYPALSVOGE KDPOGGDIDMODDAULGITYLEAOTOAPEGYALEPALDLIE FTERNOPILDELMELSIFLAQRAVELSEEADVLSVSQFOLAPAIL GOGTKEKVITWSVEURDICKLISLOLOHLPMILASPRIVORTY EFLOQKLEADISKRYSGRVALMISTSI PEPLORKLOSOLLALKKELMVQKQQEALEEQAALEPKLDLILEE FRICKLIKOSOLLALKKELMVQKQQEALEEQAALEPKLDLILEE FRICKLIKOSOLLALKKELMVQKQQEALEEQAALEPKLDLILEE TRELQXLIEADISKRYSGRVALMISTSI VVKSVTDATATRAVEGDDYVLKVDVVMKPAKITEKKEE NDHKVEYGGOLKOVCATAGNYDEPISMSEPDOSLVNSFMOSDDS GORTKRYVVENNOTLYPNEVGRREEGSYTCFAENOVGKDERVRV VKVVTAPATITRAVTCLAVOYPEPISMSEPDOSLVNSFMOSDDS GORTKRYVVENNOTLYPNEVGRREEGSYTCFAENOVGKDERVRV VKVVTAPATITRAVTCLAVOYPEPISMSEPDOSLVNSFMOSDDS GORTKRYVVENNOTLYPNEVGRREEGSYTCFAENOVGKDERVRV VKVVTAPATITRAVTCLAVOYPEPISMSEPDOSLVNSERMOSDDS GORTKRYVVENNOTLYPNEVGRREEGSYTCFAENOVGKDERVRV VKVVTAPATITRAVTCLAVOYPEPISMSEPDOSLVNSERMOSDDS PITKVIPTSSEKVOTYOOGTLLIOKAGRSDSGNYTCLANGAGE DRIVWHINVOYDEPISMSERVILDEAECHPEVTUKNOSLDISTSIKANGAG COLVCARREGERALIVOLTUTLEPPERTYPTUTCLANGAGE DRIVWHINVOYDEPISMSERVILDEAGCTICHTUTCHANGAGE DRIVWHINVOYDEPISMSERVILDEAGCTICHTUTCHANGAGE TISLICASADOTPPSLUVVLPPCTDLOSGQCQRFYHKADDMIH ISGLSSVDAAGARTACVARRAAGHTERLVSIKVGUKPEANKQYHIL VSIINGETLKLPCTPPGAOQGGFSWTLPNSHHEEGGOTIGRVSIL LIMCTLIVRGAVVPLNTHTREGOTICHTUTCHANGAGGTPAGGGGG MILEMAMEPSPEDPPPTLKPETOPPEKRRTITELPPHKYCSFVLA YAQYI PPSKEEDBPAGSSSSPLAGBSAADSOMDASSDLRTI OTFVKKAKSKSKRAAQAGTPOGPPSRTTSSLATGPTKUTCSFVLA KKLKASLFOLDGOKVASSLSFTSLIHTISRPPALTPPVLISQGDLS HPPPKKRYNGNKKLIKGAGAGAGVOVLRPPRPTPTOCOCKASRIKKKK KKLKKARGDRIPPPOPPAPSDTDOSERSERSEEEEBBENA KKRLKKABRODRIPPPOPPAPSDTDOSERSERSEEEBBERGHE TSQUGABSSGSERWINDELINVKKLEKLKRYGAGKHEATAGVOR LEEGLARREKRIKLGGAGAGAGKGEOGPNYKLIKREEEGGEH ELELIRINVYDEDEOLKKRRALBERFTGIN	L		ļ	VPSDVDS
EKINAJQOMPESBELAQLISGSYIHYFICURILLIKGTEAST KNIFGRYSGSKRKOMGH TLAYEKDNYTYURISLILUKROTANYE I PSILKKOTAKCOOLOGYSKKEBECOAGAARMREOFYHSCKYGTI TGENVÄGBLILAUVEDJESQLABIGAAAGOLGATIOVYOASVGP VCESPTEQVIJEMLEFTQKKGNSTYYEMRTGTEPSVVERHLEEL PEQVAEDAIDMGDFGVEAVESGTDSGISAEAAGIDMGIFPESDS KDROGGIIMGDDAVALQITVILBAGTQARGVARGEDAITLILEY TETRNOFLDELMELEIFLAQRAVELSEEADVLSVSOOLAPAIL QGOTKEMMYTMVSVLEDLIGKISLSCLOHLMATLASPRYVDRVT EFIQOKLKOSQLAALKKELMYQKQGPALEEQAALEPKLDLLLEK TETRNOFLDELMELEIFLAQRAVELSEEADVLSVSOOLAPAIL QGOTKEMYTMVSVLEDLIGKISLSCLOHLMATLASPRYVDRVT EFIQOKLKOSQLAALKKELMYQKQGPALEEQAALEPKLDLLLEK TETRNOFLDELMELEIFLAQRAVELSEEADVLSVSOOLAPAIL QGOTKEMYTWINVSVLEDLIGKISLSCHOLLMATLASPRYVDRVT EFIQOKLKOSQLAALKKELMYQKQGPALEEQAALEPKLDLLLEK TETRLOKALEADISKRYSGEPVILMGTSL PTRKVIPOKANTON TON THE SINSLPDOSLVNSFMOSDLOS GGRTRXVVIVADATIRNITCLANQVPYGDVATVACEAKGEPMEKTUBL VKVSVTADATIRNITCLANQVPYGDVATVACEAKGEPMEKTUBLS PTIKKVIPTSSEKVOIQOGTLLIOKAQRSDSGNYTCHENNAGE DRITVWIHVNVQPPKINGNPPPTTVTREIAAGGSRKLIDCKAGG IPTPRVIMAPPEGVVUPAPYYGNRITVHGNOSLDIRSIKKSDSV QUCVARARGEGRALIVQVITLEPMEKIPDISEKTAMAGH TISLNCSAAGTPTPSLVAVLDNOTDLOGGQQLQRYFKADMIH ISGLSSVDAGAYRCVARRAAGHTERUVSLKYGLKPBANKQYHHI VSIINGETLKLPCTPPGAGQGRFSWTLPNCHHLEGGOTLGRVSL LDMOTLTVREASVPDRGTYVCRMETEYGGPOGGGGAGAFGKAGAAGHTALVSL LDMOTLTVREASVPDRGTYVCRMETEYGGAGAGAGAGAGAAGHTALVSL LDMOTLTVREASVPDRGTYVCRMETEYGGAGAGAGAGAGAGAAGHTALVSL LDMOTLTVREASVPDRGTYVCRMETEYGGAGAGAGAGAGAAGHTALVSL VAGYIPPSKEGSDWPASGSSPLRGGSAADSDGDBABSDLRTI QTTYKKAKSKRRAAQAGPTOPPSPRSTSTSITHISPPRAALTVPLSQGOLS HPPRKKDEKNKLGGAGAAGAGVGVLRRPPPTGARPSRTKLEKK KKKLKKARGAGDILPPGPPAPTSTSPAALTVPLSQGOLS HPPRKKDEKNKLGGAGAAGAGVGVLRRPPTYCQKKKELPPSAC TVYGGABAVSKRRAAQAGAPTGPPAPTTSTSPAALTVPLSQGOLS HPPRKKDEKNKLGGAGAAGAGVGVLRRPPTYCQKKKELPPSAC TVYGGABAVSKRAAQAGPTYDPPSPTTSTGARPSTKKSK KKKLKKARGAGAADAATCKTCNSD ### MINSSYNLPRYAPTYDECACAMODGKKGGAYAGKMEATTAGVGR PHIECSLOOTWIHLISCAKIKKTNVDPFTYCQKKERPARIAG GPPKSGED ### LEEVDLAMLABARKHARTKKTKOKRDOEPTYKLLINLADYTTRQGNO NELLELIKLHLIPDHOSVHKJSNSYTYTPOTTELDSIPERNI LKGGBBASAVDAATTGKTCNS ### MINSSYNLPRYAPTYDTEELBSIPERNI LEEVDLANLAB	6428	1982	444	SGSGGKMEDHOHVPIDIOTSKLLDWLVDRRHCSLKWOSLATTTP
NNITGRYSSQRMKDWGEITALYERDTYLVELSSLLVRNVNYEL	ŀ			EKINAAIODMPESEBIAOLLSGSYIHYFHCLRILDLLKGTERST
PSEKKOTAKCOGLOGYSTEKKEBECOAGAABERGEOTYISCKYGI TGENVIGBLALVKDIPSGLAEIGAAAQGEAIDVYQASVGV VCESPTEQVLEMERFUCKKGNSTVYBHRIGTEPSVVERPHLEEL PEQVAEDAIDWGDFOVEAVSEGTDSGIGAEAAGIDWGIFPESDS KDPGGGIDWGDDAVALOITVLEAGTGAEOVARGEDAITLEV TETTNOPLDELMELEIFLAQRAVELSEEADVLSVSCOLAPAIL QGGTKEKMYTWSVLEDLIGKITSLOCHEMTILASPRYVDRVT EFLQOKLKOSOLAALKKELMVOKOGEALSEGAALEPKLDLLEK TETTNOPLDELMELEIFLAQRAVELSEEADVLSVSCOLAPAIL QGGTKEKMYTWSVLEDLIGKITSLOCHEMTILASPRYVDRVT EFLQOKLKOSOLAALKKELMVOKOGEALSEGAALEPKLDLLEK TKELGKLIE BADISKRYSGEPVINLMGTSL VVKSVTDKDAGDYLCVARNKVGDDYVULKVDVVMKENTEKEE NDHKVPYGGDLKVDCVATGLENPEISWSLEPDSILVNSFMOSDDS GGRTKRYVVFNNGTLYFNEVGMEEGDYTCFAEROVGEDERVR VKVVTAPAITINNTCLAVQVSTGDVTVACEAKGEPMPKVTULS PTINKVPYGGDLKVDCVATGLENPEISWSLEPGSILVNSFMOSDDS GGRTKRYVVFNNOTLYFNEVGMEEGDYTCFAEROVGEDERVR VKVVTAPAITINNTCLAVQVSTGDVTVACEAKGEPMPKVTULS PTINKVPYPSSEKYOLVODGTLLIOKAQRSDSGNYTCLVENSAGE DRITVWIHVNOPPKINGNPPTTTVREIGGSRKLIDCKASG IPPTRVLARPEGVULPAPYYGNRITVHGNGSLDIRSIRKSDSV QLUCMARNECGEARLIVQLTVLEPMEKPITPUBISKTAMAGH ISGLSSVDAGAYRCVARRAAGHTERLVSLKVGLKPEAAKKYTHIL VSIINGETLKLPCTPPGAGGGRSWTLFUNEGGFVLIANGAM VOARLYGRRPLHPQGSLTIQHATQRDAGFYKCMAKNILGEGKVL LDMGTITVREASVFDRGTYVCRHETEYGPSVTSIPYULAYPPR ITSETPYLYTYTREGNIVCHKOMMADIPALDEGGFVLGRVSL LDMGTITVREASVFDRGTYVCRHETEYGPSVTSIPYULAYPPR ITSETPYLYTYTREGNIVCHKOMMADIPALDTHELPDKSSHLKAG VOARLYGRRPLHPQGSLTIQHATQRDAGFYKCMAKNILGDSKT TYLHVF 6430 1946 602 RTRVSTGLRRTLLWSEAVGASSTRGDTGIPGGGGGAGFGGGGG AMLEAMAEPSPEDPPPTLKPETQPPEKRRTISDPNKCSFVLA YAGYIPPSKEESDWPAGSSSPLRGGSAADDBSARSULRI OTFVKKAKSSKRRAAQAGPTQFGPPRSTFSRLQADDSARSLURI OTFVKKAKSSKRRAAQAGPTQFGPPRSTFSRLQADDSARSLURI OTFVKKAKSSKRRAAQAGPTGFGFPSTTSGREEREBEEBEMA KKKDSLFPLOGPKVASPLSTSTIJHTTSRFTALTVPLSGODLS HPPRKXDRKORKLIGGAGAGAGVGRRPPTDTDGEREREBEEBEEBEM KKKLKABERGDRAGAGAGAGVGRRPPTDTDGEREREBEEBEEBEM TVVGGEAPVVUDTTPBERFPRDTTUPPETGDEKRRTLKSK KRLKKABERGDRAGAGAGAGVGRRPPTDTGGEREBEBEBEBEM TVVGGEAPVVUDTTPPELRSTGFTLSDEFREFEREBEBERGKH RELRIRRYVPEDEDLKKRTVPQARVAVERKVKGLEBARKFBFV LEEBALRRKERLKALREKTGROKEDGEGRYTTGILBEEBEGGKH RELRIRRYVPEDEDLKRRTVONATKLITTGRING MBELLSTLIKKD JUDDGV	ľ			KNIFGRYSSORMKDWOEIIALYEKDNTYLVELSSLLVENVNYET
TGENVRGELLALVKUDLPSQLAEIGAAQQSLGEAIDVYQASVGP VCESPTEQULPMRIFYQKRKSTYYBNRGTGPSVVERPHLEEI PEQVAEDAIDMGDPGVEAVSECTISGISAEAAGIDMGIPPESDS KDPGGGIDMGDDAVALQITVLEAGTQAFEGVARGPDALTLEY TETRNQPLDELMELEIILAQRAVELSEEDALEPKUDLITLEY TETRNQPLDELMELEIILAQRAVELSEEDALEPKUDLLILEK TERLQQLLEADISKNYSGRPVILMGTSL GQTYRKMYTWVSVLEDLIGKLTSLOLGHLEMILASPYVDRVT EFLQQKLOSQLLALKKELMWYQQGSALEGAALEPKUDLLILEK TKELQKLLEADISKNYSGRPVILMGTSL 6429 3413 3442 EPSSWTAERFOPLAAMPLEAAVGEDDRALSFDSRIKVPANGTL VVKSVTDKDAGDVLCVARNKVGDDYVVLKVDVVMKPAKLEIKEE TKELQKLLEADISKNYSGRPVILMGTSL GGTRKYVVPNNGTLYFNEVGMREBGDTTCTAENQVGKDEMRVR VKVVTAPATIRINITCLAVQPYCDVVTVACEAKGEMPKVTWLS PTNKVIPTSSEKVQIVQDGTLLOKAQRSGNYTCLVANSAGE DRITVWIHVNVQPPKINGNPPITTVRELAAGGSRKILDCKAG IPTPRVLAMPFGGVVLIPPYGNRITVVRINSLDCKAGE PTYRKVIPTSSEKVQIVQDGTLLOKAQRSGNYTCLVANSAGE DRITVWIHVNVQPPKINGNPPITTVRELAAGGSRKILDCKAG IPTPRVLAMPFGGVVLIPPYGNRITVLOKSGLDIKSLKKSDSV QLUCMARNEGGEARLIVQLTVLEPPHKRIFHDPISKITAMGH TISLACSAAGTPTPSLVVVLINGTDLOGGQLQRFYHAAOMMI ISGLSSVDAGAYRCVARNAAGHTERLVSLKVGLKPEAMKQYHNL VSIINGETLALPCTPPGAGQGRFSWTLPNGHLLEGOSLICHAUPHOHLISCHLKAG VQARLYGMRFUHPGGVSLIPPYGNVLNGTNGSGDGJAGPGTGGGG AMLEAMAPPSGDPPPTLKVPTOPPFSKRRTIEDPINKFCSFVLA YAQYIPPSKERSVPHGGGTTVCRRETEYGPSVTSIPVIVIAYPPR ITSEPTEVITTREGNTVKLNCMAMGIPRADITTHELPDKSHLKAG VQARLYGMRFUHPGGSSLICHGATQRAGGFKCMAKNILGSDSKT TYIHVF 6430 1946 602 RTRVSTGLRKTLLWSEAVGASSTRGDTGIPGSGEGGAGPGGGG AMLEAMAPSPSBDPPPTLKPTOPPFKRRTIEDPINKFCSFVLA YAQYIPPSKERSONPAGSSSPLRGBSAADSGDUSAPSDLRTI OTFVKKAKSSKRRAQAGFTQPGPPSTTSRLQAPDGSATLEEM KLKNDLFDLLGGVKASSELSFTSLITTTSRPPAALTTVPLSGGDLS HPPRKDRKNKLGFGGAAGRGVAFKRERPTLSGGNLSRSKKKK KKKLKAERGDBLPPPGPQAPPSTDSEEERBEEBEBEMA TVVGGEAPVVLDTPPERAPPPATVHPSGCREKSBRSKKGSTE TSQGGDASSEGEMRWDEDIMVESGDDSMDLITTYCRFPPAGG PPHSGGLGTWILLSCAKIKKTNVPDFFYCCKKELEFBARGG PPHSGGE GPPKSGGP SURGERTURLSCAKIKKTNVPDFFYCCKKCELFREPARGG GPPKSGGP LEEBALBRKRIKALRKRIKARDKREDGENKGGAYAGKMEATTAGVGR LEEBALBRKRIKALRKRIKKALRKFTROKREDGEPKTIGHREEEEGGKH RELEILARYVPEDEDLKRRTVPQAKPAVPEKVKGLEAARPBPV IEBVDLANLARPKPMOHLKRAVPQAKPKVAVEKVKGLEAARPBPP IEBVDLANLARPKYDMLKRAUTSRNILTSVPTPTRELBS				PSLKKQIAKCQQLQQEYSRKEEECQAGAARMREOFYHSCKQYGT
VCESPTEQVI.PMLRFVQKRGNSTVYENRTGTEPSVVERPHLEBI. PEQVAEDADIMOGPOSYRAVSECTIBGE JERAGIDIMOG IP PSDISS KDPGGDSIDMOGDAVALOITVLEAGTQAPEGVARGPDALTILEY TETRNQPLDELMELEIFLAQRAVELSEEAGULSVSGCLAPAIL QGGTKERMYTMYSVLEDLIGKLTSLOCHLFMTLASPRYVDRVT EFLQKLKGSGLLALKKELMVQKQQEALERQALERKDLLLEK TKELGKLI EADISKRYSGPVYLMMSTGS FKELGKLI EADISKRYSGPVYLMMSTGS EPSSWTAAPRGPLAAHPLERAVGEDDRRALSFDSRIKVPANGGT. VKVSKYDKDKANGOVLCVARKVGODYVVLKVDVWKAPKTEIKEE MDHKVFYGGDLKVDCVATGLPNPEISMSLEDGGLNVSMGODSS GGRTRYVVFRNGTLYPNSVGREEGDYTCFAENGVGKDEMRVR VKVVTAPATINNTCLAVOPYDGDVYVLKVDVWKMPAKIEHKEE MDHKVFYGGDLKVDCVATGLPNPEISMSLEDGGLNSKMGSDDS GGRTRYVVFRNGTLYPNSVGREEGDYTCFAENGVGKDEMRVR VKVVTAPATINNTCLAGVGREEGDYTCFAENGVGKDEMRVR PTHKVIPTSSEKYQIVQDGTLLIOKAGRSDSGNYTCLVRNSAGE DRRITVWIHNVQPPKINGNPPITTVCAERAGSPMKLTGCKAEG IPTPRVLWAPPEGVULPAPYYGNRITVHCMGSLDIRSLRXGDSV QLUCMARMEGGEAALIVQLTVLEDWELAGGSKKLIDCKAEG IPTPRVLWAPPEGVULPAPYYGNRITVHCMGSLDIRSLRXGDSV QLUCMARMEGGEAALIVQLTVLEDWELAGGSKKLIDCKAEG IPTRVTHLHPOPTSHSKTVCHKRAGHTUSLKVGLKEANKQYIHL VSIINGETTLKUPCTPPGAGGGGFSSWITHPIPPISKFCHAMGHH ISGLSSVDAGAYRCVARNAAGHTERLVSLKVGLKEANKQYIHL VSIINGETTLKUPCTPGAGGGGFSSWITHPIPPISKFCHRWSLIKAG VQARLYGRRPLHPQGSLTIQHATQRDAGFYKCMAKNILGSDSKT TYTHVB 115ENTELMPLYTYTRCHTVKLNCMANGISTWELEPOKRILKGDGWSL LDNGTLTVREASVPDRGTTVCCMSTETGGPSVTSIPVIVIAYPPR ITSEPTPIVYTYRCHTVKLNCMANGISTWELEPOKRIKLKGD VQARLYGRRPLHPQGSLTIQHATQRDAGFYKCMAKNILGSDSKT TYTHVB 6430 1946 602 RTRVSTGLRRTLLWSEAVGASSTRGDTGIPGSGGGGGGGGGG AMLEAMABPSPBDPPPTLKPETGPPERRRTITEPDRIKCCFVLA YAGYY PPSKEESDMPASSSSSPLEGSSADASGMADSAPBAPSLIRIT QTFVKKAKSSKRRAQAGFTQPGPPRSTSTSRLQAADSATLLEKM KLKDSLFJDLOPKVASPLSPTSILHTTSRPAALTPVLLGGOLS HPPRKKDRKNIKLGPGAGAGGVURRYRPPPDGDGKRSRIKKSK KRALKKARSKRRAQAGFTQPGPPRSTSTSRLQAADSATLLEKM TVVGGBAPVEVLPTTPEAPRPPATUTPEGVPPANDSEKSEVGSTE TSQDGASSEGGBRVMMEDIMVESGDDSWDLITCYCRKPFAGR PMIECSLCGWWILLSGLKKKTNVPQAKPVAVEEKVBQLEAKRPSPV LEEVLALAHAPRYDDDLKRRVPQARPYADESKYLEGOSTE TSQDGASSEGGBRVMMEDIMVESGDDSWDLITCYCRKPFAGR PMIECSLCGWWILLSHAKKRTQRATAGLUG LEEVLALAHAPRYDDBLKRRVPAARFURDTREDGSTPPRN LTEVVANDVNMLHALAPRDDDBLKKRTQRATAGUGBPRFVLTDDIDS	1			TGENVRGELLALVKDLPSQLAEIGAAAOOSLGEAIDVYOASVGP
PEQVAEDATDMODFOVEAVBEGTOSGISAERAGIDMOTIPESDIS KDPGGDSIDMODDAVALQITVLEAGTOAPBGVARGPDALTLEY TETRNOPLDELMELEIILAGRAVELSEEADVLSVSOFQLAPAIL QQQTKEKMVTMVSVLEDLIGKUTSLQLGHLFMILLASPRYDRIVI EFIQQKIKGSQLLALKKELMVQKQQEALEGAALEPKLDLLLEK TKELQKLIEADISKRYSGRPVKLMGTSL 6429 3413 3442 EPSSWTAAPGFPLARHPLEAVGEDBDRALSFPSRIKVPANGTL VVKSVTDKDAGDYLCVARNKVGDDVVVLKVDVVMKPAKIEHKEE NDHKVFYGGDLKVDCVATGLPNPEISKSLEDGSLINSFMGSDS GGRTKRYVVFNNGTLIYNBVGKREEGDYTCFAENOVGKDEMRVR VKVVTAPATIRNKTCLAVQVPYGDVTVACEAKGSPMEKVTWLS PTINKVIPTSSEKYQIVGDGTLIVCKAGSGNYTCLWRNSAGE DRKTVWIHNVQPPKINGHPNPITTVREIAAGGSRKLIDCKASG IPTPRVLWAPPEGWULPAPYYCMRITVHGNGSLDIRSIRKSDSV QLVCMARNEGGEARLIVQLTVLEPMERLFIHNPISEKITAMAGH TISLASSAGTPTPSLVWVLNNGTDLQSGQLQRFYHKADGMHH ISGLSSVDAGSAGRVCARAAGHTERLVSLKVGLKPEANKQYHNL VSIINGETLKLPCTPGGAQGFFSWTLPNGMILEGFOTLGRVSL LDNGTLTVREASVPBRGTVYCKMETEGYDTSIPVTVLAYPPR ITSEPTPVIYTREPONTVKLNCMAMGIPKADITHELPDKSHLKAG VQARLYGMRPLHPQGSLTIQHATQRDAGFFKCMAKNILGSDSKT TYHHV 6430 1946 602 RTRVSTGLRRTLLWSEAVGASSTRGDTGIPGSGGAGGAGGGG MLEAMABPSBDDPPPTLKPTOPDEKRRTITEDPNKFCSFVLA VAGYIPPSKESDWPASGSSSPLAGBSAADSDGWDSAPSDLRTI QTFVKKAKSSKRRAAQAGFTQPGPPRSTTSRLQAPDSATLLEKM KLKDSLFPDLOPFVASPLSFTSLHTARFPAALTPVLSGGOLS HPPRKKDRKNRKLGFGAGGGGVURRPRTFTGDGCRKSRIKKSK KKRLKKARFGORLPPPGQAPPSDTDSEEBEREEBEERMA TVVGGBAPVPULTTPEBAPRPATVHEGVPPADSEEKEVGSTE TSQGGABSGGEMRVMDEDIMVESGDDSWDLITCYCRCPPAGR PMIECSLCGTWIHLGCAKIKKTNVPDFFYCKKKEREPERMA TVVGGBAPVPULTTPEBAPRPATVHEGVPPADSEEKEVGGTE TSQGGCMSSGGGGRKWNDEDIMVESGDDSWDLITCYCRCPPAGR PMIECSLCGTWIHLGCAKIKKTNVPDFFYCKKKEREPERMA TVVGGBAPVPULTTPEBAPRPATVHEGVPPADSEEKEVGGEREMAL EEEBLRRKGRLKARLREKTGRKDKEDGPKYKHLREEEEBGEKH RELLRLRNYVPEDEDLLKKRRVPQAKPVAVEEKVKGQLEAAKEPBV LEEVDLANLAPRKDPWDLKRDVAKLEKLKKRTQRATASLIRER LKGGGBLASAVDAATEGKTCDSD GGLGTMGSRIKKNSKTKAPTTPTUTDLDSKOR PGFCRLSSGRASCFCILSYLPWFFVYLLULADYTTKRGENQ NNELLETLIKLPIPPDGGVSVLLSVHISYFTVVDTREEPSIPERSRN LTEYVAVDVNNMLHLVASMLYSERILIICSKLSTTACHGSSA MALYPMYMOVIVPULJPHLDVCCAPPPLLDTOCTHSHLSMEKVRN	1	ĺ		VCESPTEQVLPMLRFVQKRGNSTVYEWRTGTEPSVVERPHLEEL.
KDPGGDSIDMGDDAVALQITVLEAGTQAPEULSEAPOLAPAIL TETRINGPLEMEMELIFLAQRAVELSEAPOLAPAIL CQGTKERMYTMYSVLEDLIGKLISLQLQHLFMILASPRYVDRVT EFLQOKLKGQSLLALKKELMVQKQGEALERQAALEFUDLLLEK TRELQKLLEADISKRYSGRPVNLMMTSL EPSSWTAABRGFLAAHBLERAVQEDDRRALSFDSRIKVPANGTL VKSVTUNDKONGTYLCVARKVGODPVLWVDVMKPAKIERKER MDHKVFYGGDLKVDCVATGLPNPEISMSLEDGSLVMSFMGSDDS GGRTKRYVVFNNGTLYPMSVGMREEDGYTCPENOVGKDEMKVR VKSVTAPATIRNKTCLAVQVPYGDVTVACEAKGEPMFKVTWLS PINKVIPTSSKRYOIYQDGTLLIOKAGGSSKRINTCKARS DRITWHIHVNVQPPKINGNPPITTVERLAAGGSRKLIDCKAEG IPTFRVLWAPPEGVVLDAPYYGNRITVHGRGSLDIRSLRXSDSV QLOVMARMEGGEARLIVQITVLEMPERIPHDISEKTAMAGH ISGLSVDAGAJRCVARMAAGHTERLVSLRVGLKPAANKQTHNL VSIINGETLKLPCTPPGAGQGRFSWTLPNNMHLEGFOTLGKVSL LDNGTLTVREASVPDRGTTVCCMTETEYGFSVTSITVIVIAYPPR ITSETPTYLYTRFCATVYLKNCMAMGIF KADITWELPPKSKLKAG VQARLYGMRPLHPQGSLTIQHATQRDAGFYKCMAKNILGSDSKT TYTHVB 6430	1		•	PEQVAEDAIDWGDFGVEAVSEGTDSGISAEAAGIDWGIFPESDS
TETRNOPLDELMELSITEAQRAVELSSEADVLSVSOFGLAPAIL QQTYKRMYTMYSVLEDLIGKLITOLGHLFMILASPRYUDRVT EFLQOKLKGSQLLALKKELMVQKQQEALEEQAALEPKLDLLLEK TKELQKLISQLIALKKELMVQKQQEALEEQAALEPKLDLLLEK TKELQKLISQLISRAYSGRPVNLMGTSL EPSSWTAAPRGPLAAHPLEAAVQEDDRRALSFDSRIKVPANGTL VVKSVTDKDAGDYLCVARNKVGDDYVVLKVDVVMKPARITERKEE NDHKVPYGGDLKVDCVARGLNPGDSLOVSHGNGSTDGSRIKVPANGTL VVKSVTDKDAGDYLCVARNKVGDDYVVLKVDVVMKPARITERKEE NDHKVPYGGDLKVDCVARGLNPGDDYVVLKVDVVMKPARITERKEE NDHKVPYGGDLKVDCVARGLNPGDDYVVLKVDVVMKPARITERKEE NDHKVPYGGDLKVDCVARGLNPGDDYVTVACERAGEPMEKVTWLS PTNKVLPTSSEKYQIYQDGTLLICARGESBCHLIVCLTVLNSAGE DRKTVWIHNVQPPKINGNPPTTTVRETAAGSSRKLIDCKAEG DRKTVWIHNVQPPKINGNPPTTTVRETAAGSSRKLIDCKAEG DRKTVWIHNVQPPKINGNPPTTTVRETAAGSSRKLIDCKAEG DRKTVWIHNVQPPKINGNPPTTTVRETAAGSSRKLIDCKAEG DRKTVWIHNVQPPKINGNPPTTTVRETAAGSSRKLIDCKAEG OLVCMARNSGEBALIVQLTVLEPMEKPTFHDPISEKITAMGH TISLNCSAAGTPTPSLVWVLPNGTDLQSGQLQFPYKAGGHH ISGLSSVDAGAYRCVARNAAGHTERLVSLKVGLKPEARMQYHNL VSIINGETLKLPCTPPGAGQGRSSWTLPNGHHLSGPOTLGRWSL LDNGTTITVREASVPFDRGTYVCRETERVSVSLLKAG VQARLVGARFLHPGGSTTIQHATQRDAGFYKCMAKNILGSDKT TYHVF ITSEPTPVYYTRPGNTVKLNCMMGIPKADTTMELPDKSHLKAG VQARLVGARPLPHOGGSLTIQHATQRDAGFYKCMAKNILGSDKT TYHVF THVSTGLRRTLLWSEAVGASSTRGDTG1PGSGEGGAGPGGGGG AMLEAMAEPSPEDPPPTLKPETQPPEKRRTIEDFNKFCSFVLA YAGYIPPSKESDMPASGSSPLRGSAADSGMDSAPSDLLTI OFTVKKKASSKRRAAAGAGPTOPOPPRSTFSRLQAPDSATLLEKM KLKDSLFDLDGPKVASPLSFTSLITHTSRPPAALTPVPLSQGDLS KKRLKKASSKRRAAAGAGPTOPOPPRSTFSRLQAPDSATLLEKM KLKDSLFDLDGPKVASPLSFTSLITHTSRPPAALTPVPLSQGDLS KKRLKKASKRASKRAAAGAGPTOPOPPRSTFSRLQAPDSASLEKGSTE TSOGGDASSSGEMWAWDEDINVESGDESWDLITTCYCRKPPAGR PMIECSLCGTWIHLSCAKIKKTNVPDFFYCQKCKEURPEARRG GPPKSGEP MINSSYNLPAYAPYLPCEACAMQDGRKGGAYAGKMEATTAGGGR LEEBALRRKERLKALREKTGRKEDGEDFYKKHLREEEEGGKH RELIERNYVPDEDGLKKRRVPQAKWEKVKEQLEAAKPEPV LEEVDLANLAPRKVPDDGLKKRRVPQAKWEKVKEQLEAAKPEPV LEEVDLANLAPRKVPDDGLKKRRVPQAFWEKVKEQLEAAKPEPV LEEVDLANLAPRKPDDWDLKRDVAKKLEKLKKRTQRAIAELTRER LKGGGBLASAVDAATEGKTCDSD GGLGTMGSRIVQPBFULTDIDGSKGR PSGCLSGSGASCGCTLSVLDWFEVFYYLLINILADYTTKRQENQ NNELLETLHKLPIPDFULVPPLLIDVCAGKR MNELSTLIKENGKYN NNELLETLEKURDFYLTOFTERSTYP	1		•	KDPGGDGIDWGDDAVALQITVLEAGTQAPEGVARGPDALTLLEY
GGGTKERMTITWSVLEDLIGKLTSLOLGHLFMILASPRYUDRUT EFLOKLKOSGLIALKKERLWINGORALEGAALEFKLDLLLEK TKELOKLIEADISKRYSGRPVNIKGTSL 6429 3413 3442 EPSSWTAARPGIJAAHPLEAAVGEDDRRALSFDSRIKVFANGTL VKSVTDKDAGDYLCVARNKUGDUVKVADVVMRPAKIEHKEE NDHKVFYGGDLKVDCVARGLPNPEISMSLPDGSLVNSFMGSDDS GGRKKKYVFNGGTLYNFWSGMREEGDYTCFAENOVGKDEMRVR VKVVTAPATIRNKTCLAVQVPYGDVTVTVACEAKGEPMEKVTWLS PTINKVIPTSSEKYQTYQDGTLLIOKAQRSBGSGNYTCLJURNSAGE DRRTVWIHNTVQPPKINGNPPITTHEATAGGSRKLIDCKAEG IPTPRVLMAPPEGVVLPAPYYGNRITVHGNGSLDIRSLRXGDSV QULVMARNGGEBALIVOLTVLEPMEKPIFHDPISEKITAMAGH TISLNCSAAGTPTPSLWWLPNGTDLQSGQQLQRYNKRADGMH ISGLSSVDAGAYRCVARNAAGHTERLVSLKVGLKPEANKQYHNL VSIINGETLKLPETPFGAGGGGRFWIPPNGHLESPOTLGRVSL LDNGTLTVREASVPDGTTYVCRMETEYGPSVTSIPVIVIAYPPR ITSEPTPVIYTRPGNTVKLNCMAMGIPKEADITHELPDKSHLIKAG VQARLYGNRPHHFGGSLTTQHATQRDAGFYKCMAKNILGSDSKT TYTHVF 6430 1946 602 RTRVSTGLRRTLLWSEAVGASSTRGDTGIPGSGEGGAGPGGGE AMLEAMAEPSPBDPPPTLKPETOPPEKRRTIEDPNKFCSFVLA YAGYIPPSKEESDWPASGSSSPLRGESAADDSGMSAPSDLETI QTFVKKAKSSKRRAAQAGTTQGPPPERSTFSRLQAPDSATLLEKM KLKDSLFPLODPKVASFLSFTSITHTSRPPAALTPVLSGGDLS HPPRKKDRNKLGPGAGAGVGVLRPRPTTGDGEKRSRIKKK KRKLKABERGDRLPPPGDAGAGAGVGVLRPRPTTDGDGEKRSRIKKK KRKLKABERGDRLPPPGDAGAGAGVGVLRPRPADTSESKSVGSTE TSQGGDASSSEGEMRVMDEDINTEGTRPFBATTHFSGVPPADSESKSVGSTE TSQGGDASSSEGEMRVMDEDINTGCYCRYPFAGR PMIECSLCGTWIHLSCAKIKKTNVPDFFYCQKCKBLRPEARRLG GPPKSGEP MIECSLCGTWIHLSCAKIKKTNVPDFFYCQKCKBLRPEARRLG GPPKSGEP EERLRRWYPVPDEDELKKRRVPQARVAVEKVLKOLEARAKPBPV IEEVDLAANLAPREVPDDLEKKRRVPQARVAVEKVLKOLEARAKPBPV IEEVDLAANLAPREVPDDLEKKRRVPQARVAVEKVLKOLEARAKPBPV IEEVDLAANLAPREVPDDLEKKRRVPQARVAVEKVLKOLEARAKPBPN IEEVDLAANLAPREVPDDLTRVGVRPFUTYDDTRELPSIPENN LTGYFVANDVNNKHLYSBMLYERRILIICSKLSTLTACHIGSA AMLYPMWOHVYTPUTPUTLSLPSIPENNN LTGYFVANDVNNKHLYSBMLYERRILIICSKLSTLTACHIGSA AMLYPMWOHVYTPUTPUTLICISKIREFERN	1			TETRNQFLDELMELEIFLAQRAVELSEEADVLSVSOFOLAPAIL
6429 3413 3442 EPSWTADPROPLARHPLEAAVQEDDRRALSFDSRIKVPANGTL VVKSVTDKDAGDYLCVARNKVGDDVVVLKVDVVMKPAKTEHKEE NDHKVPYGGDLKVDCVARGLNVGDDVVVLKVDVVMKPAKTEHKEE NDHKVPYGGDLKVDCVARGLNVGDDVVVLKVDVVMKPAKTEHKEE NDHKVPYGGDLKVDCVARGLNVGDDVVVLKVDVVMKPAKTEHKEE NDHKVPYGGDLKVDCVARGLNVGDDVVVLKVDVVMKPAKTEHKEE NDHKVPYGGDLKVDCVARGLNVGDDVVVLKVDVVMKPAKTEHKEE NDHKVPYGGDLKVDCVARGLNVGDDVVVLKVDVVMKPAKTEHKEE NDHKVVPTASEKYQTYQDGTLLIOKAQRSBGGNTVLVNISAGE DRKTVVHTNVTCLAVQVPYGDVVTVACKAGSPGNTVTLVNISAGE DRKTVVHTNVOPPKINGNPFTTTVRETAAGSRKLIDCKARG IPPRVLMAPPEGVVLAPPYYGKNTVCHGNSLDIRSLRKSDSV QLVCMARNEGGEARLIVQLTVLEPMEKPIFHDPISEKITAMAGH TISLNCSAAGTFTPSLWVLYPNTTDLQGGQQLQRFYHKADGMIH ISGLSSVDAGAYRCVARNAAGHTERLVSLKVGLKVEARGYHNL VSIINGETLKLPCTPFOGAGGGRFSWTLDRGHKLEGPQTLGRVSL LDMCTLTVREASVFDRGTYVCRMETSYPGSVTSIPVIVIAYPPR ITSEPTPVIYTRPGNTVKLNCMMGIPKADLTWSLPVIAYPPR ITSEPTPVIYTRPGNTVKLNCMMGIPKADLTWSLFWLSDSKT TYTHUP TTYHUP SVARLEARMADEPSPDPPPTLKVETQPPSKRRRTIEDFFNKFCSFVLA YAGYIPPSKEDSUPPASGSSSPLRGESAADDGMUSAFDLATI OTFVKKAKSSKRRAQAGPTOPOPPRSTTSRLQAPDSATLLEKM KLKDSLFDLDGPKVASPLSPTSITHTSRPFRALTPVPLSQGDLS HPPRKKDRKNRKLGPGAGAGFGVLRPRPTFTGGCEKRSIKKSK KRKLKKABRGGRLPPLGPGPDAPPSTTDSEERSEEBEEEBEEMA TVGGGAPVPVLPTPPBAPPPATHPFGCUPPADSESKVGSTE TSQDGDASSSEGEMRVMDEDIMVESGDDSWDLITCVCRCPPAGR PHIECSLCGTWIHLSCAKIKKTNVPDFFYCQKCKELRPPARRIG GPPKSGEP PHIECSLCGTWIHLSCAKIKKTNVPDFFYCQKCKELRPPARRIG GPPKSGEP LEEEALRRKYELKALREKTGRKDKEDGEPKTKHLREEEEGEKH RELRRNYVPEDEDLKKRRVPQAKPVAVEEKVLGQLEARKPEPV IEEVDLANLAPRKPDHDLKRRVPAKREKUEGCLEARKPEPK LEGGLSLASAVDAARVAVEKKUELDARAKPEPV IEEVDLANLAPRKPDHDLKRRVPARTSGTLSDFEVQROFFF DYSDGEVLQTLTKFCFFFYVDSLTVSQVGONFFFVLTDIDGKGR FGFCRLSSGASCFCLLSSLVPFFEYKLINLLADVTKRQGEN NMELLETLHKLPIPPDGDVSVHLSVHSYPTVPDTRELPSIPENN LTEYFVANDVINNLHLYASMLYERRILIICSKLSTLTACHIGGSA AMLLPMWGNVYIPLVPPLLDVCAGLUSHLSTLTACHIGGSA AMLLPMWGNVYIPLVPPLLDVCAGLUSHLSTLTACHIGGSA AMLLPMWGNVYIPLVPPLLDVCAGLUSHLSTLINGENEVKN				QGQTKEKMVTMVSVLEDLIGKLTSLQLQHLFMILASPRYVDRVT
6429 3413 3442 EPSSWTAAPRCPLAAHPLEAAVGEDDRRALSFDSRIKVFANGTL VVKSVTDKDAGDYLCVARNKVGDDYLKVDVVMKPAKIEHKEE NDHKVFYGGOLKVDCVATGLPNPEISMSLPDGSLVNSFMGSDDS GGRTKRYVVPNNGTLYFNSVGMREEGDYTCFAERQVGKDEMRVR VKVVTAPATIRNKTCLAVQVPYGVDVTVACEAKGEPMFKVTWLG PTNKVIPTSSEKYQIYQDGTLLIQKAQRSDSGNYTCLVRNSAGE DRKTVWIHNNVQPPKINGNPRPITTVREIJAGGSRKLIDCKAEG DRKTVWIHNNVQPPKINGNPRPITTVREIJAGGSRKLIDCKAEG ORKTVWIHNNVQPYKINGNPRPITTVREIJAGGSRKLIDCKAEG DRKTVWIHNNVQPYKINGNPRPITTVREIJAGGSRKLIDCKAEG OLVCMARNEGERALIVQLTVLEPMEKPIPHDPISEKITAMAGH TISLNCSAAGTPTPSLVWVLPNGTDLQSGQLQRFYHKADGMLH USSINGETIKLPCTPPGAGQGRFSWTLPNGMHLEGPOTLGRVSL LDNGTLTVKEPSVPRGTTYVCMTETYPSVVSTIPVIVIAYPPR LTSEPTPVIYTRPGNTVKLNCMAMGIPKADITMELDKSHLKAG VQARLYGNRFLHPGOSLTIQHATQRDAGFYKCMAKWILGSDSKT TYHVF 6430 1946 602 RTRVSTGLRRTLLMSEAVGASSTRGDTGIPGSGGGAGPGGGG AMLEANAEPSPPEDPPPTLKPETQPPEKRRTIEDFMKPCSFVLA YAGYIPPSKESBUMPASGSSPJLAGSSAADSDGWDSAPSDLATI QTFVKKAKSSKRRAAQAOPTQPGPPRSTFSRLQAPDSATLLEKM KKKDSIPLDDGPKVASPLSPTSLITTSRPPAALTPVPLSQGLIS HPPRKKDRNNKLGPGAGAGMGVLRRPRPTPGGEKRSRIKKSK KKKLKAERGDRLPPPGGPAPSDTDSBEEREBEEBEEBEM TVVGGBAPVPVLPTPPEARPPP APTVHPEGVPPALDESKEVOSTE TSQDGDASSEGGEMRVMDEDIMVESGDDSWDLITCYCRKPFAGR PMIECSLCGTWHLBCAKIKKTNVPDFFYCQKCKELRPEARRLG GPPKSGEP MIECSLCGTWHLBCACKIKKTNVPDFFYCQKCKELRPEARRLG GPPKSGEP 6431 3 605 WINNSSYNLDPAYPYLPCEACAMDGRKGGAYAGKMEATTAGVGR LEEBALRRKERKALREKTGRKNEXDEGPPKTKHLREEBEEGEKH RELRRNYVPEDEDLKKRRVPQAKPVAVEEKVKEQLEAAKPEPV IEEVULANLAPRKPOMDLKRDVAKKLEKLKKRTQRAIAELIRER LKGQESLASAVDAAATGOKTOBCPAKTKHLREEBEEGEKH RELRRNYVPEDEDLKKRRVPQAKPVAVEEKVKEQLEAAKPEPV IEEVULANLAPRKPOMDLKRDVAKKLEKLKKRTQRAIAELIRER LKGGESLASAVDAAATGOKTOBCPAKTKHLIDDSKOR NGELETLHKLPIPDPGVSVHLSVHSYPTVPDTRELPSIPENRN LTEYFVAVDVNNMLHLYASMLYBERTLLICSKLSTLTACHBGA AMLYPMYWGHVYIPLSPHLLDVLPAPPYLLGPLHISLMBEVVN	1			EFLQQKLKQSQLLALKKELMVQKQQEALEEQAALEPKLDLLLEK
VVKSVTDKOAGDYLOVARNKUODDYVUKVDVWKPAKIEHKEE NDHKVFYGGDLKVDCVATCHANDTUKVDVWKPAKIEHKEE NDHKVFYGGDLKVDCVATCHANDTUSWSLOPGSLVNSFMGSDDS GGRYKVVPNNOTLYFNEVGMREEGDYTCFAENQVGKDEMRVR VKVVTAPATIRKTCLAVQVPYGDVTVACEAKGEPMPKVTWLS PTNKV1PTSSEXYQ1YQDOTLLIOKAGRSDSGNYTCLVRNSAGE DRKTWHINNVQPYKINGNPHTUREIAAGSSRKLIDCKAEG 1PTPRVLWAPPEGVVLPAPYYGNRITVHGNGSLDIRSLKXSDSV QLVCMARNAGGEARLIVQLIVLEPMEKP IHTDEISELTMAGH 1SGLSSVDAGAYRCVARNAGHTERLV3LKYGLKPEANKQYHNL VSIINGETLKLPCTPPGAGGGRFSWTLPMHLEGGPOTLGRVSL LDNGTLTVREASVFDRGTTVCMRTEYGPSVTSIPVIVAPPR 1TSEPTPVYTRPGRTVKLNCMARGIPKADITWELPDKSHLKAG VQARLXGNRPHPGGSLTIQHATQRDAGFYKCMAKNILGSDSKT TYHVF 6430 1946 602 RTRVSTGLRRTLLWSEAVGASSTRGDTGIPGSGGGGAGFGGGG AMLEAMAEPSPBDPPPTLXPBTQPPEKRRTIEDFMKPCSFVLA VAGYIPPSKEESDWPASGSSPLRGBSAADSGWDSAPSDLRTI QTFVKKAKSKRRAAQAGPTQPGPRSTTSRLQAPDSATLLEKM KKUSSLFDLDGPKVASSLSFTSLTHTSRPPAALTPVPLSGGDLS HPPRKKDRKNRKLGPGAGAGFGVLRRPRPTPGDGEKRSRIKKSK KRKLKKAERGDRLPPPGAPPSDTDSEEBEBEBEBEBBEMA TVVGGBAPVPVLPTPPBARPPPATVHPEGVPPAADESKEVGSTE TSQDGDASSEGEMRVMDEDIMVESGDDSWDLITCYCRKPAGR PHIECSLCGTWIHLSCAKIKKTNVPDFFYCQKCKELRPBARRG GPPKSGEP MIECSLCGTWIHLSCAKIKKTNVPDFFYCQKCKELRPBARRG GPPKSGEP 6431 3 605 WNNSSYNLPAYPYLPCEACAMQDGRKGGAYAGKMEATTAGVGR LEEGLRRKERLKALREKTGRKOREDGEPKTKHLREEEEGEKH RELRRNYVPEDEDLKKRRVPQAKPVAVEEKVKEQLEAAKEEPV IEEVDLANLAPRKPDWDLKRDVAKKLEKLKKRTQRAIAELIRER ELGCBLASAVADAATGCKTCDG 6432 56 1692 GGLGTMGSRIKQNPETTFEVYVEVALYPRTGGTLSDFEVQRGFPE DYSOGEVLQTLTKECFFFYVDSLTUSQUGQNFTFVLIDIDSKOR NBELLETLHKLPIEDPDGVSVHLSVHSYPTVPDTRELPSIPENRN LTCYFVANDNINHLHVASMLYBRRILLICSKLSTLTACHGSA AMLYPMYNGHVYIFVLPPHLLDYCCAPMPYLLGHLISLMEVVRN	L			TKELQKLIEADISKRYSGRPVNLMGTSL
NDHKVFYGGLKVDCVATGLPNEIGNSLPDGJLVNSFMGSDDS GGRKRYVVNNMGTLYRNEGGMYEGDYTCFAENQVGKDEMKVR VKVVTAPATIRNKTCLAVQVPYGDVTVTACEAKGEMPKRVTHLS PTMKVIPTSEKYQIYQDGTLLIQKAGGEMGHTVTHLS PTMKVIPTSEKYQIYQDGTLLIQKAGGEMGHTVTHUS DRKTVHIHNVOPPKIMGHPNITTTREIAAGGSRKLIDCKAEG LPTPRVWHAPPEGVVLPAPYYGNRITVHGNGSLDIRSLRKSDSV QLVCMARNEGGEARLIVQLTVLEPMEKPIHPDISEKKTAMAGH TISLNCSAAGTPTPSLVWLIPNSTDLQSGQQLQRFYHKADGMLH ISGLSSVDAGAYRCVARNAAGHTERLVSLKVGLKPEANKQYHNL VSIINGETLKLPCTPPGAGQRFSWTLPNGMHLEGPTIGRVSL LDNGTLIVREASVFDRGTYVCKNETEYGPSVTSIPVIVTAYPPR ITSEPTPVYTYRRGNTYVKLNCMAMGIPKADITWELDDKSHLKAG VQARLYGNRFLHPGGSLTIQHATQRDAGFYKCMAKNILGSDSKT TYHVF 6430 1946 602 RTRVSTGLRTLLWSEAVGASSTRGDTGIPGSGGGAGGGGGG MLEAMAEPSPBDPPTLKPETQPPEKRRTIEDPNKFCSFVLA VAGYIPPSKEESDWPASGSSSPLRGESAADSDGWDSAFSDLRTI QTFVKKAKSSKRRAAQAGFTQFGPPRSTTSRLQAPDSATLLEKM KLKDSLFDLDGFKVASPLSFTSITHTSRPPAALTVPLSCGOLS HPPRKKDKKNRKLGFGAGAGFGVURRPRPTPDGGEKRSRIKKSK KRKLKKAERGDRLPPPGPQAPPSDTDSEEEREBEEBEEMMA TVVGGEAPVPVLFTPFEARPPATVHPEGVPPADSESKEVGSTE TSQDGDASSSECEMRWNDEDINVESGDDSWDLITCYCRKPPAGR PMIECSLCGTWIHLSCAKIKKTNVPDFFYCQKKELRPEARRLG GPPKSGEP MECSLCGTWIHLSCAKIKKTNVPDFFYCQKKELRPEARRLG GPPKSGEP 6431 3 605 WWNSSYNLPAYAPYLPCEACAMQDGRKGGAYAGKMEATTAGVGR RELRRNYVPEDEDLKKRRVPQARFVKAELIKEEEEEGEKH RELRRNYVPEDEDLKKRRVPQARFVKAELELKKRTQRAIAELIRER LKGGSDLSAAVDAATEGKTCDSD 6432 56 1692 GGLGTMGSRIKQNPETTFEVYVEVAYPRTGGTLSDFEVQRCFPE DYSDGEVLQTLTKRCFPFYVUSLVVSQCGNFTFVLTDIDSKGR FGFCLSSGAKSCFCLISLYBMFEVFYKLLNILADYTTKRGENO WNELLETLHKLPIPDBQVSVLLSVHSYFTVPDTRELPSIPENRN LTEYFVAVDVNNMHLIVASMLYERRILICSKLSTLTACHGSA AMLYPMYMOHVIPDIPPLLDYCCAPMPYLLIGHLSLMKVNN	6429	3413	3442	EPSSWTAAPRGPLAAHPLEAAVQEDDRRALSFDSRIKVFANGTL
GGRTKRYVOFNNOTLIPENEGMREEGDYTCFAENOGGKDEMRVR VKVVTAPATIRNTCLAVQPYGDVTVACEAKGEPMPKVTWLS PTNKVIPTSSEKYQIYQDGTLLIOKAQREDSGNYTCLVENSAGE DRKTVWIHVNVQPPKINGMPNPITTVREIAAGGSRKLIDCKAEG IPTPRVLMAPPEGVULPAPYGRRITVHGNGSLDIRSLRKSDSV QLVCMARNEGGEARLIVQLTVLEPMEKPIFHDPISEKTTAMAGH TISLNCSAAGTPTPSLVWVLPNGTDLQSGQOLQRFYHKADGMLH ISGLSSVDAGAYRCVARNAAGHTERLVSLKVGLKPEANKQYHNL VSIINGETLKLPCTPPGAGQGRFSWTLPNGMHLEGPQTTLGRVSL LDNGTLIVKEASYFDRGTYVCRMETEYGFSVTSIPVIVIAYPPR ITSEPTPVYTYTRFGNTVKLNCMAGIPKADITWELPDKSHLKAG VQARLYGNRFLHPQGSLTIQHATQRDAGFYKCMAKNILGSDSKT TYTHVV AMENIAABPEPPBDPPTLKPETQPPEKRRTIEDFNKPCSFVLA YAGYIPPSKEESDWPABGSSSPLRGESAADSGWBSAFSDLRTI QTFVKKAKSSKRRAAQAGFTGPPRSTTFSRLQAPDSATLEKM KLKDSLFDLDGFKVASPLSPTSLTHTSRPPAALTPVPLSQGDLS HPPRKKDRKNRKLGFGAGAGGGVLRRFPPTGOGEKRSRIKKSK KKKLKKAERGBLPPPGSPPPSTFSRLQAPDSSTLEEM TVVGGGAPVPVLDTPPBAPRPPATVHPEGVPPADSESKEVGSTE TSQDGASSSEGEMRVMDEDIMVESGDDSWDLITCYCRKPFAGR PMIECSLCGTWTHLSCAKIKKTNVPDFFFYCQKCKELRPEARRLG GPPKSGEP 4431 3 605 WWNSSYNLPAYAPYLPCEACAMQDGRKGGAYAGKMEATTAGVGR LEEEALRRKERLKALREKTGRKDKEDGEPKYKHLREEEEGGEKH RELIRINVYPFDEDLLKKRVPQAKPVAVEEKVKEQLEAAKPEPV IEEVDLANLAPRKPDWDLKRDVAKKLKKTTGRALELIRER LKGGEDSLASAVDAATEGKTOSD 6432 56 1692 GGLGTMGSRIKQNPETTFEVYVEVAYPRTGGTLSDPEVQRGFPE DYSDQSVLGTLTKFCFPFYVDSLTVSQCGNFTFVLTDIDSKOR FGFCRLSSGAKSCCTLSTLYBWFEVFYKLDNI LDAYTYKRGENO WNELLETLHKLPIPDPGDGVVKLSVHSYFTVDDTRELPSIPENRN LTEYFVAVDVNNMLLLYASMLYERRILICSKLSTLTACHGSA AMLYPMYMOHVYIPVLPPHLLDYCCARPMPYLLIGHLSLEMKVNN	ļ			VVKSVTDKDAGDYLCVARNKVGDDYVVLKVDVVMKPAKIEHKEE
VKVVTAPATIRNKTCLAVQVPYEDDVTVACEAKGEMPKVTULS PTIKVI PTSSEKYQI YQDGTLLIQKAQRSDSGNYTCLVRNSAGE DRITVUHIVNVQPK KINGNPHPITVREIAAGGSRKLIDCKAEG IPTPRVLWAPPEGVVLPAPYYGNRI TVIGNGSLDIRSLRKSDSV QLUCMARNEGGEARLIVQLTVLPPMEKP IFHDPI SEKTTAMAGH TISLNCSAAGTPTSLWVLPNGTDLQSGQQLQRPYHKADGMLH ISGLSSVDAGAYRCVARNAAGHTERLVSLKVGLKPEANKQYHINL VSIINGETLKLPCTPPGAGQGFSWTLPNGMHLEGPOTLGRVSL LDNGTLIVREASVPDRGTYVCRMETEYGPSVTSIPVIVIAYPPR ITSEPTPVIYTRPGNTVKLNCMANGI PKADITWELPDKSHLKAG VQARLYGNRPLHPQGSLTIQHATQDAGFYKCMAKNILGSDSKT TYIHVF 6430 1946 602 RTRVSTGLRRTLLWSEAVGASTRGDTGI PGSGEGGAGFGGGE AMLEAMAEPSPEDP PPTLKPETQPPEKRRTIEBFNKYCSFVLA YAGYI PPSKEESDWPASGSSPLRGESAADSDGMDSASPDLRTI OTFVKKAKSSKRRAAQAGPTQPGPPRSTFSRLQAPDSATLLEKM KLKDSLFDLDGPKVASFLSFTSILTTSPPAALTPVPLSQGDLS HPPRKXDRNNKLGPGAGAGFGVLRRPRPTFGDGEKKRSI KKSK KRLKKAERGDRLPPGPPDAPPDAPPDTDSEEEEBEEBEEBEBEMA TVVGGEAPVPVLPTPPEARPPPATVHEGVPPADGSEKEVGSTE TSQDGDASSSECEMRWMDEDI MVESGDDSWDLITCYCRKPPAGR PMIECSLCGTWIHLSCAKIKKTNVPDFFYCQKCKELRPEARRLG GPPKSGEP MMESSYNLPAYAPYLFCEACAMODGRKGGAYAGKMEATTAGVGR MSSYNLPAYAPYLFCEACAMODGRKGGAYAGKMEATTAGVGR LEEEALRRKERLKALREKTGRKDKEDGEPKTKHLREEEEBGEKH RELRLRNTVPEDEDLKKRRVPQAKPKVKRTQRAFAELIRER LKGQEDSLASAVDAATEQKTCDSD 6431 3 605 WMNSSYNLPRKPDWDDLKKKRVPQAKPKVKRTQRATAELIRER LKGQEDSLASAVDAATEQKTCDSD GGLGTMGSRIKONPETTFEVYVEVAYPRTGGTLSDFEVQRCFPB DYSDGEVIQTLTKFCFPFFYVDSLTVSQVGQNFTFVLTDLDSKOR FGFCRLSSGAKSCFCILSYLPWFEVFYKLINILADYTTKRQENQ WNELLETLHKLPIPDDGVSVHLSVHSYPTVPDTRELPSIPENN LTEYFVAVVDVNNMLHLVASMLSVRSTILICSKLSTLTACLINGSA AMLYPMYWONVYIPVLPPHLLDYCCAPMPYLTGIHLSCHEKSA				NDHKVFYGGDLKVDCVATGLPNPEISWSLPDGSLVNSFMQSDDS
PTNKV1PTSSEKYQ1YQDGTLLIQKAQRSDGMYTCLVRNSAGE DRKTVWHYNVNOPPKINGNPHPITTVREIAAGGSRKLIDCKAEG IPTPRVLWAPPEGVVLPAPYYGNRITVHEIAAGGSRKLIDCKAEG IPTPRVLWAPPEGVVLPAPYYGNRITVHENGSLDIRSLRKSDSV QLVCMARNEGGEARLIVQLTVLEPMEKPIFHDP1SEKTTAMAGH TISLNCSAAGTPTPSLWVLPNCTDLQGQQLQRFYHKADGMLH ISGLSSVDAGAYRCVARNAAGHTERLVSLKVGLKYEANKQYHNL VSIINGETLKLPCTPPGAGQGRFSWTLPNGHHLEGPOTLGRVSL LDMGTLTVREASVPDRGTYVCRETEYGPSVTSIPVIVIAYPPR ITSEPTPVIYTRPGNTVKLKCMANGIPKADITWELPDKSHLKAG VQARLYGNRFLHPQGSLTIQHATQRDAGFYKCMAKNILGSDSKT TYTHVF 6430 1946 602 RTRVSTGLRRTLLWSEAVGASSTRGDTGIPGSGEGGAGPGGGEG AMLEANAEPSPBDPPPTLKPETQPPEKRRRTIEDFNKRCSFVLA YAGYIPPSKEESDWPASGSSSPLRGESAADSDGWDSAPSDLRTI QTFVKKAKSSKRRAAQAGFTQPGPPRSTTSRLQAPDSATLLEKM KLKDSLFDLDGFKVASFLSFTSILHTSRPPAALTPVPLSQGDLS HPPRKKDRINRLIGPGAGAGFVLRRPRPTTPGDGEKRSRIKKSK KRLKKAERGDRLPPRGPQAAPSDTDSEEEBEEBEEBEEBEMEMA TVVGGEAPVPVLDTTPEARPRPATVHFGGVPPADSESKEVGSTE TSQGDASSSEGEMRVMDEDIMVESGDDSWDLITCYCRKPFAGR PMIECSLCGTWIHLSCAKIKKTNVPDFFYCQKCKELRPEARRLG GPPKSGEP WNNSSYNLPAYAPYLPCEACAMQDGRKGGAYAGKMEATTAGVGR LEEBALRRKERLKALREKTGRKDKEDGEPKTKHLREEEEGGEKH BELRLRNYVPEDEDLKKRRVPQAKPVAVEEKVKEQLEAAKPEPV IEEVDLANLAPRKPDWDLKRDVAKKLEKLKKTQRIAELIRER LKGQEDSLASAVDAATEGKTCDSD 6431 3 605 GGLGTMGGRIKGNPETTFEVYVEVAYRTGGTLSDPEVQRGPFE DYSDGEVIQTLTKFCFFFFYVDSLTVSQVGQNFTFTUTDIDISKGR FGFCRLSSGAKSCFCILSYLPWFEVFYKLINILADDTTRQENG WNELLETLHKLPIPDPGVSVHLSVHSYPTVPDTRELPSIPENRN LTEYFVAVOVNNMLHLYASMLYSRRILICSKLISTLTACIHGSA AMLYPMYWOHVYIPVLPPHLLDYCCAPMPYLIGHHSIEKKEKKERK	1	·		GGRTKRYVVFNNGTLYFNEVGMREEGDYTCFAENQVGKDEMRVR
DRRTVWHYNVQPPKINGNPHPITTVREIAAGGSRKLIDCKAEG IPTPRVLMAPPEGVVLPAPYYGNRITVHGNGSLDIRSLRXSDSV QLVCMARNEGEARLIVQLTVLEPMEKPIFHDPISEKTTAMAGH TISLNCSAAGTPTPSLWWVLPNGTDLQSGQQLQRPYHKADGMLH ISGLSSVDAGAYRCVARNAAGHTERLVSLKVGLKPEANKQYHNL VSIINGETLKLPCTPPGAGGGRFSWTLPNGMHEBGPOTUGRYSL LDNGTLTVREASVPDRGTYVCRMTEYGPSVTSIPVIVIAYPPR ITSEPTPVIYTRPGNTVKLNCMAGIFKADLTWELPDKSHLKAG VQARLYGNRFLHPQGSLTIQHATQRDAGFYKCMAKNILGSDSKT TYTHVF 6430 1946 602 RTRVSTGLRRTLLWSEAVGASSTRGDTGIPGSGEGGAGPGGGEG AMLEANAEPSPEDPPPTLKPETQPPEKRRRTIEDFNKPCSFVLA YAGYIPPSKEESDWPASGSSSPLRGESAADSDGWDSAFSDLRTI QTFVKKAKSSKRRAAQAGPTQPGPPRSTFSRLQAPDGATLLEKM KLKDSLFPLLDGPKVASPLSTSITHTSRPPAALTPVPLSQGDLS HPPRKKDRNRKLGPGAGAGFGVLRRPRPTTGDGEKRSRIKKSK KKKLKKAERGDRLPPPGAPPSDTDSEEEEBEBEEBBERMA TVVGGEAPVPULPTPPBAPPPAAVHPEGVPPADLSESKEVGSTE TSQDGDASSSEGEMRWNDEDIMVESGDDSWDLTTCYCRKPFAGR PMIECSLCGTWIHLSCAKIKKTNVPDFFYCQKCKELRPEARRLG GPPKSGEP MIECSLCGTWIHLSCAKIKKTNVPDFFYCQKCKELRPEARRLG GPPKSGEP MIECSLCGTWIHLSCAKIKKTNVPDFFYCQKCKELRPEARRLG GPPKSGEP LEEELARRVERLKALREKTGRKDKEDGEPKTKHLREEEEEGEKH RELRRLNVPEDEDLKKRRVPQAKFVAVEKVKGQEAAAKPEPV IEEVDLANLLAPKRPDWDLKRDVAKKLEKLKKRTQRAIAELIRER LKGQEDSLASAVDAATEQKTCDSD 6432 56 1692 GGLGTMGGRIKQNPETTFEVYVEVAYPRTGGTLSDPEVQRGFPE DYSDQEVLQTLTKFCFPFYVDSLTVSQVGQNFTFVLTDLDSKQR FGFCRLSSGAKSCFCILSYLPWFEVFYKLINILADYTTKRQENQ WNELLETLHKLPIPDPGVSVHLSVHSYPTVPDTRELPSIPENN LTEYFVAVVDVNNMLHLVASMLYERRILIICSKLSTLTACHGSA AMLYPMYWQHVYIPVLPPHLLDYCCAPMPYLIGIHLSLMEKVRN	1			VKVVTAPATIRNKTCLAVQVPYGDVVTVACEAKGEPMPKVTWLS
IPTPRVLMAPPEGVVLPAPYYCNRITVHGNOSLDIRSLRKSDSV QLVCMARNEGGEARLIVQLTVLEPMEKPIFHDPISEKITANAGH TISLNCSAAGTPTPSLVWVLPNGTDLQSGQQLQRFYHKADGMLH ISGLSSVDAGAYRCVARNAAGHTERLVSLKVGLKPEANKQYHNL VSIINGETLKLPCTPPGAGQGRFWTLPNGMHLEGPOTLGRVSL LDNGTLTVREASVFPRGTVVCRMETEYGPSVTSIPVIVIAYPPR ITSEPTPVIYTRPGNTVKLNCMAMGIPKADITMELPPKSHLKAG VQARLYGNRFLHPQGSLTIQHATQRDAGFYKCMAKNILGSDSKT TYTHVF 6430 1946 602 RTRVSTGLRRTLLWSEAVGASSTRÖDTGIPGSGEGGAGPGGGEG AMLEAMAEPSPBDPPPTLKPETQPPEKRRTIEDFNKFCSFVLA YAGYIPPSKESDWPASGSSSPLRGESAADSDGWDSAPSDLRTI QTFVKKAKSSKRRAAQAGPTQPBPPRSTFSRLQAPDSATLLEKM KLKDSLFDLDGPKVASPLSPTSLTHTSRPPAALTPVPLSQGDLS HPPRKKDRKNRKLGPGAGAGFGVLRPRPTPGGGEKRSRIKKSK KRKLKKAERGDRLPPPGPQAPPSDTDSEEBEBEEBEBEMA TVVGGEAPVPVLPTPPBAPRPTATVHPEGVPPADSESKEVGSTE TSQDGDASSSEGEMRVMDEDIMVESGDDSWDLITCYCRKPFAGR PMIECSLCGTWIHLSCAKIKKTNVPDFFYCQKCKELRPEARRLG GPPKSGEP 6431 3 605 WWNSSYNLPAYAPYLPCEACAMQDGRKGGAYAGKMEATTAGVGR LEEBALRRKERLKALREKTGRKDEEDGEPKTHLREEEEBGEKH RELRLRNYVPEDBEDLKKRRVPQAKPVAVEEKVKEQLEAAKPBPV IEEVDLANLAPRKPDWDLKRDVAKKLEKLKKRTQRAIAELIRER LKGQEDSLASAVDAATEQKTODSD GGLGTMGSRIKQNPETTFEYVVEAYPRTGGTLSDFEVQROFFE DYSDGEVLQTLTKFCFPFYVDSLTVSQVGQNFTFFVLTDIDSKQR FGFCRLSSGAKSCFCILSYLPWFEVFYKLLNILADYTTKRQENQ WNELLETLHKLPIPDPGVSVHLSVHSYPTVPDTRELPSIPENRN LTEYPVAVDVNNMLHLYASMLYERRILICSKLSTLTACHGSA AMLYPMYNQHVVIPPLPPHLDYCCAPMPYLIGHHLSLMEKVRN	1			PTNKVIPTSSEKYQIYQDGTLLIQKAQRSDSGNYTCLVRNSAGE
QLVCMARNEGGEARLIVQLTVLEPMEKPIFHDFISEKITAMAGH TISLNCSAAGTPTPSLVWLPNGTDLQSGQQLQRFYHKAGMIH ISGLSSVDAGAYRCVARNAAGHTERLVSLKVGLKPEANKQYHNL VSIINGETLKLDCTPPGAGQGRFSWTLPNGMHLEGPQTLGRVSL LDNGTLTVREASVFDRGTYVCKMETPYGPSVTSIPVIVIAYPPR ITSEPTPVIYTRPGNTVKINCMAMGIPKADITMELPDKSHLKAG VQARLYGNRPLHPQGSLTIQHATQRDAGFYKCMAKNILGSDSKT TYTHVF 6430 1946 602 RTRVSTGLRRTLLWSEAVGASSTRGDTGIPGSGEGGAGPGGGG AMLEAMAEPSPEDPPPTLKPETQPPEKRRTIEDFNKFCGFVLA YAGYIPPSKEESDWPASGSSSPLRGBSAADSDGWDSAPSDLRTI QTFVKKAKSSKRRAAQAGPTQFGPPRSTFSRLQAPDSATLLEKM KLKDSLFDLDGPKVASFLSFTSLITHTSRPPAALTPVPLSQGDLS HPPRKKDRKNRKLGPGAGAGGVQVLRPRPTPTPGGGEKRSRIKKSK KRKLKKAERGDRLPPPGPPQAPPSDTDGSEEREEBEEBEEMEMA TVVGGEAPVPVLPTPPEAPRPATVHPEGVPPADSSKEVGSTE TSQDGDASSSEGEMRVMDEDIMVESGDDSWDLITCYCRKPFAGR PMIECSLCCTWIHLSCAKIKKTNVPDFFYCQKCKELRPEARRLG GPPKSGEP MIECSLCCTWIHLSCAKIKKTNVPDFFYCQKCKELRPEARRLG GPPKSGEP LEEEALRRKERLKALREKTGRKDEEDGEPKTHLREEEEEGEKH RELRLRNYVPEDEDLKKRRVPQAKFVAVEEKVKEQLEAAKPEPV IEEVDLANLAPRKPDWDLKRDVAKKLEKLKKRTQRAIAELIRER LKGQEDSLASAVDAATEQKTCDSD GGLGTMGSRIKONPETTFEVYVEVAYPRTGGTLSDFEVQROFFE DYSDGEVLGTLTKFCFFYVDSLTVSQVGQNFTFVLTDIDSKQR FGFCRLSSGAKSCFCILSYLPWFEVFYKLLMILADYTTKRQENQ WNELLETLHKLPIPDPGVSVHLSVHSYPTVPDTRELPSIPENRN LTEYFVAVDVNNMLHLYASMLYERRILICSKLSTLTACHGSA AMLYPMYNQHVVIPPLPPHLLDYCCAPMPYLIGHILSLMEKVRN				DRKTVWIHVNVQPPKINGNPNPITTVREIAAGGSRKLIDCKAEG
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ISGLSSVDAGAYRCVARNAAGHTERLUSLKVGLKPEANKQYHNL VSIINGETLKLPCTPPGAGQGRFSWTLPNGMHLEGPQTLGRVSL LDNGTLTVREASYPDRGTYVCRMETEYGPSVTSIPVIVIAYPPR ITSEPTPVIYTRPGNTVKLNCMAMGIPKADITWELPDKSHLKAG VQARLYGNRPLHPQGSLTIQHATQRDAGFYKCMAKNILGSDSKT TYIHVF 6430 1946 602 RTRVSTGLRRTLLWSEAVGASSTRGDTGIPGSGEGGAGPGGGEG AMLEAMAEPSPEDPPPTLKPETQPPEKRRRTIEDPNKFCSFVLA YAGYIPPSKEESDWPASGSSSPLRGESAADSDGWDSAPSDLRTI QTFVKKAKSSKRRAAQAGPTQPBPRSTFSRLQAPDSATLLEKM KLKDSLFDLDGFKVASPLSTTSLTHTSRPPAALTPVPLSQGDLS HPPRKKDRKNRKLGPGAGAGFYGVLRRPRPTPGDGEKRSRIKKSK KRKLKKAERGDRLPPPGDPQAPPSDTDSEEEEEBEBEEBEMA TVVGGEAPVPVLPTPPEAPRPPATVHPEGVPPADSESKEVGSTE TSQDGDASSESGEMRVMDEDIMVESGDDSWDLITCYCRKPFAGR PMIECSLCGTWIHLSCAKIKKTNVPDFFYCQKCKELRPEARRLG GPPKSGEP 6431 3 605 WWNSSYNLPAYAPYLPCEACAMQDGRKGGAYAGKMEATTAGVGR LEEEALRRKERLKALREKTGRKDKEDGEPKTKHLREEEEEGEKH RELRLRNYVPEDEDLKKRRVPQARPVAVEEKVKEQLEAAKPBFV IEEVDLANLAPRKPDWDLKRDVAVKLEKLKKRTQRAIAELIRER LKGGEDSLASAVDAATEQKTCDSD DYSDQEVLGTLTKFCFPFFVDSLTVSQVGQNFTFVLTDIDGKQR FGFCRLSSGAKSCFCILSYLPWFEVFYKLLNILADYTTKRQENQ WNELLETLHKLPIPDPGGSVHLSVHSYFTVPDTRELPSIPENRN LTEYPVAVDVNNMLHLYASMLYERRILICSKLSTLTACHGSA AMLYPMYWOHVYIPVLPPHLDVCCAPMPYLIGIHLSLMEKVRN	1			QLVCMARNEGGEARLIVQLTVLEPMEKPIFHDPISEKITAMAGH
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RELRLRNYVPEDEDLKKRRVPQAKPVAVEEKVKEQLEAAKPEPV IEEVDLANLAPRKPPWDLKRDVAKKLEKLKKRTQRAIAELIRER LKGQEDSLASAVDAATEQKTCDSD 6432 56 1692 GGLGTMGSRIKQNPETTFEVYVEVAYPRTGGTLSDPEVQRQFPE DYSDQEVLQTLTKFCFPFYVDSLTVSQVGQNFTFVLTDIDSKQR FGFCRLSSGAKSCFCILSYLPWFEVFYKLLNILADYTTKRQENQ WNELLETLHKLPIPDPGVSVHLSVHSYFTVPDTRELPSIPENRN LTEYFVAVDVNNMLHLYASMLYERRILIICSKLSTLTACHGSA AMLYPMYWQHVYIPVLPPHLLDYCCAPMPYLIGHLSLMEKVRN		1		LEEEALRRKERLKALREKTGRKDKEDGEPKTKHLREEEEEGEKH
IEEVDLANLAPRKPDWDLKRDVAKKLEKLKKRTQRAIAELIRER LKGQEDSLASAVDAATEQKTCDSD GGLGTMGSRIKQNPETTFEVYVEVAYPRTGGTLSDPEVQRQFPE DYSDQEVLQTLTKFCFPFYVDSLTVSQVGQNFTFVLTDIDSKQR FGFCRLSSGAKSCFCILSYLPWFEVFYKLLNILADYTTKQENQ WNELLETLHKLPIPDPGVSVHLSVHSYFTVPDTRELPSIPENRN LTEYFVAVDVNNNLHLYASMLVERRILIICSKLSTLTACHGSA AMLYPMYWQHVYIPVLPPHLLDYCCAPMPYLIGHLSLMEKVRN		l		RELRLRNYVPEDEDLKKRRVPQAKPVAVEEKVKEOLEAAKPEPV
LKGQEDSLASAVDAATEQKTCDSD 6432 56 1692 GGLGTMGSRIKQNPETTFEVYVEVAYPRTGGTLSDPEVQRQFPE DYSDQEVLQTLTKFCFPFYVDSLTVSQVGQNFTFVLTDIDSKQR FGFCRLSSGAKSCFCILSYLPWFEVFYKLLNILADYTTKRQENQ WNELLETLHKLPIPDPGVSVHLSVHSYFTVPDTRELPSIPENRN LTEYFVAVDVNNNLHLYASMLYERRILIICSKLSTLTACHGSA AMLYPMYWQHVYIPVLPPHLLDYCCAPMPYLIGHLSLMEKVRN	į į			IEEVDLANLAPRKPDWDLKRDVAKKLEKLKKRTORAIAELIRER
GGLGTMGSRIKQNPETTFEVYVEVAYPRTGGTLSDPEVQRQFPE DYSDQEVLQTLTKFCFPFYVDSLTVSQVGQNFTFVLTDIDSKQR FGFCRLSSGAKSCFCILSYLDWFEVFYKLLNILADYTTKRQENQ WNELLETLHKLPIPDPGVSVHLSVHSYFTVPDTRELPSIPENRN LTEYFVAVDVNNNLHLYASMLYERRILIICSKLSTLTACIHGSA AMLYPMYWQHVYIPVLPPHLLDYCCAPMPYLJIGIHLSLMEKVRN	 _			LKGQEDSLASAVDAATEQKTCDSD
DYSDQEVLQTLTKFCFPFYVDSLTVSQVGQNFTFVLTDIDSKQR FGFCRLSSGAKSGFCILSYLDWFEVFYKLINILADYTTKRQENQ WNELLETLHKLPIPDPGVSVHLSVHSYFTVPDTRELPSIPENRN LTEYFVAVDVNNMLHLYASMLYERRILIICSKLSTLTACHGSA AMLYPMYWQHVYIPVLPPHLLDYCCAPMPYLIGHLSLMEKVRN	6432	56	1692	GGLGTMGSRIKQNPETTFEVYVEVAYPRTGGTLSDPEVOROFPE
FGFCRLSSGAKSCFCILSYLPWFEVFYKLLNILADYTTKRQENQ WNELLETLHKLPIPDPGVSVHLSVHSYFTVPDTRELPSIPENRN LTEYFVAVDVNNMLHLYASMLYERRILIICSKLSTLTACIHGSA AMLYPMYWQHVYIPVLPPHLLDYCCAPMPYLIGIHLSLMEKVRN			ł	DYSDQEVLQTLTKFCFPFYVDSLTVSQVGQNFTFVLTDIDSKOR
WNELLETLHKLPIPDPGVSVHLSVHSYFTVPDTRELPSIPENRN LTEYFVAVDVNNMLHLYASMLYERRILIICSKLSTLTACIHGSA AMLYPMYWQHVYIPVLPPHLLDYCCAPMPYLIGIHLSLMEKVRN	<u> </u>	į		FGFCRLSSGAKSCFCILSYLPWFEVFYKLLNILADYTTKRQENO
LTEYPVAVDVNNMLHLYASMLYERRILIICSKLSTLTACIHGSA AMLYPMYWQHVYIPVLPPHLLDYCCAPMPYLIGIHLSLMEKVRN				WNELLETLHKLPIPDPGVSVHLSVHSYFTVPDTRELPSIPENRN
AMLYPMYWQHVYIPVLPPHLLDYCCAPMPYLIGIHLSLMEKVRN			ł	LTEYFVAVDVNNMLHLYASMLYERRILIICSKLSTLTACIHGSA
MALDDVVILNVDTNTLETPFDDLQSLPNDVISSLKNRLKKVSTT			ŀ	AMLYPMYWQHVYIPVLPPHLLDYCCAPMPYLIGIHLSLMEKVRN
				MALDDVVILNVDTNTLETPFDDLQSLPNDVISSLKNRLKKVSTT

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ı	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ľ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
<u></u>	sequence	_	\=possible nucleotide insertion)
			TGDGVARAFLKAQAAFFGSYRNALKIEPEBPITFCEBAFVSHYR
:			SGAMRQFLQNATQLQLFKQFIDGRLDLLNSGEGFSDVPEEEINM
ı		i	GBYAGSDKLYHQWLSTVRKGSGAILNTVKTKANPAMKTVYKFDI
1			AENGCAPTPEEQLPKTAPSPLVEAKDPKLREDRRPITVHFCOVP
j		•	PPRPHVVKRPKSNIAVEGRRTSVPSPEQNTIATPATLHILQKSI
			THFAAKFPTRGWTSSSH
6433	1524	484	APVTKRKEVFAKDSKGSALDAGRDPKRPALPETLCESGWASNTA
j			PTTPPQPGWCLCGKDPKSSCQTPGREKERRLATMHGSCSFLMLL
Ì	ļ		LPLLLLVATTGPVGALTDEEKRLMVELHNLYRAOVSPTASDML
Į			HMRWDEELAAFAKAYARQCVWGHNKERGRRGENLFAITDEGMDV
ı	1		PLAMEEWHHEREHYNLSAATCSPGQMCGHYTQVVWAKTERIGCG
			SHFCEKLQGVEETNIELLVCNYEPPGNVKGKRPYQEGTPCSQCP
1			SGYHCKNSLCEPIGSPEDAQDLPYLVTEAPSFRATEASDSRKMG
6434	40	2002	AEGPDKPSVVSGLNSGPGHVWGPLLGLLLLPPLVLAGIF
	''	2002	MPQLNFGMADPTQMGGLSMLLLAGEHALGTPEVFSGTCRPDVSE
1			SPELRQKSPLFQFAEISSSTSHSDASTKQCQTSALFQFAEISSN
	ł l	·	TSQLGGAEPVKRCGKSALFQLAEMCLASEGMKMEESKLIKAKES DGGRIKBLEKGKEEKEIKMEKTDETRLQKEABFEKSAKENLRDS
			KELRNFEALQIDDIMAIKMEDPKEIRKEELEEDHKCSHPPDFSY
			SASSKIIISDVPSRKDHMCHPHGIMIIEDPAALNKPEKLKKKKK
			KSKMDRHGNDKSTPKKTCKKRQSSESDIESVIYTIEAVAKGDWG
			IEKLGDTPRKKVRTSSSGKGSILDAKPPKKKVKSREKKMSKEKS
1			SDTTKESRPPDFISISASKNISGETPEGIKAEPLTPMEDALPDS
1			LSGQAKPEDSDCHRKIETCGSRKSERSCKGALYKTLVSEGMLTS
1	1		LRANVDRGKRSSGKGNSSDHEGCWNEESWTFSOSGTSGSKKPKK
1			TKPKEDCLLGSAKLDEEFBKKFNSLPQYSPVTFDRKCVPVPRKK
}			KKTGNVSSEPTKTSKGSGDXWSNKQLFLDAIHPTEAIFSEDRNT
	ł		MEPVHKVKNIPSIFNTPEPTTTARTFGGQPKEKSKENPDYSPCQ
6435	2227	657	DTQRAGYHHEEVLWMTNLMNNCGGVYLKQLRHTAMTNA
	/	937	ALQRDAAAAYAHPEYEERFLQEETVSQQINSIELLQTRPLALPE
1			VVKSQRPLQRQVHLRGRPASQPTVIRGITYYKAKVSEEENDIEE
	İ		QQDEFFSGDNGVDLLIEDQLLRHNGLMTSVTRRPAATRQGHSTA VTSDLNARTAPWSSALPQPSTSDPSIANHASVGPTLQTTSVSPD
1	i		PTRESVLQPSPQVPATTVAHTATQQPAAPAPPAVSPREALMEAM
1			HTVPVPPTTVRTDSLGKDAPAGRGTTPASPTLSPEBEDDIRNVI
1 1			GRCKDTLSTITGPTTQNTYGRNEGAWMKDPLAKDERIYVTNYYY
1			GNTLVEFRNLENFKQGRWSNSYKLPYSWIGTGHVVYNGAFYYNR
1 1			AFTRNIIKYDLKQRYVAAWAMLHDVAYEEATPWRWQGHSDVDFA
			VDENGLWLIYPALDDEGFSQEVIVLSKLNAADLSTOKETTWRTG
] [1		LRRNFYGNCFVICGVLYAVDSYNORNANISYAFDTHTNTOIUPR
			LLFENEYFYTTQIDYNPKDRLLYAWDNGHOVTYHVIFAY
6436	1295	341	GACRPPVRQDPDSGPDYEALPAGATVTTHMVAGAVAGILEHCVM
	Ĭ	[YPIDCVKTRMQSLQPDPAARYRNVLEALWRIIRTEGLWRPMPGT.
	1	ĺ	NVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANGAAGC
	t		VATLLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVWQNEGAG
[]	ł	1	AFYRSYTTQLTMNVPFQAIHFMTYEFLQBHFNPORRYNPSSHVI.
	ļ		SGACAGAVAAAATTPLDVCKTLLNTQESLALNSHITGHITGMAS
		J	AFRTVYQVGGVTAYFRGVQARVIYQIPSTAIAWSVYEFFKYLIT
6437	1828	360 .	KRQEEWRAGK
	0	360 .	PPAPAPPASPARHVTRTARGHLEGGSRAPPLLQAVFLQIKNMVK
			LIHTLADHGDDVNCCAFSFSLLATCSLDKTIRLYSLRDFTELPH
			SPLKFHTYAVHCCCFSPSGHILASCSTDGTTVLWNTENGQMLAV
	ļ	1	MEQPSGSPVRVCQFSPDSTCLASGAADGTVVLWNAQSYKLYRCG SVKDGSLAACAFSPNGSFFVTGSSCGDLTVWDDKMRCLESEKAH
			DLGITCCDFSSQPVSDGEQGLQFFRLASCGQDCQVKIWIVSFTH
		1	ILGFELKYKSTLSGHCAPVLACAPSHDGQMLVSGSVDKSVIVYD
			OIA 1 A PURCHE SUPPRING A SUPPRINCE OF A SUPPRINCE

SEO	Predicted	Predicted end	Lamino colid communication
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ŀ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
			THIENILHTLIQHTRYVTTCAFAPHTLLLATGSMDKTVNIWQFD
	}		LETLCQARSTEHQLKQFTEDWSEEDVSTWLCAQDLKDLVGIFKM
i			NNIDGKELLNLTKESLADDLKIESLGLRSKVLRKIEELRTKVKS
1			LSSGIPDEFICPITRELMKDPVIASDGYSYEKEAMENWDPAKRN
			RTSPP
6438	109	901	
į.		501	EVQILRAKMPQTGGLIVFYGLLAQTMAQFGGLPVPLDQTLPLNV
}		·	NPALPLSPTGLAGSLTNALSNGLLSGGLLGILENLPLLDILKPG
1 1			GGTSGGLLGGLLGKVTSVIPGLNNIIDIKVTDPQLLELGLVQSP
1			DGHRLYVTIPLGIKLQVNTPLVGASLLRLAVKLDITAEILAVRD
1			KQERIHLVLGDCTHSPGSLQISLLDGLGPLPIQGLLDSLTGILN
6439	23	412	KVLPELVQGNVCPLVNEVLRGLDITLVHDIVNMLIHGLQFVIKV
' ' '		114	SIQTASAITTEMASQSQGIQQLLQAEKRAAEKVADARKRKARRL
1.			KQAKEEAQMEVEQYRREREHEFQSKQQAAMGSQGNLSAEVEQAT
6440	3	517	RRQVQGMQSSQQRNRERVLAQLLGMVCDVRPQVHPNYRISA
1		317	RARWINSDMGDLPGLVRLSIALRIQPNDGPVFYKVDGQRFGQNRT
1 1		•	IKLLTGSSYKVEVKIKPSTLQVENISIGGVLVPLELKSKEPDGD
			RVVYTGTYDTEGVTPTKSGERQPIQITMPFTDIGTFETVWQVKF
6441	234	1373	YNYHKRDHCQWGSPFSVIEYECKPNETRSLMWVNKESFL
	251	13/3	KSGGLRRRQRPGRSAAVGEEELPPGMEKFKAAMLLGSVGDALGY
			RNVCKENSTVGMKIQEELQRSGGLDHLVLSPGEWPVSDNTIMHI
1 1			ATABALTTDYWCLDDLYREMVRCYVEIVEKLPERRPDPATIEGC
			AOLKPNNYLLAWHTPFNEKGSGFGAATKAMCIGLRYWKPERLET
1 1			LIEVSVECGRMTHNHPTGFLGSLCTALFVSFAAQGKPLVQWGRD
1 1	j		MLRAVPLAEEYCRKTIRHTAEYQEHWFYFEAKWQFYLEERKISK
1 :	Ĭ		DSENKAIFPDNYDAEEREKTYRKWSSEGRGGRRGHDAPMIAYDA
! !			LLAAGNSWTELCHRAMFHGGESAATGTIAGCLFGLLYGLDLVPK
6442	34	796	GLYQDLEDKEKLEDLGAALYRLSTBEK
		750	AEDPAGGLAGQDTMFARGLKRKCVGHBEDVEGALAGLKTVSSYS
1	· ·		LORQSLLDMSLVKLQLCHMLVEPNLCRSVLIANTVRQIQEEMTQ
1 1			DGTWRTVAPQAAERAPLDRLVSTEILCRAAWGQEGAHPASGLGD
1 1	İ	·	GHTQGPVSDLCPVTSAQAPRHLQSSAWEMDGPRENRGSFHKSLD
1 1		i	QIFETLETKNPSCMEELFSDVDSPYYDLDTVLTGMMGGARPGPC
6443	2	555	EGLEGLAPATFGPSSSCKSDLGELDHVVEILVET
1	-	333	MASPAASSVRPPRPKKEPQTLVIPKNAAEEQKLKLERLMKNPDK
1 1			AVPIPEKMSEWAPRPPPEFVRDVMGSSAGAGSGEFHVYRHLRRR
] [BYQRQDYMDAMAEKQKLDAEFQKRLEKNKIAAEEQTAKRRKKRQ
1			KLKEKKLLAKKMKLEQKKQEGPGQPKEQGSSSSAFASGTEEEEE VPSFTMGR
6444	390	899	
1		0,79	GSTPRGKMRAPIPEPKPGDLIEIFRPFYRHWAIYVGDGYVVHLA
	1.	1	PPSEVAGAGAASVMSALTDKAIVKKELLYDVAGSDKYQVNNKHD
	İ		DKYSPLPCSKIIQRAEELVGQEVLYKLTSENCEHFVNBLRYGVA
6445	2	753	RSDQVRDVIIAASVAGMGLAAMSLIGVMFSRNKRQKQ
	-	133	AGAAGAAGAARSPRPQAHTKGVRGLPSRRRSPDCGRMELAAGSF
1		1	SEEQFWEACAELQQPALAGADWQLLVETSGISIYRLLDKKTGLY
]]		}	BYKVFGVLEDCSPTLLADIYMDSDYRKQWDQYVKELYEQECNGE
]	1		TVVYWEVKYPFPMSNRDYVYLRQRRDLDMEGRKIHVILARSTSM
l f		•	PQLGERSGVIRVKQYKQSLAIESDGKKGSKVFMYYFDNPGGQIP
6446	1	1651	SWLINWAAKNGVPNFLKDMARACQNYLKKT
	-		RCPTRSPPPDTPGSRGTTAMCSLASGATGGRGAVENREDLPELS
	·		DSGDEAAWEDEDDADLPHGKQQTPCLFCNRLFTSAEETFSHCKS
i i	i i		EHQFNIDSMVHKHGLEFYGYIKLINFIRLKNPTVEYMNSIYNPV
1		1	
		1	PWEKEEYLKPVLEDDLLLQFDVEDLYEPVSVPFSYPNGLSENTS
			VVEKLKHMEARALSAEAALARAREDLOKMKOFAODFVMHTDVRT
			PWEKEEYLKPVLEDDLLLQFDVEDLYEPVSVPFSYPNGLSENTS VVEKLKHMEARALSAEAALARAREDLQKMKQFAQDFVMHTDVRT CSSSTSVIADLQEDEDGVYFSSYGHYGIHEEMLKDKIRTESYRD FIYQNPHIFKDKVVLDVGCGTGILSMFAAKAGAKKVLGVDQSEI

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ĺ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ł	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown *-Ston
1	amino acid	sequence	Codon, /=possible nucleotide deletion
	sequence		\=possible nucleotide insertion)
			LYQAMDIIRLNKLEDTITLIKGKIERVHLPVEKVDVIICRUMCV
1	}		FLLFESMLDSVLYAKNKYLAKGGSVYPDICTISLVAVEDVNIKUA
			DRIAFWDDVYGFKMSCMKKAVIPEAVVEVLDPKTLIGEPCCIVU
	}		IDCHTTSISDLEFSSDFTLKITRTSMCTAIAGVEDIVERNOLDI
			RVVFSTGPQSTKTHWKQTVFLLEKPFSVKAGEALKGKVTVHKNK
6447	1554	1020	KDPRSLTVTLTLNNSTQTYGLQ
]	1 233	1068	RLGPAEWHLSGPCHATLGAANRGRALGVRAAWRGAPLCQRVMMP
1 1	ĺ		SRTNLATGIPSSKVKYSRLSSTDDGYIDLQFKKTPPKIPYKAIA
1 1			LATVLFLIGAFLIIIGSLLLSGYISKGGADRAVPVLIIGILVFL
6448	74	559	PGFYHLRIAYYASKGYRGYSYDDIPDFDD
1		339	GQVLSHCYHYRSSRWRRGGLSRGRGAGVMALVPYBETTEFGLQK
			FHKPLATFSFANHTIQIRQDWRHLGVAAVVWDAAIVLSTYLEMG
1 1			AVELRGRSAVELGAGTGLVGIVAALLACRIRYERDNNFLAMLER QFIVRKVHYDPEKDVHIYEAQKRNQKEDL
6449	597	1876	EYGVCENLRKLEITGVSCRDVYAKLLHRYRHILGLWQPDIGPYG
1 1			GLLNVVVDGLFIIGWMYLPPHDPHVDDPMRFKPLFRIHLMERKA
1			ATVECMYGHKGPHHGHIQIVKKDEFSTKCNQTDHHRMSGGRQEE
1 1			FRTWLREEWGRTLEDIFHEHMQELILMKFIYTSQYDNCLTYRRI
]]			YLPPSRPDDLIKPGLFKGTYGSHGLEIVMLSFHGRRARGTKITG
			DPNIPAGQQTVEIDLRHRIQLPDLENQRNFNELSRIVLEVRERV
i I			RQEQQEGGHEAGEGRGRQGPRESQPSPAQPRAEAPSKGPDGTPG
1			KDGGEPGDAVAAAEQPAQCGQGOPFVLPVGVSSRNEDVDDTCDM
1 . 1	1		CFYGTGLIAGHGFTSPERTPGVFILFDEDRFGFVWLELKSFSLV
6450			SRVQATFRNADAPSPQAFDEMLKNIOSLTS
0450	848	269	FVPAPRTVSGKRSLPGEWEERGEGEORTGREFSGNGGPAVEAAR
1 1			MRLLCGLWLWLSLLKVLQAQTPTPLPLPPPPMOSFOGNOFOGEWE
1	i		VLGLAGNSPRPEHRALLNAFTATFELSDDGRFRVWNAMTRGOHC
			DTWSYVLIPAAQPGQFTVDHRVWTHEQAGRPQDQPAGQELVAAS
6451	232	939	RDAGPVHLPGQSSGPLG
		233	HSPTPPTSPRASTMEDVKLEFPSLPQCKEDAEEWTYPMRREMQE
1			ILPGLFLGPYSSAMKSKLPVLQKHGITHIICIRQNIEANFIKPN
			FQQLFRYLVLDIADNPVENIIRFFPMTKEFIDGSLQMGGKVLVH
			GNAGISRSAAFVIAYIMETFGMKYRDAFAYVQERRFCINPNAGF VHQLQEYEAIYLAKLTIQMMSPLQIERSLSVHSGTTGSLKRTHE
			EEDDFGTMQVATAONG
6452	1	652	RTRGESSNMEPLAAYPLKCSGPRAKVFAVLLSIVLCTVTLFLLQ
1	1		LKFLKPKINSFYAFEVKDAKGRTVSLEKYKGKVSLVVNVASDCQ
			LTDRNYLGLKELHKEFGPSHFSVLAFPCNQFGESEPRPSKEVES
i j		ļ	FARKNYGVTFPIFHKIKILGSEGEPAFRFLVDSSKKEPRWNFWK
			YLVNPEGQVVKFWRPEEPIEVIRPDIAALVROVIIKKKEDI.
6453	827	223	HRRWLPGLSMSPRRTLPRPLSLCLSLCLCLCLAAALGSAOSGSC
1			RDKKNCKVVFSQQELRKRLTPLOYHVTOEKGTESAFEGEVTHUV
ļ			DPGIYKCVVCGTPLFKSETKFDSGSGWPSFHDVINSEATTETDD
}		l l	FSYGMHRVETSCSQCGAHLGHIFDDGPRPTGKRYCINSAALGET
6454	827		PADSSGTAEGGSGVASPAQADKAEL
	02/	223	HRRWLPGLSMSPRRTLPRPLSLCLSLCLCLCLAAALGSAQSGSC
ŀ			RDKKNCKVVFSQQELRKRLTPLQYHVTOEKGTESAFEGEYTHHK
1		i	DPGIYKCVVCGTPLFKSETKFDSGSGWPSFHDVINSEATTETDD
1	1	1	F5YGMHRVETSCSQCGAHLGHIFDDGPRPTGKRYCINSAALSET
6455	1042		PADSSGTAEGGSGVASPAQADKAEL
		173	RVHLATVSASAAWDALGLPVRSHMQGSTRRMGVMTDVHRRFLQL
1		ľ	Y Market Comment of the Comment of t
1		i	LMTHGVLEEWDVKRLQTHCYKVHDRNATVDKLEDFINNINSVLE
			LMTHGVLEEWDVKRLQTHCYKVHDRNATVDKLEDFINNINSVLE SLYIEIKRGVTEDDGRPIYALVNLATTSISKMATDFAENELDLE
			LMTHGVLEEWDVKRLQTHCYKVHDRNATVDKLEDFINNINSVLE

Degianing No: location corresponding coation corresponding cofirst amino acid amino acid amino acid residue of amino acid amino acid sequence sequen	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Mucleotide Cocation Corresponding to first amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid sequence Security	1	l .		
Coctain Corresponding Coffice Corresponding Coffice Corresponding Coffice Coffic	No:			Glutamic Acid. F=Phenylalanine G=Glycine
corresponding to first amino acid residue of amino acid residue of amino acid residue of amino acid sequence solvent sets amino acid sequence solvent sets amino acid sequence solvent sets amino acid sequence solvent sequence so	1			Halistidine. Talsoleucine Kalvoine
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	. 1			
0464 1 12 1 1154 CTT.DOVED DEDNID TUVVDTT DT. DUTTINTO CEMCCT CONTINUETA	64.53	4.5		
GIDAQAEREENAKIRAAELDF DERLUDA VESEMSSESGRAQUIVEG	6464	12	1154	GILROKEREERNRIHKKEILFLEHLLVVPSEMSSLSGKVQTVLG

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
į	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
l	corresponding	to first	LaLeucine, MaMethionine, NaAsparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
<u> </u>	sequence	_	\=possible nucleotide insertion)
			LVEPSKLGRTLTHEHLAMTPDCCYCPPPPCQEAISKEPIVMKNL
,			YWIQKNAYSHKENLQLNQETEAIKEELLYFKANGGGALVENTTT
1			GISRDTQTLKRLABETGVHIISGAGFYVDATHSSETRAMSVEQL
1			TDVLMNEILHGADGTSIKCGIIGEIGCSWPLTESERKVLQATAH
	ł	ł	AQAQLGCPVIIHPGRSSRAPFQIIRILOBAGADISKTVMSHLDR
1			TILDKKELLEFAQLGCYLEYDLFGTELLHYOLGPDIDMPDDNKR
ŀ			IRRVRLLVEEGCEDRILVAHDIHTKTRLMKYGGHGYSHILTNVV
L		1	PKMLLRGITENVLDKILIENPKQWLTFK
6465	126	1396	KMTVFFKTLRNHWKKTTAGLCLLTWGGHWLYGKHCDNLLRRAAC
1		·	QEAQVFGNQLIPPNAQVKKATVFLNPAACKGKARTLFEKNAAPI
]			LHLSGMDVTIVKTDYEGQAKKLLELMENTDVIIVAGGDGTLORV
		1	VTGVLRRTDEATFSKIPIGFIPLGETSSLSHTLFAESGNKVQHI
	ĺ	1	TDATLAIVKGETVPLDVLQIKGEKEQPVFAMTGLRWGSFRDAGV
			KVSKYWYLEPLKIKAAHFFSTLKEWPQTHQASISYTGPTERPPN
İ]	EPEETPVQRPSLYRRILRRLASYWAQPQDALSQEVSPEVWKDVQ
	ļ,	İ	LSTIELSITTRNNQLDFTSKEDFLNICIEPDTISKGDFITIGSR
1		'	KVRNPKLHVEGTECLQASQCTLLIPEGAGGSFSIDSEEYEAMPV
6466	1134	828	EVKLLPRKLQFFCDPRKREQMLTSPTQ
1	1117	020	VARGTELSQLEKAHPPADMGRRKSKRKPPPKKKMTGTLETQFTC
1		·	PFCNHEKSCDVKMDRARNTGVISCTVCLEEFQTPITYLSEPVDV YSDWIDACRAANQ
6467	301	2571	GBLRVLALAHGELACHAVLTASLLSLRSRLMDSDMDYERPNVET
			IKCVVVGDNAVGKTRLICARACNATLTQYQLLATHVPTVWAIDQ
1	•		YRVCQEVLERSRDVVDDVSVSLRLWDTFGDHHKDRRFAYGRSDV
			VVLCFSIANPNSLHHVKTMWYPEIKHFCPRAPVILVGCQLDLRY
1.	•		ADLEAVNRARRPLARPIKPNEILPPEKGREVAKELGIPYYETSV
ľ		•	VAQFGIKDVFDNAIRAALISRRHLQFWKSHLRNVORPLLOAPFI.
1			PPKPPPPIIVVPDPPSSSEECPAHLLEDPLCADVILVLOERVRI
	•		FAHKIYLSTSSSKFYDLFLMDLSEGELGGPSEPGGTHPEDHOGH
1 1			SDQHHHHHHHHHGRDFLLRAASFDVCESVDEAGGSGPAGLRAST
1			SDGILRGNGTGYLPGRGRVLSSWSRAFVSIQEEMAEDPLTYKSR
1 . 1			LMVVVKMDSSIQPGPFRAVLKYLYTGELDENERDLMHIAHIAEL
1 1			LEVFDLRMMVANILNNEAFMNQEITKAFHVRRTNRVKECLAKGT
1	,	•	FSDVTFILDDGTISAHKPLLISSCDWMAAMFGGPFVESSTREVV
			FPYTSKSCMRAVLEYLYTGMFTSSPDLDDMKLIILANRLCLPHL
			VALTEQYTVTGLMEATQMMVDIDGDVLVFLELAQFHCAYQLADW
]	·]		CLHHICTNYNNVCRKFPRDMKAMSPENQEYFEKHRWPPVWYLKE
	·		EDHYQRARKEREKEDYLHLKRQPKRRWLFWNSPSSPSSSAASSS
6468	3	1374	SPSSSSAVV
	, ,	***	DAWAGTINMAALAPVGSPASRGPRLAAGLRLLPMLGLLQLLAEPG LGRVHHLALKDDVRHKVHLNTFGFFKDGYMVVNVSSLSLNEPED
			KDVTIGFSLDRTKNDGFSSYLDEDVNYCILKKQSVSVTLLILDI
1	•	. 1	SRSEVRVKSPPEAGTQLPKIIFSRDEKVLGQSQEPNVNPASAGN
		·	QTQKTQDGGKSKRSTVDSKAMGEKSFSVHNNGGAVSFQFFFNIS
] [ſ		TDDQEGLYSLYFHKCLGKELPSDKFTFSLDIEITEKNPDSYLSA
			GEIPLPKLYISMAFFFFLSGTIWIHILRKRRNDVFKIHWLMAAL
1.1	,		PFTKSLSLVFHAIDYHYISSQGFPIEGWAVVYYITHLLKGALLF
]]	J		ITIALIGTGWAFIKHILSDKDKKIFMIVIPRRVLANVAYIIIES
		· [TEEGTTEYGLWKDSLFLVDLLCCGAILFPVVWSIRHLQEASATD
			GKGKFSRAHFVLLSLL
6469	3	1374	DAWAGTNMAALAPVGSPASRGPRLAAGLRLLPMLGLLQLLAEPG
			LGRVHHLALKDDVRHKVHLNTFGFFKDGYMVVNVSSLSLNEPED
			KDVTIGFSLDRTKNDGFSSYLDEDVNYCILKKQSVSVTLLILDI
			SRSEVRVKSPPEAGTQLPKIIFSRDEKVLGQSQEPNVNPASAGN
		1	QTQKTQDGGKSKRSTVDSKAMGEKSFSVHNNGGAVSFQFFFNIS
			TDDQEGLYSLYFHKCLGKELPSDKFTFSLDIEITEKNPDSYLSA
	-		

Mo: nucleotide location corresponding to first amino acid residue of amino acid residue of amino acid residue of amino acid sequence e	SEQ	Predicted	Predicted end	Tamino agid cogment combain
Corresponding to first amino acid residue of service amino acid sequence Service amino acid	ID			Amino acid segment containing signal peptide
Corresponding to first animo acid amimo acid amimo acid amimo acid amimo acid amimo acid amimo acid asquence of residue of amimo acid asquence of acid amimo acid asquence of acid	NO:	nucleotide	location	Glutamic Acid F-Phonylalarina C. Clark
corresponding to first amino acid residue of amino acid residue of amino acid residue of amino acid sequence solvent amino acid sequence solvent amino acid sequence solvent amino acid sequence solvent amino acid sequence solvent amino acid sequence solvent amino acid sequence solvent amino acid sequence solvent amino acid sequence solvent amino acid sequence solvent amino acid sequence solvent amino acid sequence solvent amino acid sequence solvent amino acid sequence solvent amino acid sequence solvent amino acid sequence solvent acid sequence solvent amino acid sequence solvent amino acid sequence solvent amino acid sequence solvent acid sequence s		location	corresponding	H=Histidine T=Tsoleucine V=Lycine,
amino acid	1			L=Leucine, M=Methionine N=Asparagine
residue of amino acid sequence solve of amino acid sequence sequen	i	to first	amino acid	P=Proline. O=Glutamine P=Arginine
### ### ### ### ### ### ### ### ### ##		amino acid	residue of	S=Serine, T=Threonine V=V=line
sequence seq	1	residue of	amino acid	W=Tryptophan, Y=Tyrosine Y=Unknown +-Ge
GETLPRIVITS MART FFFLSGT INTHITERRENDVEXTHEMANAL GETLPRIVITS MART FFFLSGT INTHITERRENDVEXTHEMANAL PETRALSLAVEHAIDYMYLSSOG PPIEGMANVYYTHHLAGAL PETRALSLAVEHAIDYMYLSSOG PPIEGMANVYYTHHLAGAL FEGTTEYGLMKDSLFLAVOLLCGAILPPVWSTRHLQEASATO GKOKPSRAMPULSLL AASSOVSSRADAFULAQISASAGNORDETERVPGSRRHESAPER GPHPEDGGTPGOGLLPPROLLEPRILSPRIVERSRHESAPER GPHPEDGGTPGOGLLPPROLLEPRILSPRIVERSHDOT QHESSGGRCRGGTESPSSAAGRADAMARAEEDCHISDTVRADDDE EMESPASTILOAGOLOWFRANGMELAFOLUSSSNILBERPCHASTRHOT QHESSGGRCRGGTESPSSAAGRADAMARAEEDCHISDTVRADDDE EMESPASTILOAGOLOWFRANGMELAFOLUSSSNILBERPCHASTRHOT GERPANTANGOLOWFRANGMELAFOLUSSSNILBERPCHASTRHOT GERPANTANGOLOWFRANGMELAFOLUSSSNILBERPCHASTRHOT GERPANTANGOLOWFRANGMELAFOLUSSSNILBERPCHASTRHOT PETRALTREPDOGUVGMENT LIPOWOUS SILDMINGHERREN SLOKTSADTYKKOOONAGESLIKSULPREVIPRONUS SILDMINGHERREN GERMANGOLOWFRANGMENT LIPOWOUS SILDMINGHERREN GERMANGOLOWFRANGOLOWFRANGMELAFOLOWFRANGOLOFFRANGO PETRALTREPDOGUVGMENT SILDMINGHERREN GERMANGORGERSSNICHTENT SILDMINGHERREN GERMANGORGERSSNICHTENT SILDMINGHERREN GERMANGORGERSSNICHTENT SILDMINGHERREN GERMANGORGERSSNICHTENT SILDMINGHERREN GERMANGORGERSSNICHTENT SILDMINGHERREN GERMANGORGERSSNICHTENT SILDMINGHERSEN LIMBSATRANGORDOVERSILLENGOLOPPERVERADOR LIMBSATRANGORDOVERSILLENGOLOPPERVERADOR ARMEDIAGNICHT SILDMINGHERSEN ARMEDIAGNICHT SILDMINGHERS ARMEDIAGNICHT SILDMINGHERS ARMEDIAGNICHT SILDMINGHERS A	1	amino acid	sequence	Codon. /=possible mucleotide dolotion
GEILPINTISMATFFILGGTIHILTEKERNDUFKTHMIAGALIP PFTKRSLSUFHAINDYKTISSGOFP TERMAVUYTHKAGALIP PFTKRSLSUFHAINDYKTISSGOFP TERMAVUYTHEVLANNATITIES TEEGTTEVGIMKDSLPLVOLLCGGATLPPVWSTRHLQEASATO GKOKPSERAHFVLLSLL GKOKPSERAHFVLLSLL GKOKPSERAHFVLLSLL GHPEDOCRTEGOLLPLPGALLRPTILISAALETGRSRHIPDT GHPSSGGRCGGTES PSAGAGRASMARAEGECISTIVKADGE EWESPARTDLQAQLQWFRQOMWFELAGWISSANLERNERFCRARAEG SLOKTSADTKOKOGOAKSEKARELPLGAVEEGOKGALVEARFY RARAGLYPHIEVERTHATSSOORGUSTYTENDDSKMADLLS YRQQLIFFGESVIKLCOPELSSGIHISVLPMEVLMYIFRRVUS SILDLKRSLGVISUKCGFYLCARDEFUNKLAKTIKOGOGLOGFYRAMHO VEYLYNIRFPOROVISKTTIKOGOGLOGFYRAMHO VEYLYNIRFPOROVISKTTIKOGOGLOGFYRAMHO VEYLYNIRFPOROVISKTTIKOGOGLOGFYRAMHO VEYLYNIRFPOROVISKTTIKOGOGLOFPOROMHOTPERSGILKSEVEN FFDOMMAGGSGVOGKRSSKSDADGSFIGHRFTSVOPPALKRRSK VPAPKANCHARDEFUNKHTKTOKORKSILLKKFULEVULLIKKFULEVULLIKKFUL VPAPKANCHARDEFUNKHTKOROPENSUKLERTSGILLSERAN ELLFFUUTGSKEKGLIKKRTKVOKKSILLKKFULEVULLIKKFULEVULLIKKFULEVULL LINPSATRAKFORODTVERPPVILKADDRYLDVOLGEFTENGGLISERAN ELLFFUUTGSKEKGLIKKRTKVOKKSILLKKFULEVULLIKKFULUKKFULEVULLIKKFULEVULLIKKFULEVULLIKKFULEVULLIKKFULEVULLIKKFULEVULLIKKFULEVULLIKKFULEVULLIKKFULEVULLIKKFULEVULLIKKFULEVULLIKKFULEVULLIKKFULEVULLIKKFULLIL BAHTALTTYPOVARKFULEVULLIKKFULEVULLIKKFULDERANINEVULLIL LIKOSARPAGOKALIGINIKEVELLILIKKFULDERANINEVULLILLIDER LIKOSARPAGOKALIGINIKEVELLILIKKFULEVULLIKKFULDERANINEVULLILLIDIKASARORIKULTIKKFULTIKKFULTIKKFULTIKKFULTIKKFULTIKKFULTIKKFULTIKKFULTIKKFULTIKKFULTIKKFULTIKKFULTIKKFULTIKKFULTIKKFULTIKKFULTIK	<u> </u>	sequence	l -	\=possible nucleotide insertion)
PPTKSLSLVFHAIDTHYTSSGGPPLEGMAVVYTTHILKGALANDAYIIIS TEGTTEYGLMKDSLFLVOLLCCGAILFPVVMSIRHLQEASATD CKKKPSRAIPFULSLL AAASGVSSRADAFULAGISPASAGMGRESTERVFGGRRHPSAFRS GLOKTSTATIKGCOMMELAGAUSSTNALEGASATD OKKSPSRAIPFOQULPLPGALLAPRTLISSAAETGSSRHPSAFRS GLOKTSTATIKGCOMMELAGAUSSSNLERFCKARAFG SLOKTSTATIKGCOMMELAGAUSSSNLERFCKARAFG SLOKTSTATIKGCOMMELAGAUSSSNLERFCKARAFG SLOKTSTATIKGCOMMELAGAUSSSNLERFCKARAFG SLOKTSTATIKGCOMMELAGAUSSSNLERFCKARAFG SLOKTSTATIKGCOMMELAGAUSSSNLERFCKARAFG SLOKTSTATIKGCOMMELAGAUSSSNLERFCKARAFG SLOKTSTATIKGCOMMELAGAUSSSNLERFCKARAFG SLOKTSTATIKGCOMMELAGAUSSSNLERFCKARAFG SLOKTSTATIKGCOMMELAGAUSSSNLERFCKARAFG SLOKTSTATIKGCOMMELAGAUSSSNLERFCKARAFG SLOKTSTATIKGCOMMELAGAUSSSNLERFCKARAFG SLOKTSTATIKGCOMMELAGAUSSSNLERFCKARAFG SLOKTSTATIKGCOMMELAGAUSSSNLERFCKARAFG SLOKTSTATIKGCOMMELAGAUSSSNLERFCKARAFG SLOKTSTATIKGCOMMELAGAUSSSNLERFCKARAFG VEYNRYTTFFPGHAMMUTTFEEDGSIVPTRAMT SSLOLLARGELGUSDOMMANTTFEEDGSIVPTRAMT STATALFORDOMSTATIKGTOMMANTTFEEDGSIVPTRAMT SCHAMPSTOMMANTTFEEDGSIVPTRAMT SCHAMPSTOMMANTTFEEDGSIVPTRAMT SCHAMPSTOMMANTATICHTERFORSUMMANTATICHTSTATALATOR SCHAMPSTOMMANTATICHTSTAT			·	GEIPLPKLYISMAFFFFISGTIWIHTLPKPPNDVEYTUWI MAAY
1TTALIGTOMAP INHILISHOKKIT PMIVIPR VILANVATITIES TEEGTTEYGIMDSI-LVULLCGAILFPVWS TRHIQASATO GKKPSBAHFVILSIL 6470 2726 1437 AAASOVSSKADAFVILSIL GPIPREDGCTTGOLIPPALLIPRTILISSAAETORSRHEDT OHPSSGGRCGGTSSPSSAAGA PSAMPARABEDTVADDDE ENESPASTILOAULOMPROMPELAGVSSNILBUR PCRARGE SLOKTSADTYKKGKONKEKEKARELFILOGUSSNILBUR PCRARGE SLOKTSADTYKKGKONKEKEKARELFILOGUSSNILBUR PCRARGE SLOKTSADTYKKGKONKEKARELFILOGUSSNILBUR PCRARGE SLOKTSADTYKKGKONKEKEKARELFILOGUSSNILBURDSKAADLIS YFOQOLTPOESVIKILOOPELESSOIHISULPREVIATITIKOGOSLOGYPAMPA SDILLARSIGOLISULORGFYICARDEPINHALOKEKKORGSCIKLV PTYSWREMPLERPRVEFDGYISKTTIKGGGSLOGYPAMPA SSILDIARSIGOLISULORGFYICARDEPINHALOKEKKORGSCIKLV PTYSWREMPLERPRVEFDGYISKTTIKGGGSLOGYPAMPA SPANDULAGOPHENVILGERFUNGGLISEPAN GERMKKGKREHALGPELGELVOOPHENVILGERFUNGGLISEPAN ELIFPUTGSKEKGLTKURTKVOKKSLLLKKPLEVDILLERPRE GRAKKGKREHALGPELGELVOOPHENVILGERFUNGGLISEPAN ELIFPUTGSKEKGLTKURTKVOKKSLLLKKPLEVDILLERPRE GRAKKGKREHALGPELGELVOOPHENVILGERFUNGGLISEPAN LINPSATRAKPOOPDTVERPPTDUMASDRPLORPLOGDEPENRAG ELIFPUTGSKEKGLTKURTKVOKKSLLLKKPLEVDILLERPRE GYKKKGKGREHALFTENGGAADATOGSTFOELCGGLISE SEDGGEGGGGGPFAGGBAVCTPARALTTEKSGAAVAURALBELERRORP GYKKKGKGKREHALTTEKSGAAVAURADATOGSTFOELCGGLISE ESDGGEGFAGGGBVETARANTATOGSTFOELCGGLISE SEDGEFAGGGBPEGGBAVCTPARALTTEKSGAAVAURALBELERRORP ROARREABADFRAGGRIKANGLAPATGGAATOGSTFOELCGGLISE SEDGEFAGGGBPEFODALTETARATOTIKATERATORTIKATATORTICATA VURIRVOQAALKARATIKTSGAAVAURALBELERRORP ROARREABADFRAFFAGGRIKKVALPVUKLVEKRAPREIOTIL LIKKSYADATOON LIKKSGARPAKKAA IIG JIVVOYKLEVULDREANIREVEPLICL LIKKSYALTATOVONNOVI 1EGFFARGINERVEPLICL LIKKSYALTATOVONNOVI 1EGFFARGINERVEPLICL LIKKSYALTATOVONNOVI 1EGFFARGINERVEPLICL LIKKSYALTATOVONNOVI 1EGFFARGINERVEPLICL LIKKSYALTATOVONNOVI 1EGFFARGINERVEPLICL LIKKSYALTATOVONNOVI 1EGFFARGINERVEPLICL LIKKSYALTATOVONNOVI 1EGFFARGINERVEPLICL LIKKSYALTATOVONNOVI 1EGFFARGINERVEPLICH LIKKSYALTATOVONNOVI 1EGFFARGINERVEPLICH LIKKSYALTATOVONNOVI 1EGFFARGINERVEPLICH LIKKSYALTATOVONNOVI 1EGFFARGINERVEPLICH LIKKSYALTATOVONNOVI 1EGFFARGINERVER LIKKSTOOLOGIA KIKKEEKGEAGKGGAASSINGTTABEHII SRTVINVSTSRGT PST	}		İ	PFTKSLSLVFHAIDYHYISSOGPPIFGWAWYYTTULI YCALLE
6470 2726 1437 AAASGVSRADAPULGCGALIPPVWSIRHLQEASATD (KKKPSRAPVILSIL) AAASGVSRADAPULGCGALIPPVWSTRYDGSRAPGRSRIPDT (GIPSGGCCGGTRE) PSSAAGRPSYMBABERDCHSDTVRADDIB ENESPASTIDLOOLOMPSGADLIRPPTLISSAABTGRSRIPDT (OIPSGGCCGGTRE) PSSAAGRPSYMBABERDCHSDTVRADDIB ENESPASTIDLOOLOMPSGADROWNSI LEDNDODSWADLLS YFQQUITTGESVURLCOPBLESSGIHISVERGARG SLOKTSADTKGKOEQAKEEKARELPIKAVBEEROKGALVEATKRY RAMOLVPDI ERKITYTRSDGGDVCMSY IEDNDODSWADLLS YFQQUITTGESVURLCOPBLESSGIHISVERDVIMYITTRWOYS SIDLARSLEQLSLVCRFFY CARDPEIVRIACKLYKUGSKILGKYRANDLLS YFQQUITTGESVURLCOPBLESSGIHISVERDVIMYITTRWOYS SIDLARSLEQLSLVCRFFY CARDPEIVRIACKLYKUGSKILGKEARN PYTSKREWHELBERPRVTROVYISKTY IRGOSKILGFYRAWG VEYYKYTRFPDGHVWMLTTEEPEQSIVERLTR GPRINKRGWRRIAGEPIGLEVODPLEDVRLQERTSGGLISEAPN ELLFPUTTGSKEKSLTKARKTVKVKKSLILKKERPRVLILERTIKK VPAPKDULAHQUPNAKKLRKEQLIMEKLAKGGELPERVERAGAR ELLFPUTTGSKEKSLTKARKTVKVKKSLILKKERPRVLILERTIKK VPAPKDULAHQUPNAKKLRKEQLIMEKLAKGGELPERVERAGAR ELLFPUTTGSKEKSLTKARKTVKVKKSLILKKERPRVLILERTIK VPAPKDULAHQUPNAKKLRKEQLIMEKLAKGGELPERVERAGA ELLFPUTTGSKEKSLTKARTVOKKSLILKKERPRVLILERTIK VPAPKDULAHQUPNAKKLRKEQLIMEKLAKGGELPERRAGA ELLFPUTTGSKEKSLTKARTVOKKSLILKKERPRVLILERTIK VPAPKDULAHQUPNAKKLRKEQLIMEKLAKGGELPERRAGA VPARRAPADAPTRADATTERSCHOOTHELPPARRETICL TILMPSATRAKPOPOTVERPPTULMASONDHEDPLWQDDFFTEL OYKKKGWRRAARLTTERSCAPAVEVAPRAATSTERSCHOOTHELPPARRETICL GAKKGWRRAARLTHESCAPATARTTERSCAPATIONATOR TILMPSATTARABARTHOFTERSCHOOTHELPPARRETICL GAKGREPOGGGGGGGBADAEVCPTPARLATTERKTCOGRREKAR VVERRVOODALRAARCHGELFFELTVLLOCHELPPARRETICL ESDGGGGFGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	i			ITIALIGTGWAFIKHILSDKDKKIFMIVTPRRVIANVAVITTES
6470 2726 1437 AAASGVSERADAPVLAGSREASGGGRETERVENGSRRHPSAFES GPLPREDGCRTPGPQLLPLEGALLREPTLLSSAAETGISRHPDT ORPSGGGCRGGTBSPSSAGREPSATHLASSAAETGISRHPDT ORPSGGGCRGGTBSPSSAGREPSATHASTESTURADDE EMESPATDLQAQLOMPRAQOMPELAPGVSSSILENRECCARGE SLOKYSADTIKGKOQAKEKARELIKAVEEGONGALIFAKYE RRAMQLVPDI BEKITYTRSPGGDGVGNSYSIEDHDDDSSMADLLS YRQQQIFTGESVULKLQPELESSGIHISVLPMEVUMYIFAKVUS SDLURSLGLGLLVCREPTICARDPSIVELDEDDDDSSMADLLS YRQQUIFTGESVULKLQPELESSGIHISVLPMEVUMYIFAKVUS SDLURSLGLGLLVCREPTICARDPSIVELDEDDDDSSMADLLS YRQQUIFTGESVULKLQPELESSGIHISVLPMEVUMYIFAKVUS SDLURSLGLGLLVCREPTICARDPSIVELDERDDDSSMADLLS YRYRYIFTPFDGIVMMLTTPEEPGGIVFMLTTER FFFDMAAGGSGVGGKRSSKSDADSGFLGLEPTSVDFARMIO PYTSSRRMFLEERPRVRFDGVYISKTTYTRQGGSLDGFYRAMIO YRYRYIFTPFDGIVMMLTTPEEPGGIVFMLTTR GPRINKRGWRRIAGDELGUEDGPEDGUEDGETSGGLESADH ELLFYUTGSKEKGLTKKRTVQKKSLLLKKPILVULLLENTSK VAPAFOULANDVPRAKKLERGLARFGLARGGLERFEVARAGAR ELLFYUTGSKEKGLTKKRTVQKKSLLLKKPILVULLLENTSK VAPAFOULANDVPRAKKLERGLARFGLARGGLERFUNGLEFTSGELGSGLE ELLFYUTGSKEKGLTKKRTVQKKSLLLKKPILVULLTENTSK VAPAFOULANDVPRAKKLERGLARFGLARGGANETERVENGLERFUNGLEFTURGE GTKKKGVKRTARLHTKRSQAFAVEVAFAGASTVESFTCELGGGLE ESDGEGFOQGGSGFAGAVEVAFAGASTVESFTCELGGGLE ESDGEGFOQGGSGFAGAVEVAFAGASTVESFTCELGGGLE ESDGEGFOQGGSGFAGAMETEFTDVALSFRITTVLDGHLRFARGRETTLKEFG TILLDGFRKSFGRRMATERFERGLARFAKTKKKVKLVEKRAFRETGL 6472 3 897 SGGSBRAQAMEFFFTDVALFFRITTVLDGHLRFPARFSHTLKEGG TILLDGFRKSFGRRMATERFERGKFKKKVKLVEKKAFRETGL LIKDSARARGHTIT IDEIGKASAQONLSAPITASSFMQSRNTHTVLY LIKDSARFAGKGALTGFTKVGYKKLPVLLODREAURSVEDLGL DFYTHSSVGGITHGHASSLGVHLASFBRAGDTKAEDHGLIK LIKHYHLETTVQVNHFVIFFGFFTTPARSFMAN AVDDTPAAPARKLPVLGKREVPHOLAIDRSSGRRHTVEKARGDGGK NEWERGRAAFFRETGTLFFKLEAUPTHKACFDCGAK NESSARFVWEGEKMAAFFRETGTLFFKLEAUPTHKACFDCGAK NESSARFVWEGEKMAAFFRETGTLFFKLEAUPTHKACFDCGAK NESSARFVWEGEKMAAFFRETGTLFFKLEAUPTHKACFDCGAK NESSARFVWEGEKMAAFFRETGTLFFKLEAUPTHKACFDCGAK NESSARFVWEGEKMAAFFRETGTLFFKLEAUPTHKACFDCGAK NESSARFVWEGEKMAAFFRETGTLFFKLEAUPTHKACFDCGAK NESSARFVWEGEKMAAFFRETGTLFFKLEAUPTHKACFDCGAK KYKERQEANGTAPSRAGGTKABESHTISSTTUNSTSRGTP PSTLSVKGGIETGTVAUGTEN LECKYGGGFRAFTKAKKEPGAKEP			ĺ	TEEGTTEYGLWKDSLFLVDLLCCGATLFPVVWSTDHLOFACATD
6470 2726 1437 AAASSVSSRADAPULAGSPARAGIGRSFFRVPGGRRHPSAFRS GPLPSEDGCTPSPQDLIPLEGALLRPRTLLSSARIPSTSRHIPT OHPSSGGCRGGTSSPSSAGGRASHARZEBALTSBRHIPT OHPSSGGCRGGTSSPSSAGGRASHARZEBALTSBRHIPT OHPSSGGCRGGTSSPSSAGGRASHARZEBALTSBRHIPT OHPSSGGCRGGTSSPSSAGGRASHARZEBCHSDTVRADDDS EMESPASTDLQAQUMPRAQMMFELAPGYSSSNLERRECRARAG SLOKTSADTKGGCQAKEEKRELPLKAVEGGALLAGERJEGTSANALLS YFQQLIFTGESVLKLCQPELESGSIHISUPBULMYTPRWVDS SLOLRSLEGLSLVCRGFYLGARDFSIHRLACLKAVEGGSCIKLV PYTSRREMFLEEPRWYREDVISKTYTIRGGGSLDGFYRAWHQ VEYYRYTRPPDGHVMMLTTDEEPQSIVPRLETT 6471 1750 293 FFFDXMAGGSVGKRSSKSDADSGFIGLRPTSVDPALRRRRR GPRINKRGKRRLAGEFLGLEVUGFLEDWLGGSLDGFYRAWHQ VEYYRYTRPPDGHVMMLTTDEEPQSIVPRLETT GPRINKRGKRRRLAGEFLGLEVUGFLEDWLGGLETSGGLESAPA ELLFFVUTGSKEKSLTKKRTKVQKKSLLLKKPLRVDLLINTSK VPARKDLAGAVPARAKLERGOLBKLAKGGSLPREVRRAGNA LLINPSATRAKDGPQDTVERPFYDLWASDNFLDEFLYGDGLEFTBRAGDEFLGE GTKKKGVKRPRALHTKPSGGAPAVVAPAGATAVPSFEDHOTILLS AAHBVELQRQKEABKLERGLALPATGOATOSETTOPLCTGGLE ESDGGEGFQGGSGBGAGAGAPAVVAPAGATVSFFEDHOTILS AAHBVELQRQKEABKLERGLALPATGOATOSETTOPLCTGGLE ESDGGEGFQGGSGBGAGAGAPAVVAPAGATVSFFERTIKVEG VRIRKVQOAALRAARLEHOELFFLRG IKAQVALRLAELARRRR RQARREAEABVERFRLGUCYPTPARLATTKEKTGORRESAA VPERLYQOAALRAARLEHOELFFRLTGVLDGHERPPARRGFTTP ARVOLOQQIMTI IDELGKASAKQNISAPITASSAMQSINSHTIKEG NILKDRFKSFQRRMMEPRESAKFKKKVKVKVEKRAFREIGL DFYTHSSVGNGHGRELGFYUKGKRVEPHOLDREAINSVEELGIL DFYTHSSVGNGHGRELGFYUKGKRVEPHOLDREAINSVEELGIL DFYTHSSVGNGHGRAELGFYUKGKRVEPHOLDREAINSVEELGIL DFYTHSSVGNGHGRAELGFYUKGKRVEPHOLDREAINSVEELGIL DFYTHSSVGNGHGRAELGFYUKGKRVEPHOLDREAINSVEELGIL DFYTHSSVGNGHGRAELGFYUKGKRVEPHOLDREAINSVEELGIL DFYTHSSVGNGHGRAELGFYUKGKRVEPHOLDREAINSVEELGIL DFYTHSSVGNGHGRAELGFYUKGKRVEPHOLDREAINSVEELGIL DFYTHSSVGNGHGRAELGFYUKGKRVEPHOLDREAINSVEELGIL ARPRATTPPANPPRSSICKSSEGGFTFYSSGEBTRAGAVEN RAPRATTPPANPPRSSICKSSEGGFTFYSSGEBTRAGAVER LEMGVGGGRAAAARAGALGKAGGAVKSVSGEBTRAGAVENSER LEMGVGGGRAAAARAGALGKAGGAVKSSGEBTRAGAVENSER LEMGVGGRAAAARAGALGKAGGAVKSSGEBTRAGAVKSEERGGGG KVIKGEPTRASALSAKAAPPEPEPRRTSAKESTERGAGVAG KUKEBKQGAGGTAPSENGGTRATAKTKKSGETTALOKGTO ARAMAGYTGTMERGGRAWHILKKRESTHAKVSCTSGGT FSTLSVKGG	L	1	ļ	GKGKFSRAHFVLLSLL
GPLPREDGETTGFQLLPLEGALLREFTLLSSAAETGSSRIPDT QHPSSGGGKGGTSSPSSAAGREAGHANARAETGGSTTVRADDE EMESPATIDLQAQLOMFRAQMMFELAAGVSSSNLERRECRARAG SLOKTSADTMKGGOAMERKARELPLKANEGNALVEA KEY RRAMQLUPDIERKITYTRSPOGDGVGNSYIEDNDDDSKMADLLS YFQQQLFFQSSULKLQPBLESSQIHISVLPMSVMYITRWVS SDLDLRSLEQLSLUCRGFFTGARDFSINELACLKWGRSCIKLV PYTSWREMPLEERPRUPFDGVMMLTPERPGSIVPRLEGKRAG SLOKTSADTWENDERVITYTRQGGSLDGFYRAMHQ YPTSWREMPLEERPRUPFDGVMMLTPERPGSIVPRLERRER GPRINKRGWRERLAGEFLGLEVDFPLOVALDERTSGGLSEARM GRYNKRGWRERLAGEFLGLEVDFPLOVALDERTSGGLSEARM ELIFPUTGSKEKGLTKKRTVQKKSLLIKKPLRVDLILENTSK VPAPKOLLANDPRAKKLERGUMSKLAKGPLEPEVBRONG ELIFPUTGSKEKGLTKKRTVQKKSLLIKKPLRVDLILENTSK VPAPKOLLANDPRAKKLERGUMSKLAKGPLEPEVBRONG ELIFPUTGSKEKGLTKKRTVQKKSLLIKKPLRVDLILENTSK VPAPKOLLANDPRAKKEGLOMSKLAKGPLEPEVBRONGLEFTSGGLSEARM ELIFPUTGSKEKGLTKKRTVQKKSLLIKKPLRVDLILENTSK VPAPKOLLANDPRAKLTRGOLMSCLAKGLOMSKLAKGPLEPEVBRONGLE ELIFPUTGSKEKGLTKKRTVQKKSLLIKKPLRVDLILENTSK VPAPKOLLANDPRAKLTGOLMSCLAKTROTTKVQKKSLLIKKPLRVDLILENTSK VPAPKOLAARARAENGEODTVERPPTLAMGAGSYNFETSGLECGLLE ESDGGEGFQQGGGFGADAEVCTPARLATTEKKTGQGRREKA VERLRVQCAARAERAREHGPARLEGUMSKTERLIKEGG KYKKGVKRPRABLETTVADGHLEPPARTEKKEG KOARREABADKRRLGRUKYGADDIDVQLSSELTTDSLTKLKOG KULLDERFSKFGRRAMEFPERDALPFRARGUMERPASSLRGTREKTE ARVOLQQQIMTI IDBIGKASAKQNISAPITASSRMQSNSHTVYS LIKDSSARPAGKGAI IGFIKVGYKKLFVLDDREAINSVEBLCIL DFYTHSSVGNIGHGRELGYVLGKRVEPPHOTTP ARVOLQQQIMTI IDBIGKASAKQNISAPITASSRMQSNSHPVTI LIKDSSARPAGKGAI IGFIKVGYKKLFVLDDREAINSVEBLCIL DFYTHSSVGNIGHARELGYVLGKRVEPPHOLIDSPOKLIKFA AVDDTPAAPARLEPPKARGILFYSSGRICHFYSSGRICHLIKFA AVDDTPAAPARLEPPKARGILFYSSGRICHFYSSGRICHLIKFA AVDDTPAAPARLEPPKARGILFYSSGRICHFYSSGRICHLIKFA AVDDTPAAPARLEPPKARGILFYSSGRICHFYSSGRICHLIKFA AVDDTPAAPARLEPPKARGILFYSSGRICHFYSSGRICHLIKFA LERGQGAADAKKGAESSWASMALAYGELOJIDR LERGQVGGNAAATAFFRGHGCTANDANTKYNSRAAQMYBEKTRQ LGCAYGGNAAARATAFFRGHGCTANDANTKYNSRAAQMYBEKTRQ LGSAALARHGTUHLINGNARGALAVALSKEP ALGRGGHAAAAPAVPVRCFFFCTDIVIMPKRKSPENTSGRGG KYKEEKQEAGKGGTAPSRKKSLAKEPGAKISGRG KYKEEKQEAGKGGTAPSRKKSLAKEPGAKISGRGG KYKEEKQEAGKGGTAPSRKKSLAKEPGAKISGRG KYKEEKQEAGKGGTAPSRKKSLSCLSFALDDL	6470	2726	1437	
QHPSSGGRCRGGTESPSSAAGRASMARAEDENLENTRADDUS EMESPABLIDLQAQLOMFRAQMWELLAFVSSSILENTRCRARGE SLOKTSADTKGKOEOAKEKARELFLKAVEEEDNGALVEAIKY RRAMGLUPDI EFKITYTFSPDGGGVGNSY1EDNDDDSKMADLLS YFQQQLTFGESVLKLQPELESQIHISVLPMEVLMYIFAWVVS SDLDLRSLEQLSLVCRGFYYCARDPETWRLACLKWGRSCIKLV PYTSWREWFLEERPRVRFDGYTYSKTYTIRGGEQSLDGFYRAWHO VEYYMYIRFFPDGHWMLTTPEEPGSIVPFLETR FFFDRWARGGSWGGKGSSSSSDADSGFGLRPFYSVDFALRERR GFRNKKGWRELAGDFLGLEVDQFLEDVLQCRTSGGLSEADN ELIFFVUTGSKEKGLTKKFRWCKKSLLKRUDLILENTSK VPARKNGWRELAGDFLGLEVDQFLEDVLQCRTSGGLSEADN ELIFFVUTGSKEKGLTKKFRWCKKSLLKRUDLILENTSK VPARKNGWRELAGDFLGLEVDQFLEDVLGCRTSGGLSEADN ELIFFVUTGSKEKGLTKKFRWCKKSLLKRUDDIFFLE OTKKKGVKRIPARLHTKFSQAPAVEVAPAGASYNTSFEDHGTLLS ANHEVELQRGKEABEKLERQLAFPATCAATGSTTGCGLSELE ESDGGEGFGCGSGPAGDADEVCPTFARLATTEKKTEQORREKA VPERRVQQAALPARARLHTKFSQAPAVEVAPAGASYNTSFEDHGTLLS ANHEVELQRGKEABEKLERQLAFPATCAATGSTTGLCGGLLE ESDGGEGFGCGSGPAGDADEVCPTFARLATTEKKTEQORREKA VPERRVQQAALPARARLHKGVAPDIDVGLEFPARTHEGKTKJEVE ONLKROFKSFGRRWINEPERRAKFRKYKKKLVEKRAFREIGL SGGSDRAGNAMFFPFDUDALFPERTITULELPARRPEITT AAVDLQQIMTIIDELGKASAKAQNLSAPITSASRMGSKRHVY ILKDSSARPAGKGAIIGFIKVGVAFUDDREAHREVEFLCILL DFYIHSSVGRHGHGELFGYMLGKREVEHQLAFLDRFSGRKLKF LINKHYNLETTVPGVNNEVIFEGFFAHGHRPPAPSLRATHISKAA AVDPTPARAPARRLPFKAREDDIKFYSSGFEKVAVEPPWBLN RAPRRATPPAHPPPRSSSLGNSPERGFLRPFVPWBLN RAPRRATPPAHPPPRSSSLGNSPERGFLRPFVPWBLN RAPRRATPPAHPPPRSSSLGNSPERGFLRAPPYNKACEPGCGAX NPSWASITTGWFLCIDGSGVHRSLGVBLSFTKSTELDSNNNWPQ LGSAALARNGTDLWIDMMSAVPNHSPEKKNSDFFTEHTOPPAM DAPATBPSGTQQPASTESSGLADPENGPNTDLLGTSPKASLEL KENGQAADAKAARSHARAYBERGTKAREPHARLSRAGA KVKEEKGAAAKSGLAGAKNSGLAGAKNSGSFSBIERGAANIEKKRG KKEEKGAAAKSGLAGAKNSGLAGAKNSGSFSBIERGAANIEKKRG KKEEKGAAAKAGTAAPAPVFVCFTFFFTDIVHPRKSPENTTGGKGG KVTKGSPTRRSARLSAKAPAPKEEPRHRFRKSTVNVSTSRGTP PSTLSVKGGIETVVKKGTEN 6475 3 462 LORGRIPHAAPAVFVCFTFFFTDIVHPRKSPENTTGGKGG KVTKGSPTRRSARLSAKAPAPKEEPRHKRSTAKKEPGAKISRGA KKKEEKGAAKGCTAAPSROGTAABEHLISRSTVUNSTSRGTP PSTLSVKGGIETVVKGTEN CARGROWNERSARIYADAVSBALKSSTVGLVTHERKKERGREGGGE AARMSVKDEGBRWYTTSVKGTEN OADABARRARDADVFUCTETEN RGGARTANDEGERENTILERERGE RGJAKROHLEBORHV	1			GPLPREDGCRTPGPOLLPLPGALLPRPTIL SCARFORDER
SEMESPATIDLOAGLOMFRAGMMETLAPOVSSSINLENRECRARIEL SIGNER SIGNERS SUCKISATURISKOEGONALVEEGONGALVEALKRY RRAMGLVPDIEPKITYTESPOGGOVGNSYIEDNOGSKMADLLS YPOQULTPGESVIKLOPBELSSQIHISVLPMEVIMYIFRWVVS SULDLRSLEQLSLVCRGFYICARDPELWRHACLKWGRSCIKLV PYTSWREMPLERPRVRPDGVYISKTTYIRGOSGSLOFTRAWHO SUSYNYITEPPOGNYMMUTTPEEPGSLVKLOPPERAWHO EVSYNYITEPPOGNYMMUTTPEEPGSLVKUPGERTSGGLISEPAPN GFRINKKRGWRERLAGEPIGLEVOQPLEDVUPGERTSGGLISEPAPN ELLFPUTGSKERGLTKKRTKUQKKSLLLKKPLRVDLILENTSK VPAPKDULAGVUPNAKKLRKKEQLWEKLAKVGLEPREVRAGAR ELLFPUTGSKERGLTKKRTKUQKKSLLLKKPLRVDLILENTSK VPAPKDULAGVUPNAKKLRKKEQLWEKLAKVGLEPREVRRAGAR ELLFPUTGSKERGLTKKRTKUCHKLAKVGLEPREVRRAGAR ELLFPUTGSKERGLTKKRTKUCHKLAKVGLEPREVRRAGAR LLNPSATRAKPGPQDTVERFFTDLWAGASVNPSFEDHGTLIS AAHEVELGOALAPATEGALATEKKTEGORRESKA VERLRVQAALAPATELAGELAFATERKTEGORRESKA VPRIRVQAALRAALLENGLEFREGIKLAVQAAPDIDVOLSSIJTDSLKTIKPG ROARREAEADKFRRIGELKYQAAPDIDVOLSSIJTDSLKTIKPG ROARREAEADKFRRIGELKYQAAPDIDVOLSSIJTDSLKTIKPG ROARREAEADKFRRIGELKYQAAPDIDVOLSSIJTDSLKTIKPG ROARREAEADKFRRIGELKYQAAPDIDVOLSSIJTDSLKTIKPG ROARREAEADKFRRIGELKYQAAPDIDVOLSSIJTDSLKTIKPG ROARREAEAPARGRAIIGFLKYQAKDLJUKERKRESTUTTERTIKPG ROARREAEAPARGRAIIGFLKYQAKDLJUKERKRESTUTTERTIKPG ROARREAEAPARGRAIIGFLKYQAKDLJUKERKRESTUTTERTIKPG ROARVOLGARAMEFFFDVMLQKRRVERPHOLAIDREAMSVERTUTT ARVOLOQUIMTIIDELGKASAKQANLSADITTSASRMSNIHVY LIKBSSARFARGKGITIKVGYKKLPULDBEAMINEVEPLCIL DFYIHESVQRHHGRGELFFYMLQKRRVERHOLAIDREAMSVERLUKER ARVOLTPRAPARRILPPKRAGGIKYYSSSDREFLKVAVEPPWPLN RAPRATPPAPPAPHPPRSSIGNSPERGFLKARFITSAGKLEP LECQUGGNANATAFFRIGGCTAMDANTKYNSRAAMVSHLAVVENDAMA APPERPAPPAPHPPRSSIGNSTAREFULGTFREATENDERMINFG LECQUGGNANATAFFRIGGCTAMDANTKYNSRAAMMYSKRAA DAPATEPSSTOQAPPSTESSGLAQPBERGTAREFHISRTVNVSTSRGTD PSTLSVKGQIETVVKKGTEN LOGRAGHPAAAPAVPVCTTCFFTDIVIMPKRKSPENTEGKOGS KVTKGEPTRRSARLSAKAPAPKPCFTFCPFDIVIMPKRKSPENTEGKOGS KVTKGEPTRRSARLSAKAPAPKPCFTFCPFDIVIMPKRKSPENTEGKOGS KVTKGEPTRRSARLSAKAPAPKPCFTFCPFDIVIMPKRKSPENTEGKOGS KVTKGEPTRRSARLSAKAPAPKPCFTFCPFDIVIMPKRKSPENTEGKOGS KVTKGEPTRRSARLSAKAPAPKDERHTKEGTURDKARGEALVERER ROLARGVHENGERANHLLKKREGREGOMELKKISCLSFALDDLD CADABARRANGLGK	1			OHPSSGGRCRGGTESPSSAAGRPASMARAFFDCUGDTURA DDDD
SJOKTSADTIGKGCOAKEEKARELIKAVEEEGNIGALYEAIKAY RRAMGULUPDIEFKITYTESPOGGGVGNYYLENDODDSKANDLLS YRQQUIFFOESVIKLICOPELESSQTHISVLPMEVLMYTPRIVUS SULDLIRSIEGLSLUKCGEYTCARDPEIWHLACLKVWGRSCIKLV PYTSYREMFLERPRYRFDGVIJSKTTIKGGSSLDGFYRAWHQ VEYYRYIRFFPDGHWMLTTEEEPGSIVPELRITR GPRINKRGMRILAGDFLGLEVDGPLEDVRUGERTSSGULSEADN ELLFFVOTGSKEKGITKKRYKOKKSLLLKKPLRVDLILENTSK VPAPKDVLARGOPPOLEVROGPLEDVRUGERTSGULSEADN ELLFFVOTGSKEKGITKKRYKOKKSLLLKKPLRVDLILENTSK VPAPKDVLARGOPPOLWARKKRREGULWEKLAXGGELDERVRAOAN LINDSATRARPGPGOTVERFYVLWKSSLLKKPLRVDLILENTSK VPAPKDVLARGOPPOLWARKKRREGULWEKLAXGGELDERVRAOAN LINDSATRARPGPGOTVERFYVLWKSSLLKKPLRVDLILENTSK VPAPKDVLARGOPPOLWARKKRREGULWEKLAXGGELDERVRAOAN LINDSATRARPGPGOTVERPFYDLWASDDEPLAVOEDEFILE OTKKKGVRRARLHTKPSQAPAVVAPAGASYNPSFEDHOTLLS AAHEVELQRQKEAEKLERGLAJAPTEQRATGESTTGELGGLLEE ESDGEGEPGGSEPGGGBPFAGGALVEYFTARLATEKKTEQORRREKA VERLRVQQAALRARLHHGELFRLGIKAQVALILABLARRGRR RGARREABAKPRIGGLAVGAPDIDVOLSSILTDSLRTIKDEG NILKDSRRSFGRRWMIPPRERAKFRRYKYKULVEKRAFREIGL SCGSDRRQAMEPFPTOWALPAPTEGTTFP ARVOLQQIMTIIDELGKASAKAQNLSAPITSASRMQSRRHVVY ILKDSSARPAGKAPITGHAPPARRFRITTYP ARVOLQQIMTIIDELGKASAKAQNLSAPITSASRMQSRRHVVY ILKDSSARPAGKAPITGHAPPARRFRITTYPARPATTTP ARVOLQQIMTIIDELGKASAKAQNLSAPITSASRMQSRRHVVY ILKDSSARPAGKAPITGHAPPARRFRITTYPARPATTYPATHOPPAR AVDFTRARPAGKAPITGHVOYKKLFYDIKARPEPUTTERVAPPYNKACPDCGAK NESMASITYGVFLCIDCSGVRRSIGVILGFTRSTELDSMINNFO LERMOVGGRANATAFFREGDIKTSGUTKSPAGLEKVAVEPPWBLIN RAPRRATTPRAHPPARSSIGNISTAGVILGFTRSTELDSMINNFO LERMOVGGRANATAFFREGGCTANDANTRRAQMYREKIRG LGSAALARRGTDLAVILOMSSAVPNHSPEKKDSFFTEHTQPPAN DAPATEPSGTQQPAPSTSSGLAAPBHOPTDLLGTSFRASLEL KSSITGKKKPARAKKGLGAKKGLGAKKSGSFSBETRGAGVAREK KKGERKGBAGKGETAPSRNGETKABEHHISRSTVAVSTSRGTP PSTLSVKGGITTVXKGTEN LORGROHPAAAPAPVFVCTFFTPTDVIMPRKSPENTEGKDGS KVTKGSPTRRSARLSAKPAPPKPEPKPRKTSAKKEPGAKISRGA KKKEEKGBAGKGETAPSRNGETKABEHHISRSTVAVSTSRGTP PSTLSVKGGIETTVXKGTEN LORGROHPAARAPAPVFVCTFFTPTDVIMPRKSPENTEGKGGS KVTKGSPTRRSARLSAKAPAPPKPEPKPRKTSAKKEPGAKISRGA KKKEEKGBAGKGETAPSRNGETKABEHHISRSTVAVSTSRGTP PSTLSVKGGIETTVXKGTEN LORGROHPAAAPAPVFVCTFTFPTDVIMPRKSPENTEGKGGS KVT	1	∤ ·		ENESPAETDLOAOLOMFRAOWMFELA DGVSSSNI ENEDCRADO
RRAMQLVPDIEFKITTTRSPIDGOVONSYIEDDDDSKMADLLS YFQQUITFQSEVIKLOPPELSVILISULPMEVLMYIFWAVOS SDLDLRSLEQLSLVCRGFYICARDPEIWRLACLKVWGRSCIKLV PYTSWREWPIERPRWYPGVYISKTYTIRQGOGSLDGFYRAWHG VEYYRYIRFPPDGHVMMLTTPEBPQSIVPRLETR 6471 1750 299 FFFDXMAAGGSGVGGKRSSKSDADSGFLGLEFTSVDPALRHRR GPRINKRGWRRLAQDELDGLEVUQPLEGETSGGLISEAPAN EKLFYUTGSKERGLTKKRTKVQKKSLLLKKPLRVDLIESTAGN EKLFYUTGSKERGLTKKRTKVQKKSLLLKKPLRVDLIESTAGN EKLFYUTGSKERGLTKKRTKVQKKSLLLKKPLRVDLIESTAGN LLNPSATRAKGPODTVERPPYDLWASDNPLDRPLVQODEFFLE OTKKKGVKRPARLHTKFSQAPAVEAPAGASYNTSFEDHQTLLS AAHEVELQRQKARAKLERQLALPATEQAATQESTFGELGGGLE ESDGEGEGGGGPGEAGDAEVCTPARLATTEKKTEQORRESKA VERRIVQOAALRAALRIGGEFFLERGVALLVEKRTEQOKRESKA VERRIVQOAALRAALRIGGEFFLERGVALLVEKRTEGOKRESKA VERRIVQOAALRAALRIGGEFFLERGVALLVEKRTEGOKRESKA VERRIVQOAALRAALRIGGEFFLERGVALLVEKRTEGOKRESKA ROARREAEADKPREGGRAAVALVALSKALRREGLEGGLE ESDGEGEGGGGDGEAGDAEVCTPARLATTEKKTEQOKRESKA VERRIVQOAALRAALRIGGEFFLERGVALLVEKRTEGOKRESKA VERRIVQOAALRAALRIGGEFLERGVALLVEKRTEGOKRESKA ROARREAEADKPREGORDAEVCTPARLATTEKKTEQOKRESKTLKY ROARREAGABANGAEFPROGRAMPTERGETAGARVALLVEKRTEGOKRESKA VERRIVQOAALRAALRIGGEFLERGVALLVEKRTEGOKRESKA ROARREAGABANGAEFPROGRAMPTALBYGERGTTS ARVDLQQUIMTIIDELGKASAKQNLSAPITASRAMQSKRHVVY LIKBSSARPAGKAJIIGFIKVOYKKURLVEKRAPEDLCIL DFYIHESVQRHGHGEELGYMULQKERVEPHQLA DRRSCKLLKF LNKHYNLETTYPQVNHTYIFEGFFADHPAPPASPLARTHSRAA AVDETPAAPARKLIPKKRAEGIKYTSTESSLADBERGPAPPAPPLEPRISAL LNKHYNLETTYPQVNHTYIFEGFFADHAPATSSALADPPAPPAPPLENGERGAK AVPETPAAPARKLIPKKRAEGIKYTSEFTAGAVA PARATTSPAHPAPPAPPSSSLANDSANDANTKYNSRAAQMYREKIRG LGSAALARRIGTOHINTMSSAUPNISPEKKOPDTDLLGTSFKALLEL KSSIIGKKKPAAAAKGLGAKKGLGAKKGLGAKKGLGAKKCERGACKETASSKOTASKERGTAGKACH LKSQOAAAKAGAESVASMELAYQELQIDR 6474 3 462 LORQRQHFAAAPAVPVRCFTFCFTDIVIMPKRKSPENTEGKDGS KVYKQBFTRSSARLSAKPAPPEPKPKTSAKKEPGAKISRGT SKYEKGCEAGKECTAPSERGSTKAEBIHISRSTVNVSTSRGTP PSTLSVKGGIETVRVKGTEN 6475 106 1090 ARAMAQYKGTMEERGKGTAPSERGSTKAEBIHISRSTVNVSTSRGTP PSTLSVKGGIETVRVKGTEN 6476 106 1090 ARAMAQYKGTMEERGREGNEVLKKURGNIAGETIL KSOVOKRFSAHTAAVEALKKSSTVULTUMDKKRSPENTEGKDG CADAAARRAGNLCKNPOUTSFLIPDDREEERBRIKEECGER	1			SLOKTSADTKGKOEOAKEEKAPELELKAVEEPONGALVEATURV
YYQQQLTTQESSYLKLCQPELESSGIHISULPMEVLMYIPRWVUS SDLDLRSLEQLSLVCRFYICARDPEIAACLKWRGEGIKLV PYTSREMFLERPRVEPDQVYISKTTYIRQEGGLDGFYRAHIQ VEYYRYIR PPPDGHVMMLTPEBPQGIVERLETR FFFDWAAGGSGVGGRESSKSDADSGFLLRETSVDPALRERRE GFRNKKGWERLAQBELGLEVDQFLEDVSLQERTSGLISEAPN ELLFFVOTGSKEGGITKKRTVKVKSLKKLKURDLENTSK VPAPKDVLAHQVPNAKKLRREGUMEKLAKQGELPREVRAQAR LLNPSATAKPGPQDTVERPPYDLWASDNPLDENTVGCFEGLISEAPN CYKKKGVRRARLHTKYPSQAPAVEVAPGASYNDSFEDHQTLLS AAHBVELQRQKEAEKLERGLALPATEQAATQESTFQELGGGLE ESDGGEGEGGGDEPEGGADEVCTPTRATTEKTEGGOKREKA VWRLRVQQAALRAARLRIGGELFRAITEKKTLOKGKREKA VWRLRVQQAALRAARLRIGGELFRAITEKKTEGGOKREKA VWRLRVQQAALRAARLRIGGELFRAITEKKTEGGOKREKA VWRLRVQQAALRAARLRIGGELFRAITEKTEKTGGOKREKA VWRLRVQQAALRAARLRIGGELFRAITEKTEKTGGOKREKA VWRLRVQQAALRAARLRIGGELFRAITEKTEKTGGOKREKA VWRLRVQQAALRAARLRIGGELFRAITEKTEKTGGOKREKA VWRLRVQQAALRAARLRIGGELFRAIGIKAQVALLALAARGOR RQARREABAKPRRIGGIKKYQAPDIVGSSELTTSLEVDEG NILRDRFKSFORRNMIEPRERAKFKKYKVLUEKRAFREIGL DFYYHESVQRHGHGEGEASAAKQNISSTIASSRMYSRRITVY ILKDSSARPAGKGAIIGFIKVGKKFVLDDREAHREVEPLGIL DFYYHESVQRHGHGEGEASAAKQNISFIASSRMYSRRITVY ILKDSSARPAGKGAIIGFIKVGKKFVLDDREAHREVEPLGIL LNKHYNLETTVPOVNNFVIFEGFFAHQHARWEVPDLGTBRARAA AVDFTPAAPARKLPPKRAEGIKYPPVDALFPERTFUNAGCFDCGAK LNKHYNLETTVPOVNNFVIFEGFFAHQHARWEVPNKACFDCGAK AVDFTPAAPARLPPKRAEGIKYPPVV SSAVEFWEGERMAAEPRKTEIGTLFKKLRAVPFNKACFDCGAK AVPSPABSITYGVFLGIGGSWRSLGVHFIRSTEILDSMWNMPQ LRCMQVGGNANATAFFROHGCTANDANTKYNSRAAQMYREKIRQ LGSAALAARHGTDLWIDMSSAVPNHSPKRASPFTHTGYPAM DAPATEPSGTQQPAPSTESSGLAQVASSEGSFERRAQVAE KKRECKGEKGEMAABANDARCHFFFTDIVIMPKRKSPENTEGKDGS KVYKQEPTRRSARLSAKPAPPKPEPPPPRKTSAKKEPGAKISRGA KCKKEEKQBAGKEGTAPSRMGTKAEBIHISRSTVNVSTSGTT PSTLSVKGQIETVRVKGTEN 462 LQRGGHPAAAPAVVERTFFFTDIVIMPKRKSPENTEGGEGG KVYKQEPTRRSARLSAKPAPPKPEPPPPRTSAKKEPGAKISRGA KCKKEEKQBAGKEGTAPSENGETKAEBIHISRSTVNVSTSGTT PSTLSVKGQIETVRVKGTEN 6476 106 1090 ARAMAQYKGTMFEAGRAMHLLKKRERQREGMEVLKKNTCLGFFLDDLDD QADAAEAREAKSNTSULTVILIDMKARGREALVREER RQIAKROHLEEGLLOGRGREGGERREKKTSGLIGFFLOGLURGER RQIAKROHLEEGLLOGRGREGGERREKKTSGLIGFFLOGLURGER RQIAKROHLEEGLLOGRAGGGORRERKKTSGLIGFFLOGLURGER BAQREKVKD				RRAMOLVPDIEFKITYTRSPDGDGVGMSVIFDNDDDGVMADITG
SSLDLRSLEQLSLVCRGFYICARDPEIWRIACLWWGRSCIKUV PTYSREMFLERRRVPDGVISTYTYIRGGOSLDGFYRAHHO VEYYRYIR FPPDGHVMMLTTEEDQSIVPRLETR FFPDXMAAGGSGVGKRSSKADDSGFLLRFTSVDPALRRRRR GFRINKRGWRRLAQDELGLEVUQPLEDVALQERTSGGLISEAPN EKLFYUTGS KEKGLTKKRTKVOKKSLLLKKPLRVDLLIENTSK VAPAPGULAHQVPUNAKLRKERGLEURALAQGELLPREVRRAQAR LLINPSATRAKPGPOTVERPPYDLWASDNPLDRPLVQODEFFLE OTKKKGVKRPARLHTKFSQAPAVEVAPAGASYNTSFEDHQTLLS AAHBYELQRQKEABELKERGLAPARTCANTSFEDHQTLLS AAHBYELQRQKEABELKERGLAPARTCANTSFEDHQTLS AAHBYELQRQKAEABLKERGLAPARTCANTSFEDHQTLS AAHBYELQRQKAEABLKERGLAPARTCANTSFEDHQTLS BSOGGEPGGGBOPERGDAEVCTPARLATTEKKTEQORRRSKA VERLRVQOAALRAALRHOELFRIAGAVQUALLABLARQRR RQARREADKPRRLGRLKYQAPDIDVQLSSELTDSLRTLKPEG ROARREADKPRRLGRLKYQAPDIDVQLSSELTDSLRTLKPEG RQARREABAKPRRLGRLKYQAPDIDVQLSSELTDSLRTLKPEG RQARREAPARKPRRLGRLKYQAPDIDVQLSSELTDSLRTLKPEG RQARREAPARKPRRLGRULKYQAPDIDVQLSSELTDSLRTLKPEG RQARRAFFFQRWMIEFFRCHDALFPERTYLDDREAMPGTTTP ARVDLQQQIMTIIDELGKAGAKAQNLSAPITSASRMQSKRHVVY LLKDSSARPAGKGAIIDFIKVGYKLUDGREAMPEVEPLCIL DFYTHESVQRHGHGRELFQYMLQKERVEPHQLAIDRESKRLKVF LINKHYNLEITTVQVNNFVIFEGFFAHQKRPPAPSLRATHSRAAA AVDETPAAPARLIPPKRAEGDINFYSERPLKVAVDEPWPWILN RAPRRATPPAHPPPRSSSLKNSPERFLKVAVPTNKACFDCGAX NPSWASITYGVPLCIDCSGVHRSLGVHLSFIRKTSTELDSMWNFQ LRCMQVGGRANATAFFRQHGCTTANANTKNNSARAQMYREKIRQ LGGSALARAGGTHATBOMSSAVNNISPEKKDSPFFTHOPPAW DAPATEPSGTQQAPASTESSGLAQPEHGPNTDLLGTSPKASLEL KSSIIGKKRPAAKKGIGAKKGIGAKKGIGAKVSSSPSBIERQAQVAE KLREQQAADAKKQAEESMVASURLAYQELQIDR 6474 3 462 LQRQRGHPAAPAVPVRCFFFCFTDIVIMPKRKSPENTEGKDGS KVYTKGSPTTRSARLSAKPAPPKPEPKFKTSAKKEPGAKISRGA KGKKERKQGIETVRVKGTEN 6475 3 462 LQRQRGHPAABAVPVRCFFFCFTDIVIMPKRKSPENTEGKDGS KVYTKGSPTTRSARLSAKPAPPKPEPKFKTSAKKEPGAKISRGA KGKKERKQEAGKEGTAPSRNGGTKAEBIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN 6476 1060 1090 ARAMAQYKGTMREAGRAWHLLKKRRQREQMEVLKQRIAEETIL KSCVOKRTSAHYDAVEREKKSTVCUVTLINDMKARGELVRERE RQLAKROHLEEQRIQOGRRRGRERKKKISCLSFALDDLDD QAAABARARAGNICKHDPUOTSFLUDGGGRRRGEENKHLEELLRGBW BAQREKVKDEEMEVTFSVMDGSGRRTVRVNRNTVVQGFLKKAL GGLRKDFLEERSAGVVLUKEMVEKKHTP		1		YFQQQLTFQESVLKLCOPELESSOTHTSVI.PMENT.MVTEDLITATO
FPTTSMREMFLERRVKPGOVITSTTYIRGGSGLDGFYRAMHQ VSYYNYTPYPDCHWMITTEEEPGSIVOPRIETR GPRNKKRGWRIFPPDCHWMITTEEEPGSIVOPRIETR GPRNKKRGWRIAGPELGLEVDGFLEDVELGERTSGLISEAPN ELLFPVOTGSKEKGITKKRTKVCKKLKKLKGLEKFLKPLLEVELLENTSK VPAPKDVLANGVPNAKKLRREGLMEKLAKGGELGEREVRRAGAR LINPSATRAKPGFGOVTSKRPTVLNAKBPLDEPLAVGODEFFLE O7KKKGVKRTRAHHTKPSQAPAVEVAPAGASYNPSFEDHOTILIS AAHEVELGRQKEAEKLERQLALPATEQAATGESTFGELGEGLLE ESDGEGEFGGBGPERGGBEVCETPARTTEKTETGGOKREKA VHERRVQOAALRAARLRIGGELFELRGIKAQVALLABLARGGR ROARREAEADKPRRIGGRIKVQAPDIOUSSELTDSLITLKDEG NILBDRYKSFORRNMIEPRERAKFKKVKLVEKRAPREIGL 6472 3 897 SGGEDRAGMAMEFFFDVDALFPERITVLODHERPARRFGTTTP ARVDLQQIMTIIDELGKASAKAQNISAPITSASRNGSKRHVVY ILKDSSARPAGKGALIGFIKVGYADDIOUSSELTDSLFTLKDEG NILBDRYKSFORRNMIEPRERAKFKKVKLVUKKRAPREIGL DFYTHESVORHGHEELGYMLGKREPGLIADRRSGKRHVVY ILKDSSARPAGKGALIGFIKVGAPDIOUSSELTDSLFTLKDEG NILBDRYKSFORRNMIEPRERAKFKKVKLVLVEKRAPREIGL DFYTHESVORHGHEELGYMLGKREPGLIADRRSGKRHVVY ILKDSSARPAGKGALIGFIKVGAPDIOUSSELTDSLFTLKDEG NILBDRYKSFORRNMIEPRERAKFRIKVELUTHDREAHNEVEPLCIIL DFYTHESVORHGHEELGYMLGKREPGLIADRRSGKLKF INKHYNLETTVPQVNNFVIFEGFFAHQRRPPAPSPLRATHSRAA AVDETPAAPARLIPPKAREGGIKYPSSLROTHVSCALLE RAVDETPAAPARLIPKRAEGGIKYSSSTEPKLAVAVEPPWPLIN RAPRRATPPAHPPPKSSSLGNSPERGPLRFVVP 6473 22 912 SSAVEFVMEGEKMAAERNKTEIGTFFKELEDSMWNFQ LRCMQVGGNANATAFFROHGCTANDANTKYNSRAAGMYREKIRG LGSAALAARGTOLHATUMSSAVDNISPEKKDSDFFTEHTOPPAN DAPATEPSGTQQPAPSTESSGLAQPEHOPNTDLLGTSFKASLEL KSSIIGKKKPAAAKKGLGAKKGLGAKKSDFFTEHTOPPAN DAPATEPSGTQQPAPSTESSGLAQPEHOPNTDLLGTSFKASLEL KSSIIGKKKPAAAAKGLGAKKGLGAKKSDFFFTEHTOPPAN DAPATEPSGTQQPAPSTESSGLAQPEHOPNTDLLGTSFKASLEL KSSIIGKKREKQBAGKEGTAPSRNGTKABEIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN 6476 3 462 LQRGGHFAAAPAVVRCFFFCFTDIVIMPKRKSPENTEGKDGS KVTKGPFTRSARILSAKPAPPKPEFPKTSAKKEPGAKISRGA KGKKEEKQBAGKEGTAPSRNGTKABEIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN 6476 1090 ARAMAQYKGTMREAGRAMHLLKKRERGREGMEVLKKNTGULKRERE RQIAKROHLEEGRIQOGGRRERKKKTSCLSFALDDLDD QADAABARARELKSSTVGUTINDMKRKGEENLIKEEL KSOVOKRFSAHDAVAERKEKSTVGUTINDMKRKGEENLIKEEL GQARKVKDEEMEUTFSVHDOSGRRETKRVRNNTVOQFLKKAL GGRREFFAHDAVEREERENL	1	!		SDLDLRSLEQLSLVCRGFYICARDPETWRLACT.KUWGPGGTVT.
6471 1750 299 FFFDKMANGGSGVGKSSKSDSGFJGLFPTSVDPALRERRE GFRNKRGWRLAGGPLGKKSSKSDSGFJGLFPTSVDPALRERRE GFRNKRGWRLAGGPLGKEVGLFLENTSK GFRNKKGWRSLAGGELGLEAPN EKLFFVDTGSKEKGLTKKRTKVGKSLLLKKPGEUPEUENTSK VPAPKDVLAHQVPMAKKLRKRGGLPREVENGAGE LLNPSATTAKBGPQDTVERFFVDLWASDNPLDRPLVGQDEFFLE OTKKKGVKRALTKIKTSGQAPREVARGASYNPSFEDHQTLLS AAHEVELQRQXEAEKLERQLALPATEQAATQESTFQELGEGLLE ESDGGGEGGGGGPAGDABVCPTFARLATTEKKTGQARREKA VHRIRVQQAALRAARLENGELFRIGKIKAQVALRLAELARRQRE ROARREABANFRRLGRLKYQAPDIDVQLSSEITDELFTLKDEG INLEDPRKSFQORRMARENGELFRIGKIKAQVALRLAELARRQRE ROARREABANFRSCHGLKYQAPDIDVQLSSEITDELFTLKDEG INLEDPRKSFQORRMIEPPERFKSFVKVLVLVEKRAPREIQL DETYTHESVQRHENGERSFFFDVDALFFBEITVLDQHLEFPARREGTTTP ARVOLQQINTIIDELGKASAKAQNLSAPITASSRMQSNRHVVY ILKDSSARPAGKGAIIGFIKVYKLFVLDDREAHREVEPLCIL DFYTHESVQRHGIGGRELFGYMLQKERVEPHQLAIDRPSQKLLKF LNKYTHYDEVTAPARARKLPPKRAEGGIKFYSSDEFLKVAVEDPWFLIN RAPRAARALPPKRAEGGIKFYSSDEFLKVAVEDPWFLIN RAPRAARALPPKRAEGGIKFYSSDEFLKVAVEDPWFLIN RAPRAARALPPKRAEGGIKFYSSDEFLKVAVEDPWFLIN RAPRAARALPPKRAEGGIKFYSSDEFLKVAVEDPWFLIN RAPRAARATPAPHPPPRSSSLGNSPERGFLRFVD SAVEFWEGEKMAABAPFNKTEIGTFFVD AVDITAABRAK GARVAVEDPWFLIN RAPRAARATPAPHPPPRSSSLGNSPERGFLRFVD LICTGVGGGAK NPSWASTTYSVFLCIDCSGVRSLGVILSPIRSTELDSNMWFQ LRCMVGGGNANATAFFRQHGCTANDANTKKNRAAQMYKEREIRG LGCAGAAARATAFFRQHGCTANDANTKKNRAAQMYKEREIRG LGCAGAAARATAFFRQHGCTANDANTKKNRAAQMYKEREIRG KSIGKKPAAAKKGLGAKKGLGAKVSSGSFSIERQAQVAE KLRSOQAADAKQAESSWASMRLAYQELQIDR KYTKQEPTRSATLSAKAPAPKVEPKRTISAKKEPGAKISRGF KVTKQEPTRRSARLSAKAPAPKVEPKRTISAKKEPGAKISRGF KVTKQEPTRRSARLSAKAPAPKVEPKRTISAKKEPGAKISRGA KGKKEEKQEAGGGTAPSBNOETTAEEIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN 6475 3 462 LQRQRQHPAAAPAVVVRCFTFCFTDIVIMPKRKSPENTEGKDGS KVTKQEPTRRSARLSAKAPAPKVEPKRTISAKKEPGAKISRGA KGKKEEKQEAGGGGTAPSBNOETTAEEIHISRSTVNVSTSRGTP PSTLSVKGGIETVRVKGTEN 6476 106 1090 ARMAQYKGTMREAGRAMHLLKKRERGREQMEVLKORIAEETE KSGVDOKRFSAHTDAVEAGLLKSTVANGTERE RQLAKKGULEFER RQLAKKGULEFER RQLAKKGULEFER RQLAKKGULEFER RQLAKKGULEFER RQLAKKGULEFER RQLAKKOLDEFUTFOFTDIVIMPKRAGGRAUFERE RQLAKGGULEFER RQLAKKOLDEFUTFOFTDIVARGGRAUVLKSWENKHIT PSTLIABARGK SGP				PYTSWREMFLERPRVRFDGVYISKTTYIROGEOSIDGFVD AUTO
FFPDMMAGGSGVGKRSSKSDADSGFLGLEPTSVDPALRERRE GPRNKRGWRLAGEPLGLEVDQFLEDVRLQERTSGGLISEAPN EKLFFVDTGSKEKGLTKKRTKVQKSKLLLKKPLEVVDLILENTSK VPAPKDVLAHQVPNAKKLRKEQLMEKLAKGGELPREVRRAGAR LLNPSATTARKGPGOPTVERPFDLMASDNPLDRPLVQGDEFFLE GYKKKGVKRPARLHTKPSQAPAVEVAPAGASYNPSFEDHQTLLS AAHEVELQRQKEAEKLERGLALPATEQKATGOKREKA VHRLRVQQAALRAARLEHGELFRLEGIKAQVALRLAELARGOR RGARREAEADKPRIAGERLYQADPUQLSFELTGLEGGLE ESDGGGEGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG				VEYYRYIRFFPDGHVMMLTTPEEPOSIVPRIETP
GPRNKRGWRLAGEPIGLEVDQPLEDVNQERTSGGLISEAPN ELIFPVDTGSKEKGLTKKRTWQKKSLLLKKPLEVDLILENTSK VPAPKDVLAHQVPNAKKLRKREQLWEKLAKQGSLPREVRRAQAR LLNPSATTARAFGEQDTVERFYDLMASDNIDDRPLVGQDEFFLE OTKKKGVKRTARLHTKPSQAPAVEVAPAGASYMPSFEDHQTLIS. AAHEVELQRQKEABKLERQLALPATEQAATQESTFGELGGGLE ESDGEGEPGGGEGPEPAGDABVCPTPARLATTEKKTEQORREKA VHELVQQAALRAARLRHQELFRLEGIKAQVALRLAELARRQRR RQARREAEANKPRRLGRLKYQAPDIDVQLSSELTDSLRTLKPEG NILRDRFKSFQRRAMIEPPERKKFKKYKVKLVEKREKAPETQL 6472 3 897 SGGSDRAQMAMEPFFDVDALFPERTTVLDQHLRPPARRFGTTTP ARVDLQQQIMTIIDELGKASAKAQNLSAPITSASRMQSNRHVVY LLKDSSARPAGKGALIGFIKVGYKKLEVLDDREAHREVEPLCILL DFYTHESVQRHGHGRELFGYMFQKERVEPHQLAIDRPSGKLIKF LNKHYNLETTVPQVONNFVIFEGFAHQRPPAPSLEATHSRAA AVDETPAAPARKLPPKRAGGIKPYSSDREPLKVAVEPPWPLN RAPRRATPPAHPPRSSSLGNSPERGPLRFTVB 6473 22 912 SSAVEFVWECEKMAAEPKKTEIGVTLKFREAVPTNKACFDCGAK NPSWASITYGVFLCIDCSGVURSLGVHLSFIRSTELDSNMMPQ LRCMQVGGNANATAFFRQHGCTANAFKYNSRAAQMYREKIRQ LGSAALARHGTDLWIDNMSSAVPNHSPEKKDSDFFTEHTQPPAM DAPATEPSGTQQPAPSTESSCLAQPEHGPNTDLLGTSFKASLEL KSSILGKKKPAAAKKGLAKKGLAGKVSGSFSBIERQAQVAE KLESQOADAKKQAESSWASMRLAYQELQIDR 6474 3 462 LQRQQHPAAAPAVPVRCFTFCFTDIVIMPKRKSPENTEGKDGS KVYKQBPTRRSARLSAKPAPKPEPKPRKTSAKKEPGAKISRGA KGKKEEKQBAGEGTAPSENGETTAEBIHISRSTVNVSTSRGTP PSTLSVKGQIETYVKKGTEN 6475 3 462 LQRQQHPAAAPAVPVRCFTFCFTDIVIMPKRKSPENTEGKDGS KVYKQBPTRSARLSAKPAPKPEPKPRKTSAKKEPGAKISRGA KGKKEEKQBAGEGTAPSENGETTAEBIHISRSTVNVSTSRGTP PSTLSVKGQIETYVKKGTEN 6476 106 1090 ARMAQYKGTMREAGRAMHLLKKRERQREQMEVLKQRIAEETIL KSQVDKRFSAHIDAVEAGLKSTVGLVTINDMKARQBALVRERE RQLAKKQHLEEQGLQQERQRRQREQRERKISCLSFALDDLDD QAAAABARRAGHLKURDVDTSFLDPRDREBEENRLREELRQBW EAQREKVKDEMEVTFSYWDGSGHRRTVRYRKGNTVQOFLKKL GQDAKROPLELBRAAGVEQMEVTKRKNHTYDFIIAARRGK SGPLEFSFDVHDDVLLLBDATMEEDSBAAGKVVLKSWKKHHT GARRAGKKKKKKKKKHLDLDSTMEEDSBAAGKVVLKSWKKHHT SGPLEFSFDVHDDVLLLBADAMEEDSBAAGKVVLKSWKKHHT SGPLEFSFDVHDDVLLLBADAMEEDSBAAGKVVLKSWKKHHT SGPLEFSFDVHDDVLLLBADAMEEDSBAAGKVVLKSWKKHHT SGPLEFSFDVHDDVLLLBADAMEEDSBAAGKVVLKSWKKHHT	6471	1750	299	FFFDKMAAGGSGVGGKRSSKSDADSGFLGLRPTSVDDALDDDD
EKLFYDTGSKEKGLTKKRTVOKKSLLLKKPLRVDLILENTSK VPAPKOVLANGVPARKLRRTKQGELPREVRAQAR VPAPKOVLANGVPARKLRTKRGGELPREVRAQAR LLNPSATRAKPGPQDTVERPFYDLWAGDBFLDRFLVGODEFFLE GYKKKGVRFARLHTKYSQAPAVEVAPAGAGYNPSFEDHQTLLS AAHEVELQRGKEBELERGLALPATEGAAGGSTFOELGEGLE ESDGEGEGGGEBGAGAEVCPTPARLATTEKKTEQGRREKA VHRLRVQQAALRAARLHRUGLFFLRGIKAQVALRLAELARQRR RQARREAEADKPRIGRLKYAGDIDVOLSSELTDSLRTLKPEG NILRDRFKSFGRRMMISPRERAKFKKYKKLVEKRAFRETOL 6472 3 897 SGSDFAQMABEFFFDVDALFPERITVLDQHLR PPARRFGTTFF ARVDLQQIMTIIDELGKASAKQNLSAPITSASRMQSNRHVVY ILKDSSARPAGKGAIIGFIKVGYKKLFVYLDDREAINEVEPLCILL DFYTHESVQRIĞHGRELFGYMLQKERVEPHQLALDRPSGKLLKF LNKHYNLETTVPQVNNFVIFEGFFAHQHRPPAPSLRATRHSRAA AVDPTPAAPARKLPPKRAEGDIKPYSFOR LNKHYNLETTVPQVNNFVIFEGFFAHQHRPPAPSLRATRHSRAA AVDPTPAAPARKLPPKRAEGDIKPYSFOR LRCMQVGGNANATAFFRQHGCTANDANTKYNSRAAQMYRELIRQ LGSAALARHGTDLWINMSSAVPNNSPEKKDSDFFTEHTOPPAW DAPATEPSGTQOPAPSTESSGLOPBFFFOR LRCMQVGGNANATAFFRQHGCTANDANTKYNSRAAQMYRELIRQ LGSAALARHGTDLWINMSSAVPNNSPEKKDSDFFTEHTOPPAW DAPATEPSGTQOPAPSTESSGLOPBFFORDHTTOPPAW CKREGOADAKKQAESMVASKALGGAKKGLGAKVSQSFSEIERQAQVAR KLREQOADAAKKGAESMVASKALGGAKKGLGAKKEPGAKISRGA KVTKQBFTRRSARLSAKPAPPKPEPKPRKTSAKKEPGAKISRGA KVTKQBFTRRSARLSAKPAPPKPEPKPRKTSAKKEPGAKISRGA KCKKEEKQEAGKEGTAPSENGETKAEBIHISRSTVNVSTSRGTP PSTLSVKGQIETTVRVKGTEN 6476 106 1090 ARAMAQVKGTIRESGRANGSKAKERGRAMSVKGAESHILISRSTVNNSTSRGTP PSTLSVKGQIETTVRVKGTEN ARAMAQVKGTMERBEAGRAMILLKKRERQREQMEVLKQRIAEETIL KSQVDKRFSAHYDAVEAELKSSTVGLVTLMMKRRGEALVRERE RQLAKROHLEGGRLQQGERGRGGGRRERVEKKISCLSFALDDLDD GADAAARARGKGIKNDDVOTS-DRDREEEERMIREELRQGW EAQREKVKDEEMEVTFSYMDGSGHRRTVRVRKONTVQGFLKKNL QGLKDPLELSSAGVEQUMFIKEDLILEPHTTYDET IJRARGK GGRLFSFDVHDDVRLLSDATHEKBESSAGKVVLRSWYENKHIF				GPRNKKRGWRRLAGEPLGLEVDOFLEDVRLOFFTSGGLLSFADN
UPAPKOVLAHQVPNAKKLRREQLMEKLAKQGELPREVBRAQAR LLNPSATRAKPOPQOTVERPFYDLWASDNPLDR PLVGQDEFFLE QTKKKGVKRPARLHTKPSQAPAVEVAPAGASYNPSFEDHQTLLS AAHEVELQRQKEAEKLERQLALPATEQAATQESTFQELCEGLLE ESDGEGEGGGGSGEPAGDABVCPPARLATTEKKTEQORRREKA VHRLRVQQAALRAARLRHQELFRLRGIKAQVALRLAELARRQRR RQARREAEADKPRELGRLKYQADDIDVQLSSELTDSLBTLKPEG NILRDFRKSFGRRMISPREREAKFKKKYKVKUKVEKAPREIOL 6472 3 897 SGSDRAQMAMEFPFDVDALFPERITVLDQHLRPPARRFGTTTP ARVDLQQQIMTI IDELGKASAKAQNLSAPITASSMQSNRHVVY LIKDSSARPAGKGAIIOFIKVGYKKLFVUDDREARINEVEPLCIL DFYTHESVQRIGHGRELFQYMLQKERVEPHQLAIDRPSQKLLKF LNKHYNLETTVPQVNNFVIFGEFFAHQHRPPAPSLRARTHSRAA AVDETPAAPARKLPPKRAEGDIKPYSSSDREFLKVAVSEPPMPLN RAPRRATPPAHPPPRSSSLGNSPERGPLRFPVD 6473 22 912 SSAVEFVWEGEKMAAEPNKTEIQTLFKRLRAVFTNKACFDCGAK NPSWASITYGVFLCIDCSGYHRSLGVHLSFIRSTELDSNNMWFQ LGSAALARHGTUKINDSAVPNHSPEKKBDSFFTEHTQPPAW APATEPSGTQQPAPSTESSGLAQPEHGPNTDLLGTSPKASLEL KSSIIGKKRPAAKKGLGAKKGLGAQKVSQSFSEIERQAQVAE KLRBQOADAKKQAESEMVASMALAYQELQIDR 6474 3 462 LQRQRQHPAAAPAVPVRCFTFCFTDIVIMPKRKSPENTEGKDGS KVYKQBFTRRSALBAKAQAESEMVASHLSHKTSRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN 6475 3 462 LQRQRQHPAAAPAVPVRCFTFCFTDIVIMPKRKSPENTEGKDGS KVYKQBFTRRSALBSAKPAPPKPEPKPRKTSAKKEPGAKISRGA KGKKEEKQEAGKGTAPSRNGETKAEBIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN 6476 106 1090 ARAMAQYKGTMREAGRAMHLLKKRERGREOMEVLKQRIAEETIL KSQVDKRFSAHYDAVEABLKSSTVGLVTLNDMKARQEALVRENE RQLAKRQHLEGRLQGERGREGGREREKKISCLSFALDDLDD QADAABARRAGIGKNPDUTDTS-DRDREEEERNIKEELINGBW EAQREKVKDEEMEVTFSVWDGSGHRRTVRVRKGNTVQQFLKKAL QGLKDFLEERSAGVGEMFILEKDERGSGGRRTCHRREAGRARGERGE EAQREKVKDEEMEVTFSVWDGSGHRRTVRVRKGNTVQQFLKKAL QGLKDFLEERSAGVGEMFILESDATSHEVBERGERGEMEVLKALL QGLKDFLEERSAGVGEMFILESDATSHEVBERGERGREWEREELRGGBW EAQREKVKDEEMEVTFSVWDGSGHRRTVRVRKGNTVQQFLKKAL QGLKDFLEERSAGVGUMFILKEDLILEPHTTFDT ITARARGK SGPLFSFDVHDDVRLLSDATHEKDESSAGKVVLRSWYMSKHKHIF				EKLFFVDTGSKEKGLTKKRTKVOKKSLLLKKPLRVDLTLENTSK
LLNPSATRAKPGPGDTVERPYDLWAGNDFLDRPLVGQDEFFLE OTKKKGVKR PARLHTHY PSQAPAVEVA PAGASYNPSFEDHQTILS AAHEVELQRQKEAEKLERQLALPATEQATQESTFOELCEGLLE ESDGEGEPGGGEPAGDAEVCPTPARLATTEKKTEQORREEKA VURLHAVQQAALARAARLINGERLEKIG KGAVQALKLAELARRQRR RQARREAEADKPRRLIGILKYQAPDIDVQLSSELTDSLPTLKPEG NILROPPKSFQRRNMIEPRERAKFKKKVKLVEKRAFRETQL 6472 3 897 SCGSDRAQWAEFPFDVDALPFERTVLLOGHLRPPARREGTTP ARVDLQQIMTIIDELGKASAKAQNLSAPITSASRMQSNRHVVY ILKDSSARPAGKGAIIGFIKVYSKLFVLDDREAHREVEPLCIL DFYTHESVQRIGHGRELEVYMLQKERVEPHQLAIDRESGKLLKF LNKHYNLETTVPQVNNFVIFFGFFAHGRPEPPAPSLRATRHSRAA AVDPTPAAPARKLPPKRREGILFYYSSSDERPLKVAVEPPWPLN RAPRRATPPAHPPPRSSSLGNSPERGPLRPFVP 6473 22 912 SSAVEFWEGEKMAAEPNKTEIQTLFKKLRAVPTNKACFDCGAK NPSWASTTYGVFLCIDCSGVHSIGSVHLSFSSDLRAFTHSTRAA AVDETPAAPARKLPPKRREGITSTSGLBINMNWFQ LRCMQVGGNANATAFFRQHGCTANDANTKYNSRAAQMYREKIRQ LGSAALARHGTDLWIDMMSSAVPNHSJEKKDSDFTEHTQPPAN ARSTIGKKPAAAKKGLGAKKGLGAQKVSSQSFSEIERQAQVAE KLRSQQAADAKKQAEESMVASMRLAYQELQIDR KSSIIGKKPAAAPAVPVECFTFCFTDIVIMPKRKSPENTEGKDGS KVTKQBETRRSARLSAKPAPPKPPFKPKTSAKKEPGAKISRGA KCKKEEKQEAGKEGTAPSENGETKAEBIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN 462 LQRQRQHPAAAPAVPVRCFTFCFTDIVIMPKRKSPENTEGKDGS KVTKQBETRRSARLISAKPAPPKPPBKPKTSAKKEPGAKISRGA KGKKEEKQEAGKEGTAPSENGETKAEBIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN 6476 106 1090 ARAMQYKGTMREAGRAMHLLKKRERQREQMEULKORIAEETIL KSQVDKRFSAHYDAVEAELKSSTVGLVTLNDMKARQEALVRERE RQLAKKQHLEEGRLQQERQREGGRAFGRERKKISCLSFALDDLDD QADAAPARRRANICKMPDUTSFLDPDREEBEERNLERELINGBW EAQREKVKDEEMBYTFSYMGGGHRTVRVRKGNTVQQFLKKAL GQLRKOPLERSAGVEQLWFIKEDLILPHYTTYDF IJARAGGK SGPLFSFDVHDDVRLLSDATMEDSSHAGKVVLRSWYEENKHIF		i i		VPAPKDVLAHQVPNAKKLRRKEOLWEKLAKOGELPREVRRAOAD
GTKKKGVKRPALHTKPSQAPAVEVAPAGASYNPSFEDHQTLLS AAHEVELGRQKREKLERQLAPATEQATQESTFQELCEGLLE ESDGEGEPQQGGPBAGDAEVCPTPARLATTEKKTEQQRREKA VHRIRVQQAALRAALRHQELFRLIGIKAQVALRIABELARRQRR RQARREAEADKPRRIGGIKAVQADDIDVQLSSELTDSLEPLTKPEG NILRDRPKSFQRRNMIEPRERAKFKKYKVKLVEKRAPRETQL 6472 3 897 SCGSDRAQWAMEFPFDVDALFPERITVLDQHLRPPARRPGTTTP ARVDLQQQIMTI IDELGKARQMISAPITSASRMQSNRHVVY ILKDSSARPAGKGAIIGFIKVGYKKLFVLDDREAHNEVEPLCIL DFYTHESVQRHGHGRELGYMLQKRFVEPHQLAIDRPSQKLLKF LIKKHYNLETTVPQVMFVIFFSFFAHCHRPPAPSLARATHSRAA AVDTPPAAPARKLPPKRAEGDIKPYSSDREPLKVAVEPPWPLN RAPRRATPPAHPPRSSSIGNSPERGLRFVFV 6473 22 912 SSAVEFVWEGEKMAAEPNKETGTIFKKLRAVPTNKACFDCGAK NPSMASTTYGVFLCIDCSGVHRSLGVHLSFIRSTELDSNNMWFQ LRCMQVGGNANATAFFRQHGCTANDANTKYNSRAAAQMYREKIRQ GSAALARHGTDLWIDMMSSVMNSPEKKDSDFFTEHTOPPAW DAPATEPSGTQQPAPSTESSGLAQPBHGPNTDLLGTSPKASLEL KSSIIGKKKPAAAKKGLGAKKGLGAKKGLGAKVSGGSPSIERQAQVAE KLREQQAADAKKQAESMVASMALAYVSLOIDR 6474 3 462 LQRQRGHBAAPAVPVRCFTFCFTDIVIMPKRKSPENTEGKDGS KVTKQEPTRRSARLSAKPAPPKPEPKPRKTSAKKEPGAKTSRGA KGKKEEKQEAGKEGTAPSENGETKAEBIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN 6475 3 462 LQRQRQHPAAPAVPVRCFTFCFTDIVIMPKRKSPENTEGKDGS KVTKQEPTRRSARLSAKPAPPKPEPKPRKTSAKKEPGAKTSRGA KGKKEEKQEAGKEGTAPSENGETKAEBIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN 6476 106 1090 ARRMAQYKGTMREAGRAMHLLKKRERQREQMEVLKORIAEETIL KSOVDKRFSAHYDAVEAELKSSTVGLVTLNDMKARQEALVRERE RQLAKROLEGQRIQQERGREGGRERKRKISCLSFALDDLDD QADABARARRAGNLGKMPDUPTSFLDPDREEEEEEPINLREELINGBW EAQREKVKDEEMBYTSYMDGSGHRTVRVRKGNTVQQFLKKAL GQLRKDFLERSAQCLMFIKEDLIHPHTTYDFILARAGGK SGPLFSFDMIDDVLLSDATMENDSSHAGKVVLRSWYERKHIF	1	1		LLNPSATRAKPGPODTVERPFYDLWASDNPLDRPLVGODEEELP
AAREVELQRQKEABEKLERQLAIPATEQATQESTFOELCEGLLE ESDESEETQGEGPEAGDAEVCPTPARLATTEKKTEQQRRREKA VHRLRVQQAALRAARLRIQELFRLEGIKGVALRLAELARRQRR RQARREABADKERRIGGIKYQAPDIDVQLSSELTDSLETLKPEG ROARREABADKERRIGGIKYQAPDIDVQLSSELTDSLETLKPEG RILDROFKES FORRMIEPERRAKFKRKYKVKLVEKRAFREIQL 897 SCGSDRAQWAMEFFFDVDALFPERITVLDQHLRPPARREGTTF ARVDLQQQIMTIIDELGKASAKAQNLSAPITSASRMQSNRHVVY LIKUSSARPAGKGAIIGFIKVYGYKKLFVULDDREAHNEVEPLCIL DFYIHESVQRHGHGRELGYMLQKERVEPHQLAIDRESGKLLKF LNKHYNLETTVPQVNNFVIFESFFAHQRPPAPSLRATRHSRAA AVDPTPAAPARKLPPKRAEGDIKPYSSDREFLKVAVEPPWPLN RAPRRATPPAHPPRSSSLGNSPERGPLRPFVP 6473 22 912 SSAVEFVWEGERMAAEPNKTEIQTLFKRLRAVPTNKACFDCGAK NPSWASITYGVFLCIDCSGVHRSIULHSFIRSTELDSNNNWFQ LRCMQVGGNANATAFFRGHGCTANDANTKNNSRAAQMYREIRQ LGSAALARHGTDLWIDMSSAVPNHSPEKKDSDFFTEHTOPPAM DAPATEPSGTQQPAPSTESSGLAGKGIGAQKVSSQSFSEIRRQAQVAE KLRRQQAADAKKQAEESWASMRLAYQELQIDR 6474 3 462 LQRQRQHPAAPAVPVRCFTFCCFTDIVIMFKRKSPENTEGKDGS KVTKQBPTRRSARLSAKPAPPKPPFRFKTSAKKEPGAKISRGA KGKKEERQEAGKEGTAPSENGETKAEBIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN 6475 3 462 LQRQRQHPAAPAVPVRCFTFCFTDIVIMPKRKSPENTEGKDGS KVTKQEPTRRSARLSAKPAPPKPPRKPTSAKKEPGAKISRGA KGKKEERQEAGKEGTAPSENGETKAEBIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN 6476 106 1090 ARAMAQYKGTMREAGRAMHLLKKRERQREQMEVLKQRIAEETIL KSQVDKRFSAHYDAVEBELKSSTVGLVTLINDMKARQGALVRERE RQLAKRQHLEGQRLQQERQREGGREGTRRKKISCLSFALDDLDG QADABEARRAGNLGKMPDUDTSFLPDRDREEEENRLREELIGGW EAQREKVKDEEMBYTFSYMDGSGHRETVRVKKGNTVQQFLKKAL QGLRKDFLEIRSAGVQLMFIKKUFLIPHTFYDFIIARARGK SGPLFSFDHNDDVRLLSDATMERDSSHAGKVVLRSWYENKHIF	1	İ		QTKKKGVKRPARLHTKPSOAPAVEVAPAGASYNPSFEDHOTLI.S
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VHRLEWQQAALRAARLEHOELERIGIKAQVALRLAELARRQRR RQARREAEADKPRRIGILKQVAPDIDVQLSSELTDSLRTLKPEG NILRDFKSFQRRNMIEPRERAKFKRKYKVKLVEKRAFREIQL SGSDRAQWAMEPPFDVALFPERITVLDQHLRPPARRPGTTTP ARVDLQQQIMTIIDELGKASAKAQNLSAPITASRMQSNHIVVY ILKDSSARPAGKGAIIGFIKVGYKKLFVLDDREAHREVEPLCIL DFYIHESVQRHGHGRELFQYMLQKERVEPHQLAIDRPSQKLLKF LNKHYNLETTVPQVNNFVIFEGFRAKQHRPPAFSLRATRHISRAA AVDETPAAPARKLPPKRAEGDIKPYSSDREPLKVAVEPPWPLN EAPRRATPPAHPPPRSSIGNSPERGPLRPFVP SSAVEFVWEGEKMAAEPNRTEIGTFKRLEAVFTNKACFDCGAK NPSWASITYGVFLCIDCSGVHRSLGYHLSFIRSTELDSNNNWFQ LRCMQVGGNANATAFFRQHGCTANDANTKYNSRAAQMYREKIRQ LGSAALARHGTDLWIDNMSAVPNHSPEKKDSDFFTEHTOPPAN DAPATEPSGTQQPAPSTESGLAQPBHGPNTDLLGTSPKASLEL KSSIIGKKKPAAAKKGLGAKKGLGAQKVSSQSFSELERQAQVAE KLEBQQAADAKQAESMVASMRLAYQELQIDR CKSSIIGKKKPAAAPAVVPRFFFFFTDIVIMPKRKSPENTEGKDGS KVTKQEPTRRSARLSAKPAPPKPEPKPRKTSAKKEPGAKISRGA KGKKEEKQEAGKEGTAPSENGSTKAEEIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN 6475 3 462 LQRQRQHBAAPAVVPKCFFFCFTDIVIMPKRKSPENTEGKDGS KVTKQEPTRRSARLSAKPAPPKPEPKPRKTSAKKEPGAKISRGA KGKKEEKQEAGKEGTAPSENGSTKAEEIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN 6476 106 1090 ARAMAQYKGTMREAGRAMHLLKKRERQREQMEVLKQRIAEETIL KSQVDKRFSAHYDAVEABLKSSTVGLVTINDMKARQEALVRERE RQLAKKGHLEGQRLQQERQRRGQQRERKRKISCLSFALDDLDD QADAAEARRAGNIGKNPDVDTSFLPDRDREEEENLREELRGEW EAQREKVKDEEMBVTFSYWOGSGHRRTVRVRKGNTVQQFLKKAL GGLKKDFLELRSAGVEQLMFTKEULILPHYHTFYDFIIARARGK SGPLFFSPUNDDVURLLSDATMEKDESHAGKVVLRSWYRKKHIF)]		ESDGEGEPGQGEGPEAGDAEVCPTPARLATTEKKTEOORREKA
RQARREAEADKPRRLGRLKYQAPDIDVQLSSELTDSLRTLKPEG NILRDRFKSFQRRMMIEPREAKKFKRYKVKLVEKRAFREIQL SCGSDRAQWAMEFFFDVDALFPERITVLDOHLEPPARRPGTTP ARVDLQQQIMTIIDELGKASAKAQNLSAPITSASRMQSNRHVVY ILKDSSARPAGKGAIIGFIKVGYKKLFVLDDREAHNEVEPLCIL DFYHHESVQRHGHGRELFQYMLQKBRVEPHQLAIDRPSQKLLKF LNKHYNLETTVPQVNNFVIFEGFFAHQHRPPABSLRATRHSRAA AVDFTPAAPARKLPPKRAEGDIKPYSSSDREFLKVAVEPPWPLN RAPRRATPPAHPPPKSSSGNPERFLKVAVEPPWPLN RAPRRATPPAHPPPRSSIGNSPERGPLRFVVP SSAVEFVWEGEKMAAEPNKTEIQTLFKKLRAUPTNKACFDCGAK NPSWASITYGVFLCIDCSGVHRSLGVHLSFIRSTELDSNWNWFQ LRCMQVGGNANATAFFRQHGCTANDANTKYNSRAAQMYREKIRQ LGSAALARHGTDLWIDNMSSAVPNHSPEKKDSDFTEHTOPPAW DAPATEPSGTQQPAPSTESSGLAQPEHGPNTDLLGTSPKASLEL KSSIIGKKKPAAAKKGLGAKKGLAQKVSSQSFSBIERQAQVAE KLRSQQAADAKKQAEESMVASMRLAYQELQIDR 6474 3 462 LQRQRQHFAAAPAVPVRCFTFCFTDIVIMPKRKSPENTEGKDGS KVTKQEPTRRSARLSAKPAPPKPEPKPRKTSAKKEPGAKISRGA KGKKEKEKQEAGKEGTAPSENGETKAEBIHISRSTVNVSTSRGTP PSTLSVKQQIETVRVKGTEN 6475 3 462 LQRQRQHPAAAPAVPVRCFTFCFTDIVIMPKRKSPENTEGKDGS KVTKQEPTRRSARLSAKPAPPKPEPKPRKTSAKKEPGAKISRGA KGKKEKQEAGKEGTAPSENGETKAEBIHISRSTVNVSTSRGTP PSTLSVKQQIETVRVKGTEN 6476 106 1090 ARAMQVKGTMREAGRAMHLLKKRERQREQMEVLKQRIAEETIL KSQVDKRFSAHYDAVEABLKSSTVGLVTLMDMKARQEALVRERE RQLAKRQHLEEQRLQGGRGGGGRERERKKISCLSFALDDLDD QADAAEARRAGNLGKNPDVDTSFLPDRDREEEENRLREELRQGW EAQREKVKDEEMEVTFSVMGGSGHRRTVRVKKGNTVQQFLKKAL GGLKKPLERGRQCGRGGGGGRGRERERKKISCLSFALDDLDD QADAAEARRAGNLCKNPDVDTSFLPDRDREEEENRLREELRQGW EAQREKVKDEEMEVTFSVMGGSGHRRTVRVKKGNTVQQFLKKAL GGLKKPLERGRQVELKSSTVGLVTLMTMKARGELLVRERE EAQREKVKDEEMEVTFSVMGGSGHRRTVRVKKGNTVQFLKKAL GGLKKPLERGRQUERGEGRAGGGGRAGEGRAFTREELRQGW EAQREKVKDEEMEVTFSVMGGSGHRRTVRVKKGNTVQFLKKAL GGLKKPLERGRAVGLLKSSTVALVERWYEKNKHIF	1			VHRLRVQQAALRAARLRHQELFRLRGIKAQVALRLAELARRORR
897 SCGSDRAQWAMEFPERUNDLOPHERPPARRPEIOL 897 SCGSDRAQWAMEFPFFDVDALFPERITVLDQHLRPPARRPETTT ARVDLQQIMTIIDELGKASAKAQNISAPITSASRMQSNRHVVY ILKDSSARPAGKGAIIGFIKVGYKKLFVLDDHEAPHARRPETTIT DFYIHESVQRHGHGRELFÇYMLQKERVEPHQLAIDRPSQKLLKF LNKHYNLETTVPQVNNFVIFEGFFAHQRHPPAPSLRATHRISAA AVDPTPAAPARKLPPKRAEGDIKPYSSSDREPLKVAVEPPWPLN RAPRRATPPAHPPPRSSSLGNSPERGPLRPFVP 6473 22 912 SSAVEFVWECKMAAEPNKTEIQTFKRLRAVPTNKACPDCGAK NPSWASITYGVFLCIDCSGVHRSLGVHLSFTRSTELDSNNNWFQ LRCMQVGGNANATAFFRQHGCTANDANTKYNSRAAQMYREKIRQ LGSAALARHGTDLWIDNMSSAVPNHSPEKKDSDFFTEHTQPPAW DAPATEPSGTQQPAPSTESSGLAQPEHGPNTDLLGTSPKASLEL KSSIIGKKKPAAARKGLGAKGLGAKGLGAQKVSSQSFSBIERQAQVAE KLREQQAADAKKQAESMVASMRLAYGELDIDR KKSLIGKKPAAAPAVVVCFTFCFTDIVIMPKRKSPENTEGKDGS KVTKQEPTRSARLSAKPAPPKPEPKPRKTSAKKEPGAKISRGA KGKKEEKQEAGKGGTAPSRNGETKAEEIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN 6475 3 462 LQRQRQHPAAPAVVVCCFTFCFTDIVIMPKRKSPENTEGKDGS KVTKQEPTRSARLSAKPAPPKPEPKPRKTSAKKEPGAKISRGA KGKKEEKQEAGKEGTAPSENGETKAEEIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN 6476 106 1090 ARAMAQYKGTMREAGRAMHLLKKRERQREQMEVLKQRIAEETIL KSQVDKRFSAHYDAVEAELKSSTVGLVTLMDMKARQEALVRERE RQLAKKGHLECGRLQGERGGGGRGGGGRRERKKISCLSFALDDLDD QADAAEARRAGNLCKNPDUDTSFLPDDRBEEEERRLBEELRGEW EAQREKVKDEEMEVTFSVMGGSGHRRTVRVKKGNTVQQFLKKAL QGLKKDFLELRSAGVEQLMFIKEDLLLPHYTYDFILARARGK SGPLFSFDVHDDVKLLSDATMERDSSHAGKVVLRSWYEKNKHIF	1			ROARREAEADKPRRLGRLKYQAPDIDVOLSSELTDSLRTLKPEG
SCSDRAQWAMEFPFUNDALFPERITULDQHLRPPARRPGTTTF ARVDLQQQIMTI IDELGKASAKAQNLSAPITSASRMQSNRHVVY ILKDSSARPAGKGAI IGFIKVGYKKLFVLDDREAHNEVEPLCIL DFYIHESVQRHGHGRELFQYMLQKERVEPHQLAIDRESGKLLKF LNKHYNLETTVPQVNNFVIFGGFFAHQHRPPAPSIRATHHSRAA AVDFTPAPAPARKLPPKRAEGDIKPYSSDREPLKVAVEPPWPLN RAPRRATPPAPAPAKLPPKRAEGDIKPYSSDREPLKVAVEPPWPLN RAPRRATPPAHPPPRSSSLGNDERGPLRPFVP 6473 22 912 SSAVEFVWEGEKMAAEPMKTEIQTLFKRLRAVPTNKACFDCGAK NPSWASITYGVFLCIDCSGVHRSLGVHLSFIRSTELDSNWNWFG LRCMQVGGNANATAFFRQHGCTANDANTKVNSRAAQMYREKIRQ LGSAALARHGTDLWIDNMSSAVPNHSPEKKDSDFFTEHTQPPAW DAPATEPSGTQQPAPSTESSGLAQPBHGPNTDLLGTSPKASLEL KSSIIGKKKPAAAKKGLGAKGLGAQKVSSQSFSEIERQAQVAE KLREQQAADAKKQAEESMVASMRLAYQELQIDR 6474 3 462 LQRQRQHPAAAPAVPVRCFTFCFTDIVIMPKRKSPENTEGKDGS KVTKQEPTRRSARLSAKPAPPKPEPKPRKTSAKKEPGAKISRGA KGKKEEKQEAGKEGTAPSENGETKAEEIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN 6475 3 462 LQRQRPAAAPAVPVRCFTFCFTDIVIMPKRKSPENTEGKDGS KVTKQEPTRRSARLSAKPAPPKPEPKPRKTSAKKEPGAKISRGA KGKKEEKQEAGKEGTAPSENGETKAEEIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN 6476 105 1090 ARAMQYKGTMREAGRAMHLLKKRERQREQMEVLKQRIAEETIL KSQUVDKFSAHYDAVEAELKSSTVGLVTLNDMKARQEALVRERE RQLAKKQHLEEGRLQQERQRROEGRREKKKISCLSFALDDLDD QADAAEARRAGNLGKNPDVDTSFLPDRDREEEENRLREELRQEW EAQREKVKDEEKEVTFSYWGSGRRRTVRVRKSNTVQOFLKKAL QGLKKPFLELRSAGVEQLMFIKEDLILPHYHTFYDFIIARARGK SGPLFSFDVHDDVRLLSDATMEKDESHAGKVVLRSWYEKNKHIF				NILRDRFKSFQRRNMIEPRERAKFKRKYKVKLVEKRAFRETOL.
ARVDLQQQIMTIDELGKASAKQNLSAPITSASRMQSNRHVVY ILKDSSARPAGKGAIIGFIKVGYKKLFVLDDREAIREVEPLCIL DFYIHESVQRHGHGRELFQYMLQKERVEPHQLAIDRPSQKLKF LNKHYNLETTVPQVNNFVIFEGFFAHQHRPPAPSLRATHHSRAA AVDFTPAAPARKLPPKRAEGDIKPYSSSDREFLKVAVEPPWPLN RAPRRATPPAHPPPRSSSLGNSPERGPLRPFVP SSAVEFVWEGEKMAAEPNKTEIQTLFKRLRRAVPTHKACFDCGAK NPSWASITYGVFLCIDCSGVHRSLGVHLSFIRSTELDSMWNWFQ LRCMQVGGNANATAFFRQHGCTANDANTKKNSRAAQMYREKIRQ DAPATEPSSTQQPAPSTESSGLAQPEHGPNTDLLGTSPKASLEL KSSIIGKKKPAAAKKGLGAKKGLGAQKVSSQSFSEIERQAQVAE KLRSQQAADAKKQAEESNVASMRLAYGELOIDR 6474 3 462 LQRQRQHPAAPAPVFKTFFFTDIVIMPKRKSPENTEGKDGS KUTKQEPTRRSARLSAKPAPPKPEPKPRKTSAKKEPGAKISRGA KGKKEEKQEAGKEGTAPSENGETKAEEIHISRSTVNVSTSRGTP PSTLSVKGQIETTVRVKGTEN 6475 3 462 LQRQRQHPAAPAPVFFCFFTFFFTDIVIMPKRKSPENTEGKDGS KVTKQEPTRRSARLSAKPAPPKPEPKPRKTSAKKEPGAKISRGA KGKKEEKQEAGKEGTAPSENGETKAEEIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN 6476 106 1090 ARAMAQYKGTMREAGRAMHLLKKRERQREQMEVLKQRIAEETIL KSSVJKRESAHVDAVEAELKSSTVGLVTLNDMKARQEALVRERE RQLAKRQHLEEQRLQQERQREGEGRERKKKISCLSFALDDLDD QADAAEARRAGNLGKMPDVDTSFLPDRDREEEENRLREELRQEW EAQREKVKDEEMEVTFSYMGSGRRTVRVRKGNTVQGFLKKAL QGGRKDFIELRSAGVEQLMFIKEDLILPHYHTFYDFIIARARGK SGPLFSFDVHDDVRLLSDATMEKDESHAGKVVLRSWYEKNKHIF	64/2	3	897	SCGSDRAQWAMEFPFDVDALFPERITVLDOHLRPPARRPGTTTP
ILKDSSARPAGKGAIIGFIKVGYKKLIPULDDREAHNEVEPLCIL DFYIHESVQRHGHGRELFQYMLQKERVEPHQLALDRPSCKLIKF LNKHYNLETTVPQVNNFVIFGFFAHQHRPPAPSLRATRHSRAA AVDPTPAAPARKLPPKRAEGDIKPYSSSDREPLKVAVEPPWPLN RAPRRATPPAHPPPRSSSLGNSPERGPLRPFVP SSAVEFVWEGEKMAABEPNKTEIQTLFKRLRAVPTNKACFDCGAK NPSWASITYGVFLCIDCSGVHRSLGVHLSFIRSTELDSNWNWFQ LRCMQVGGNANATAFFRQHGCTANDANTKYNSRAAQMYREKIRQ LGSAALARHGTDLWIDNMSSAVPNHSPEKKDSDFFTEHTQPPAN DAPATEPSGTQQAPPSTESSGLAQPEHGPNTDLLGTSPKASLEL KSSIIGKKPAAAKKGLGAQKVSSQSFSEIERQAQVAE KLREQQAADAKKQAEESMVASMRLAYQELQIDR 6474 3 462 LQRGRQHPAAPAPVPVCFTFCFTDIVIMPKRKSPENTEGKDGS KGKKEEKQEAGKEGTAPSENGETKAEBIHISRSTVNVSTSRGTP PSTLSVKGGIETVRVKGTEN 6475 3 462 LQRGRQHPAAPAPVPVCFTFCFTDIVIMPKRKSPENTEGKDGS KGKKEEKQEAGKEGTAPSENGETKAEBIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN 6476 106 1090 ARAMAQYKGTMEEAGRAHLLKKRERGREQMEVLKGRIAEETIL KSQVDKRFSAHYDAVEABILKKRERGREQMEVLKGRIAEETIL KSQVDKRFSAHYDAVEABILKKRERGREQMEVLKGRIAEETIL KSQVDKRFSAHYDAVEABILKKRERGREQMEVLKGRIAEETIL CQADAAEARRAGNLGKNPDVDTSFLPDRDREEEENRLREELRQBW EAQREKVKDEEMEVTFSYWDGSGHRRTVRVKKGNTVQOFLKKAL QGABAEARRAGNLGKNPDVDTSFLPDRDREEEENRLREELRQBW EAQREKVEDEEMEVTFSYWDGSGHRRTVRVKKGNTVQOFLKKAL GGGUKKDFLELRARGVULRSHYEKBGHLILPHYHTFYDFIIARARGK SGPLFSFDVHDDVRLLSDATMEKDSSHAGKVVLRSWYEKNKHIF		Ì		ARVDLQQQIMTIIDELGKAŞAKAQNLSAPITSASRMOSNRHVVV
LINKHYNLETTVPQVNNFV1FEGFFAHQHRPPAPSLRATRHSRAA AVDPTPAAPARKLPPKRAEGDILKPYSSSDREFI,KVAVEPPWPLN RAPRRATPPAHPPPRSSSLGNSPERGPLRPFVP SSAVEFVWEGEKMAAEBNKTETQTLFKRLRAVPTNKACFDCGAK NPSWASITYGVFLCIDCSGVHRSLGVHLSFIRSTELDSNWNNFQ LRCMQVGGNANATAFFRQHGCTANDANTKYNSRAAQMYREKIRQ LGSAALARHGTDLWIDMSAXVPNHSPEKKDSDFFTEHTQPPAW DAPATEPSGTQQPAPSTESSGLAQPEHGPNTDLLGTSPKASLEL KSSIIGKKKPAAAKKGLGAKKGLGAQKVSSQSFSEIERQAQVAE KLREQQAADAKKQAEESMVASMRLAYQELQIDR KKSKIIGKKPAAARAVENGTERN 462 LQRQRQHPAAAPAVPVRCFTFCFTDIVIMPKRKSPENTEGKDGS KVTKQEPTRRSARLSAKPAPPKPEPKPRKTSAKKEPGAKISRGA KGKKEKQEAGKEGTAPSENGETKAEEIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN 6475 3 462 LQRQRQHPAAAPAVPVRCFTFCFTDIVIMPKRKSPENTEGKDGS KVTKQEPTRRSARLSAKPAPPKPEPKPRKTSAKKEPGAKISRGA KGKKEKQEAGKEGTAPSENGETKAEEIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN 6476 106 1090 ARAMAQYKGTMREAGRAMHLLKKRERQREQMEVLKQRIAEETIL KSQVDKRFSAHYDAVEABLKSSTVGLVTLMDMKARQEALVRERE RQLAKRQHLEEQRLQQERQREQEQRRERKRKISCLSFALDDLDD QADAAEARRAGNLCKNPDVDTSFLPDRDREEEENRLREELRQEW EAQREKVKDEEMSVTFSYWDGSGHRRTVRVRKGNTVQQFLKKAL GGLRKDFLEIRSAGVEQLMFIKEDLILDHYHTFYDFIIARARGK SGPLFSFDVHDDVRLLSDATMEKDESHAGKVVLRSWYEKNKHIF				ILKDSSARPAGKGAIIGFIKVGYKKLFVLDDREAHNEVEPLCTI.
AVDPTPAAPARKLIPPKRAEGDI KPYSSSDERPLKVAVEPPWPLN RAPRRATPPAHPPRSSSIGNSPERGPLRPFVP SSAVEFVWEGEKMAAEPNKTEIQTLFKRLRAVPTNKACFDCGAK NPSWASITYGVFLCIDCSGVHRSLGVHLSFIRSTELDSNWNWFQ LRCMQVGGNANATAFFRQHGCTANDANTKYNSRAAQMYREKIRQ LGSAALARHGTDLWIDNMSSAVPNHSPEKKDSDFFTEHTQPPAW DAPATEPSGTQQPPASTESSGLAQPEHGPNTDLLGTSPKASLEL KSSIIGKKKPAAAKKGLGAKKGLGAQKVSSQSFSBIERQAQVAE KLREQQAADAKKQAEESNVASMALAYQELQIDR 6474 3 462 LQRQRQHPAAAPAVPVRCFTFCFTDIVIMPKRKSPENTEGKDGS KVTKQEPTRRSARLSAKPAPPKPEPKPRKTSAKKEPGAKISRGA KGKKEKQEAGKEGTAPSENGETKAEBIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN 6475 3 462 LQRQRQHPAAAPAVPVRCFTFCFTDIVIMPKRKSPENTEGKDGS KVTKQEPTRRSARLSAKPAPPKPEPKPRKTSAKKEPGAKISRGA KGKKEKQEAGKEGTAPSENGETKAEBIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN 6476 106 1090 ARAMAQYKGTMREAGRAMHLLKKRERQREQMEVLKQRIAEETIL KSQVDKRFSAHYDAVEABLKSSTVGLVTLNDMKARQEALVRERE RQLAKRQHLEEQRLQQERQRBQEQRRERKRKISCLSFALDDLDD QADAAEARRAGNLGKNPDVDTSFLPDDRBEBEENRLREELRQEW EAQREKVKDEEMBVTFSYWDGSGHRRTVRVRKGNTVQPILKKAL GGLRKDFLELRSAGVEQLMFIKEDLILPHYHTFYDFIIARARGK SGPLFSFDVHDDVRLLSDATMEKDESHAGKVVLRSWYEKNKHIF		ľ		DFYIHESVORHGHGRELFQYMLQKERVEPHQLAIDRPSQKLLKF
AVDPTPAAPARKLIPPKRAEGDI KPYSSSDERPLKVAVEPPWPLN RAPRRATPPAHPPRSSSIGNSPERGPLRPFVP SSAVEFVWEGEKMAAEPNKTEIQTLFKRLRAVPTNKACFDCGAK NPSWASITYGVFLCIDCSGVHRSLGVHLSFIRSTELDSNWNWFQ LRCMQVGGNANATAFFRQHGCTANDANTKYNSRAAQMYREKIRQ LGSAALARHGTDLWIDNMSSAVPNHSPEKKDSDFFTEHTQPPAW DAPATEPSGTQQPPASTESSGLAQPEHGPNTDLLGTSPKASLEL KSSIIGKKKPAAAKKGLGAKKGLGAQKVSSQSFSBIERQAQVAE KLREQQAADAKKQAEESNVASMALAYQELQIDR 6474 3 462 LQRQRQHPAAAPAVPVRCFTFCFTDIVIMPKRKSPENTEGKDGS KVTKQEPTRRSARLSAKPAPPKPEPKPRKTSAKKEPGAKISRGA KGKKEKQEAGKEGTAPSENGETKAEBIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN 6475 3 462 LQRQRQHPAAAPAVPVRCFTFCFTDIVIMPKRKSPENTEGKDGS KVTKQEPTRRSARLSAKPAPPKPEPKPRKTSAKKEPGAKISRGA KGKKEKQEAGKEGTAPSENGETKAEBIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN 6476 106 1090 ARAMAQYKGTMREAGRAMHLLKKRERQREQMEVLKQRIAEETIL KSQVDKRFSAHYDAVEABLKSSTVGLVTLNDMKARQEALVRERE RQLAKRQHLEEQRLQQERQRBQEQRRERKRKISCLSFALDDLDD QADAAEARRAGNLGKNPDVDTSFLPDDRBEBEENRLREELRQEW EAQREKVKDEEMBVTFSYWDGSGHRRTVRVRKGNTVQPILKKAL GGLRKDFLELRSAGVEQLMFIKEDLILPHYHTFYDFIIARARGK SGPLFSFDVHDDVRLLSDATMEKDESHAGKVVLRSWYEKNKHIF	1			LNKHYNLETTVPQVNNFVIFEGFFAHOHRPPAPSLRATRHSRAA
SSAVEFVWEGEKMAAEPNKTEIQTLFKRLRAVPTNKACFDCGAK NPSWASITYGVFLCIDCSGVHRSLGVHLSFIRSTELDSNWNWFQ LRCMQVGGNANATAFFRQHGCTANDANTKYNSRAAQMYREKIRQ LGSAALARHGTDLWIDNMSSAVPNHSPEKKDSDFFTEHTQPPAW DAPATEPSGTQQPAPSTESSGLAQPEHGPNTDLLIGTSPKASLEL KSSIIGKKKPAAAKKGLGAKKGLGAQKVSSQSFSEIERQAQVAE KLREQQAADAKKGAESMVASMRLAYQELQIDR 6474 3 462 LQRQRQHPAAAPAVPVRCFTFCFTDIVIMPKRKSPENTEGKDGS KVTKQEPTRRSARLSAKPAPPKPEPKPRKTSAKKEPGAKISRGA KGKKEEKQEAGKEGTAPSENGETKAEEIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN 6475 3 462 LQRQRQHPAAAPAVPVRCFTFCFTDIVIMPKRKSPENTEGKDGS KVTKQEPTRRSARLSAKPAPPKPEPKPRKTSAKKEPGAKISRGA KGKKEEKQEAGKEGTAPSENGETKAEEIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN 6476 106 1090 ARAMAQYKGTMREAGRAWHILLKKRERQREQWEVLKQRIAEETIL KSQVDKRFSAHYDAVEABLKSSTVGLVTLNDMKARQEALVRERE RQLAKRQHLEEQRLQQERQREQEQRREKRKISCLSFALDDLDD QADAAEARRAGNLGKNPDVDTSFLPDRDREEEENRLREELRQEW EAQREKVKDEEMBVTFSYWDGSGHRRTVRVRKGNTVQQFLKKAL GGLRKDFLERSAGVEQLMFIKEDLILPHYHTFYDFIIARARGK SGPLFSFDVHDDVRLLSDATMEKDESHAGKVVLRSWYEKNKHIF	1			AVDPTPAAPARKLPPKRAEGDIKPYSSSDREFLKVAVEPPWDIN
NPSWASITYWEGEUNALSPHKETQTLFKRLRAVPTNKACFDCGAK NPSWASITYWEGEUNALSPHKSIGVHLSFIRSTELDSNWNWFQ LRCMQVGGNANATAFFRQHGCTANDANTKYNSRAAQMYREKIRQ LGSAALARHGTDLWIDNMSSAVPNHSPEKKDSDFFTEHTQPPAW DAPATEPSGTQQPAPSTESSGLAQPEHGPNTDLLGTSPKASLEL KSSIIGKKKPAAAKKGLGAKKGLGACKUSQSFSBIERQAQVAE KLREQQADADAKKQAEESMVASMRLAYQELQIDR LQRORQHPAAAPAVPVRCFTFCFTDIVIMPKRKSPENTEGKDGS KVTKQEPTRRSARLSAKPAPPKPEPKPRKTSAKKEPGAKISRGA KGKKEEKQEAGKEGTAPSENGETKAEBIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN LQRORQHPAAAPAVPVRCFTFCFTDIVIMPKRKSPENTEGKDGS KVTKQEPTRRSARLSAKPAPPKPEPKPRKTSAKKEPGAKISRGA KGKKEEKQEAGKEGTAPSENGETKAEBIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN 6476 106 1090 ARAMAQYKGTMREAGRAMHLLKKRERQREQMEVLKORIAEETIL KSQVDKRFSAHYDAVEABLKSSTVGLVTLNDMKARQEALVRERE RQLAKROHLEEQRLQQERQREQEORRERKRKISCLSFALDDLDD QADAAEARRAGNICKNPDVDTSFLPDRDREEEENRLREELRQEW EAQREKVKDEEMKVTFSYWDGSGHRRTVRVRKGNTVQQFLKKAL GCLRKDFLELRSAGVEQLMFIKEDLILPHYHTFYDFIIARAGK SGPLFSFDVHDDVRLLSDATMEKDESHAGKVVLRSWYEKNKHIF	6473			RAPRRATPPAHPPPRSSSLGNSPERGPLRPFVP
LRCMQVGGNANATAFFRQHGCTANDANTKYNSRAAQMYREKIRQ LGSAALARHGTDLWIDNMSSAVPNHSPEKKDSDFFTEHTQPPAW DAPATEPSGTQQPAPSTESSGLAQPEHGPNTDLLGTSPKASLEL KSSIIGKKKPAAAKKGLGAKKGLGAQKVSSQSFSEIERQAQVAE KLREQQAADAKKQAEESMVASMRLAYQELQIDR 6474 3 462 LQRQRQHPAAPAVPVRCFTFCFTDIVIMPKRKSPENTEGKDGS KVTKQEPTRRSARLSAKPAPPKPEPKPRKTSAKKEPGAKISRGA KGKKEEKQEAGKEGTAPSENGETKAEEIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN 6475 3 462 LQRQRQHPAAAPAVPVRCFTFCFTDIVIMPKRKSPENTEGKDGS KVTKQEPTRRSARLSAKPAPPKPEPKPRKTSAKKEPGAKISRGA KGKKEEKQEAGKEGTAPSENGETKAEEIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN 6476 106 1090 ARAMAQYKGTMREAGRAMHLLKKRERQREQMEVLKQRIAEETIL KSQVDKRFSAHYDAVEAELKSSTVGLVTLNDMKARQEALVRERE RQLAKRQHLEEQRLQQERQREGEQRRERKRKISCLSFALDDLDD QADAAEARRAGNLGKNPDVDTSFLPDDRDREEEENRLREELRQEW EAQREKVKDEEMBVTFSYWDGSGHRRTVRVRKGNTVQQFLKKAL QCLRKDFLELRSAGVEQLMFIKEDLILPHYHTFYDFIIARARGK SGPLFSFDVHDDVRLLSDATMEKDESHAGKVVLRSWYEKNKHIF	04/3	44	912	SSAVEFVWEGEKMAAEPNKTEIQTLFKRLRAVPTNKACFDCGAK
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6478 2 1495 PYSSRILPESIASSERSTLEAMGRKEEDDCSSWKKOTTNIERTF IPMEVLIGSGAFSEVFLVKORLTOKLFALKCIKKSPAPENDSLEN ELAVLKKIKHENTVIEDIEVSSTHYLVKORLTOKLFALKCIKKSPAPENDSLEN ELAVLKKIKHENTVIEDIEVSSTHYLVKORGELPPRILE GROVTEKDASLVIOQULSAVKYLHERIETVERDLKYLTPE ENSKIMITTPDELISOMERONGIMSTACGTPGVVAPEVLAQKPYSKA VDCWSIGVITYILLCOYPPYEETESKLFEK KUPKKYRYBYESFEPP DDISESAKDPICHLGKOPPRANAVVHHERIEVSPHESFEPP DDISESAKDPICHKERIEN DEN STANDAVHHERIEN STUPPEN BEVERRPPETQASETSRPSSETTITEAPVLORUSVALPAITCLPC GHORRYTAPGGSERICKLIVNOSSHISSLEVWERVBIAAPGCOCC SSCLNIGSKOKSSYCSBYLLKANKKOPKSEVWUPVALAGSS HCRAGGTOVICHM 6479 3 949 SCROFGMIPAGGQAGAMBLISALSIGELALSFSEVPLPPVEDLS YFVISILLIKKYBGAVELSRIPILASHLCAMHACYGSYLLADLL LGBELIDYFSNNSSILLASAVWALIFTCPIDLPYKCCUPPUK IPVISILLIKKYBGAVELSRIPILASHLCAMHACYGSYLLADLL LGBELIDYFSNNSSILLASAVWALIFTCPIDLPYKCCUPPUK IPVISILLIKKYBGAVELSRIPILASHLCAMHACYGSYLLADLL LGBELIDYFSNNSSILLASAVWALIFTCPIDLPYKCCUPPUK IPVISILASKYBGAVELSTEVEN STANDAVAN KAKAAD LMSNFFOLLROWKBETNEILSINSFPTKASLYGAILFTLQTRK KAKAAD LDFNSTYFFILTPLPWVSCKYFLIATHISHSBPDALGGYLCPVK GSACGODHHDNHGGSHSGCOGAGASMANAVELTACKYKGGAA LMSNFFOLLROWKBETNEILSINSFPTKASLYGAILFTLQTRK KAKAAD LDFNSTYFFILTPLPWVSCKYFLIATHISHSBPDALGGYLCPVK GSACGODHHDNHGGSHSGCOGAGASMANAVELTACKYKGGAA KKAKAD LDFNSTYFFILTPLPWVSCKYFLIATHISHSBPDALGGYLCPVK GGSACGODHHDNHGGSHSGCOGAGASMANAYPHYSDWSGIANGY GUPPDSBPDRCCKIKRRIESIVVEPTEGGVESGELRWPPEETL VQEDEGDONGETAKNIKGU SVAVEKPHOLTOSTAKOH MILSVYKELGGAAAVEKTPLIFSTPEEMSEMLQLC SVAVEKPUPGLIGAULVANATHISHTYNY GWENTLGMONYSPERSTENDAM GOOGAGAAVANAYPHYDDWSGIANLACKING SVAVEKPUPGLIGAULVANATHINFYRKLIPLIFYSEMSHALQLC SVAVEKPUPGLIGAULVANATHINFYRKLIPLIFYSEMSHALQLC SVAVEKPUPGLIGAULVANATHINFYRKLIPLIFYSEMSHALQLC SVAVEKPUPGLIGAULGLAVENTHINFYRKLIPLIFYSEMSHALQLC SVAVEKPUPGLIGAULVANATHINFYRKLIPLIFYSEMSHALQLC SVAVEKPUPGLIGAULGLAVENTHINFYRKLIPLIFYSEMSHALQLC SVAVEKPUPGLIGAULGLAVENTHINFYRKLIPLIFYSEMSHALQLC SVAVEKPUPGLIGAULGLAVENTHINFYRKLIPLIFYSEMSHALQLC SVAVEKPUPGLIGAULGLAVENTHINFYRKLIPLIFYSEMSHALQLC ALALSE BLAUGHANATHINFYRKLIPTHINFYRKLIPTHRUPGLIGAULGHAD HANGKET ARGENTALTEN GROPPENDAM THE GOOGAGA THE GOOGAGA	1			IISYVSKIITLEEGDIILTCTDYGUGDUVTDDIAGETSSMIFSIPY
1495	1		ļ	TEKVEKDEY
ITMENUGSGAFSEVFLVKORLIGELINGSGGELADRILE BEJALKKIKHNITUTEDITYSSTHYHLMUGSGGELADRILE ROVTERDASLVIOOVLSAVKYLHENGIUHROLKSGGELADRILE ROVTERDASLVIOOVLSAVKYLHENGIUHROLKSGGELADRILE ROVTERDASLVIOOVLSAVKYLHENGIUHROLKSGGELADRILE ROVTTERDASLVIOOVLSAVKYLHENGIUHROLKSGGELADRILE ROVTTERDASLVIOOVLSAVKYLHENGIUHROLKSGENLLYLTPE ERSKIMITTOFOISMMERGINGINSTACGTDGYVAPPEVLAQKYTSKA UDCHSIGVITYILLCGYPPFVEETESKLEEKIKEGYTSFESPFM DDISESAKDFICHLEKDPBRRYTCEKALSHEWILDATALHROI YESVSLJOIGKAFAKSKKROARNAAVVHAMKKUNFALHEPGURE EVERNPFETQASETSRPSSPEITITEAPVLDHSVAKPHOGSILAADPGGCC SSCLNIGSKGSSTCSRPTLLKKANKKONFKSEVMVPVKASGSS HCRAGGTGGCLIM 6479 3 949 SCREPGWHEDAGGOAGMELLSALSIGELALSFSRVPLPPVFDLS VFIVSILYLKYBPGAVELSRRIPIASMLCANLHKONFKSEVMVPVKASGSS HCRAGGTGGCLIM LOSPLIDTFSNNSSILLASAVWLIFFCFLDIFYKCVCFLPVKL ITVAMKEVVRVRIANGTHHAHHHYHHOWFWILATGWKCSGVA LMSNFFGLLGRVWKPTERE LHMSPFTKASGAILFTTGOTER LPVSKASLIFIFTLFWVSCKVFLIJAHSHSSPPDALGSILGTOFTV LPVSKASLIFIFTLFWVSCKVFLIJAHSHSSPPDALGSTLADFIL LPVSKASLIFIFTLFWVSCKVFLIJAHSHSSPPDALGSTLOTTV FGSACGGHHHDHHGSHISGGGGAQHSAMPKSKEELSEGSRK KAKKAKAD 6480 192 514 DPMSIYFPHCPDYLESAKMTEUMMTOPMEETGLSPRKODLSY OIPPDSDPDRCCKLKDRLPSIVVEPTEGSVESGELRWPPEBFL VOURDEQDNCEETKARKNEQ OIPPDSDPDRCCKLKDRLPSILVEPTEGSVESGELRWPPEBFL VOURDEQDNCEETKARKNEQ OIPPDSDPDRCCKLKDRLPSILVEPTEGSVESGELRWPPEBFL OVERLEUMMTOPMSVENHEDVYGVTSFRCRPGHKRSILMHLOTSPERMSEMLQLC SVERKVDGOLTGGLVDVRIFHNDFYRKLPLEIVSEKSRYSLIQ MKNILVYPTOJIWGKOQOVILDVGADMLAKSILMUCC SVURKVDGOLTGGLVDVRIFHNDFYRKLPLEIVSEKSRYSLIQ MKNILVYPTOJIWGKOQOVILDVGADMLAKSILMUCC SVURKVDGOLTGGLVDVRIFHNDFYRKLPLEIVSEKSRYSLIQ MKNILVYPTOJIWGKOQOVILDVGADMLAKSILMUCC SVURKVDGOLTGGLVDVRIFHNDFYRKLPLEIVSEKSRYSLIQ MKNILVYBOJIWGKSVKSYBALLEESTRKAVQUEEHOG HVVMERPRKTARLIIDPLASVHNDIDNKKLD 6482 2517 568 EPVSKVSGSRRKAGVYTANTESGGVARANVDPMAEVCEKPOA ALASRVELIKHRIGHENDFYKKYSVARALLEESTRKAVGUEEHOG NEMKILVYTOJIWGKGUGAAVEKSUPLOTSELKKAUCHSTENDA KARGTANTATATASOFYINKICHTERLUCHTUCHTHA KRQLEHNAYHPIEMAINAATLSOFYINKICHTERLUCHTUCHTHA KRQLEHNAYHPIEMAINAATLSOFYINKICHTERLUCHTUCHTHA KRQLEHNAYHPIEMAINAATLSOFYINKICHTERLUCHTUCHTHA KRQLEHNAYHPIEMAINAATLSOFYINKI	6478	2	1495	
EIAULKKIKHENIVTEDIYSETHYYLVMQLVSGGELDRILLE RGVYTERDASJVIQOULSGAVYKLHENSIVERPENLYTTPE RGSAINTTDFGLSKMEQNGIMSTACGTPGYVAPPULARPYCARPYSER UDCUSIGUTYTILLCGYPPYEPTERSKERELEKEGYPETESPR UDCUSIGUTYTILLCGYPPYEPTERSKERELEKEGYPETESPR DDISESAKDPICHLLEKDDNRRYTCEKALSHPWIDGNTALHRDI YPSVSLQIQKIPAKSKURQAPNAAAVVHHMIKKLHMELHSJGVRP EVENRPPETQASETSRPSSPSITITRSRVDSAAPPALTOLPC QHGRRPTAPGGGSLNCLVNGGSLHISSSLVPHKGGSLAAPGGGC SSCLNIGSKGSSCSEPTLKKANKKQNFSEVMYPVKASGSS HCRAGGTGVCLIM 6479 3 949 SCROFFMHPBAGGQAGMELLSALSIGELALSFERVPLPPVFDLS YFIVSILVLKYEPGAVELSRRIPTJASMLCAMLHCFGSYILADLL LGBELIDYSSNSSILLASAJVAVIJEPFCDLFYKCVCLPVKL LGBELIDYSSNSSILLASAJVAVIJEPFCDLFYKCVCLPVKL LFVAMKEVVRVRXLAVGTHHAHHHYHGRPWIATGWVKGSGVA LMSNFFQLLGAVWKPSTNSILLASAJVAVIJEPFCDLFYKCVCLPVKL LFVAMKEVVRVRXLAVGTHHAHHYHGRPWIATGWVKGSGVA LMSNFFQLLGAVWKPSTNSILLASSPRADASSPLAGVICPVL PGSACGGDHHIDHIGGSHSGGGFGAQHSAMPAKSKEELSGGSR KAKKAAD 6480 192 514 DFMSIYFPIHCPDYLESAKWTEVMNTQPMEEIGLSPRKDGLSY QIPPDSSPFDRCCKLKDRLPSIVVEFTEGEVESGELRWPPEEFL VQEDEQDNCEETAKENKEQ 6481 110 1131 SSRNDLDVVNNFVIAGGTAFT PLAPVASPLLWFSALTRIYWY WRRTLGMQVRVWHEDYOPCVSFRGRPGHKRSILMLHGFSAHKD MINSVKIPPLENHHJVCVDMDGHEGTTRSSLDLGINGVRRH OFWSCLKLINKKPPHLVGTSMSGVAGVYANYYESDVSSLMLVCP AGLQISTDNGFVGLKELQGSAVEKIPLIFSTPEEMSHLQCC SVUREKVPQQILQGLDVDRYHNNFYRKLIEIGVSEKSRYSLMQ NMDKIKVPTQIINGKOQVALDVSGADMLAKSIANCOVELLENGG SVVREKVPQQILQGLDVDRYHNNFYRKLIEIGVSEKSRYSLMQ NMDKIKVPTQIINGKOQVALDVSGADMLAKSIANCOVELLENGG SVVREKVPQQILQGLDVDRYSHNDYRKLILESTDEEMSHLQCC SVUREKVPQQILGGLDVDRYSHNDYRKLILLGAPDEDDB RPBAEDGGAGDHALGJARAVKUPABVCCSFPQA ALLASRVELIKHPSEPENKSKYSABALLESSEIRKAVQVELKENG NMDKIKVPTQIINGKGGIARAKKUPGARVCCSFPQA ALLASRVELIKHPSEPENKSKYSABALLESSEIRKAVQVECKFPQA ALLASRVELIKHPSEPENKSKYSABALLESSEIRKAVQVECKFPQA ALLASRVELIKHPSEPENKSLILDRAKKERGESTRKAVQVECKFPQA NAGSMODNIGGILDLDNGSLARAKKERGESTRKAVQVECKPQA NAGSMODNIGGILDLDNGSLARAKKERGESTRKAVQVECKPQA NAGSMODNIGGILDLDNGSLARAKKERGESTRKAVQVECKPQA NAGSMODNIGGILDLDNGSLARAKKERGESTRKAVQVECKPQA MLAKFRVARLIVGALIPPENDANARATCHSTL KRQLEHAVHPIBMANINAALKYYQLFILDSLRDPKNYPBENGERIKFAVCHTER ALASRICELRHAPSANGRARAMEGNLARAFTA	1			TEMEVI GSGA FSEVEL UVORI MOVI ERI VOLUMORA ERIPAGA
RGVYTEKDASIVIQOULSAVKYLIENGIVHEDLESPEVALAÇAYSKA ENSINITIFIGISMEMCHINISTACTEPOVALFAVLAÇAYSKA VDCUSIGVITYILLCGYPPPYEBTESKLERIKEGYYEPESPP DDISESANDICHLEKEDDIREYTCEKALSHPHIDONTALHRDI VPSVSLQIQKNFAKSKURQAFNAANVHHMKKLEMELHSPGVRP EVENRPPETQASETSRPSSPEITITEAPVLDHSVARLHRDIL VPSVSLQIQKNFAKSKURQAFNAANVHHMKKLEMELHSPGVRP EVENRPPETQASETSRPSSPEITITEAPVLDHSVARLHRDILOPG QHGRRYITAGGGSINLCLVANGSHITSSLVPHQGSISAAGPGGCC SSCLNIGSKGKSSYCSEPTLLKKANNKQNFKSEWMPVVKAGGSS HCRAGGTGYCLIM 6479 3 949 SCROFGWHEAGGQAGMELLSALSIGELALSFSRVPLPPVEDLS VFIVSILIVKYEPGAVELSRRIPITAGHLACHHCPGSYILADLL LGEPLIDYFSNNSSILLASAVWYLIFFCPLDLFYKCVCFLEVKL LGEPLIDYFSNNSSILLASAVWYLIFFCPLDLFYKCVCFLEVKL LHONFEQLIRGVWKPETRE LHMSPFYTKAGALHCPGSYILADLL LGPLIDYFSNNSSILLASAVWYLIFFCPLDLFYKCVCFLEVKL LPVAKKEVVRVRKIAVGIHHAHHHYHHGWFWILATGWYKGSGVA LMSNFEQLIRGVWKPETRE LHMSPFYTKAGALHCPGSYILADLL PVSKASLIFIFTLFWVSCKVFLIATHHSHSSPPDALGSTICPTV FGSACCGOHHEDHIGGSISGGGGAGAHGASAFAKTEGISGGSRK KKAKKAD 6480 192 514 FMSIYFFIHCPDYLESAKWTEVMNTQPMEETGLSPRKODLSY QIPPDBSDPDRCCKLKDRLPSIVVEPTEGEVESGELRWPPEEFL VGREDGDNCETAKENKED VGREDGDNCETAKENKED VGREDGDNCETAKENKED KRAKKAD MINSVVKLPGHDSHGGGTAGASVEKIPLDSILDGWGVRIH QFVECLKLINKKPPHLVGTSMGGQVAGVYAAYYPSDVSSLMLVCP AGGVSTINGFVGVRIKELGGAAVEKIPLDSILDGWGRIH QFVECKKINKKPPHLVGTSMGGQVAGVYAAYYPSDVSSLMLVCP AGGVSTINGFVGVRIKELGGAAVEKIPLTSEEMSENLOL SYVRKVPQQILQGLVDVRTPHNNTYRKLFLETVSEKSRYSLHQ NMKIKVYPTQUTIGKQQDQUADVSADMLAKSILANCELLENGC SYVRKVPQQILAGLUDVRYGRHAMANVPAEEVCEKPQA ALALSRVELHKMPEEPTSKKYSAPALLEEVKALLGPAPEDEDE RPEAEDGGAGCHALGLPARVYDMMLKSLAGPAPEDEDE RPEAEDGGAGCHALGLPARVYDMGKGVARAVRUPHELLENG NALSWGRIKSTETTPAGATUSSSRALNAVYMKEVGSPPLDPTERFLPEE EKLTDORSKREPKYYTHILYYLAQVYQHLEMFEKAAHYCHSTL KRQLEHNAYHPIEWAINAALLSSERLIVRQWKEVGSPPLDPTERFLPEE EKLTDORSKREPKYYTHILYYLAQVYQHLEMFEKAAHYCHSTL KRQLEHNAYHPIEWAINAALLSSERLIVRGGGFREKAAHYCHSTL KRQLEHNAYHPIEWAINAALLSPYLINGGLAFFETDWESTRKANQGGT GELCDAISAVERKYSYLIPLDGERARRELFILAGHYVPERKEESIRKAVQGGT GELCDAISAVERKYSVIRPLDGERARRELFILAGHYVPERKEESIRKAVQGGT GELCDAISAVERKYYTHUNSALKYQLERLBARKERGESIRKAVALDE PLTVULMPQGYLLIVRGLAFFETBERSETIRKAVQG	į			EIAVLKKIKUENTUET EDIVERMUUNU INOINIO GERAFROSSLEN
ENSKIMTTDFGLSKMEQNGIMSTAGCTGGYVAPULAGKPYEKP DDISESAKDPICHLLEKDPMERTCEKALSHPRIJORTALHRDI YPSUSLJOIGNFAKSKWRQAFNAAAVYHHRKLHRWLESPGYW EVENRPPETQASETSRSSSETTITEAPVLDHSVALPALTGLPC QHGRRPTAPGGSKINCLVNOSSLHISSSLVPHUGGSLAAGPGGC SSCLMIGSSKSSYSSESPTLKKANKNEKEVMPWKASGSS HCRAGGTGYCLIM SCROFGWHRPAGGOAGMELLSALSIGELALSFSRVELPPVEDLS SCROFGWHRPAGGOAGMELLSALSIGELALSFSRVELPPVEDLS LGBPLIDYFSNNSSILLASAWYLIFFCPLDFYKCVCTPVKL LGBPLIDYFSNNSSILLASAWYLIFFCPLDFYKCVCTPVKL LGBPLIDYFSNNSSILLASAWYLIFFCPLDFYKCVCTPVKL LGBPLIDYFSNNSSILLASAWYLIFFCPLDFYKCVCTPVKL LMSNFEQLLRGVWKPETNSILLHMSFPTKASLVGALFFTCQTTRV LMSNFEQLLRGVWKPETNSILHMSFPTKASLVGALFTCQTTRV FGSACGGDHHIDNIGGSHSGGGPGAQHSAMPAKSKEELSEGSKK KAKKAKAD 6480 192 514 DFMSIYFPHCPDYLRSAKMTEVMNTQPMEEIGLSPRKDGLSY QIPPDBSDFDRCCKLKDRLPSIVVEPTEGGVESGGELRWPPEEL KKAKKAD KSRMDLDVVNNFYLAGGTLAIF ILAFVASFLLWPSALTRIYWY WRRILLGMORVVNHEDVYCYSFRGRYGHPSILMLGFSAHKD MWLSVVKFLPKNLHLUCUDMPDHBGTTRSSLDDLSIDGQVKRIH QFVECLKLMKKPPHLUCYDMPDHBGTTRSSLDDLSIDGQVKRIH QFVECLKLMKKPPHLUSTSMGGQVAGVYAAYYBGDVSSLMLVCP AGLQYSTDNQFVQRLKELJGSSAVEKTPLIPFSTEEMSSHOLDC SYVRKVPQQILQGLUDVASGAMISTANCYVELLENGG HSVWERPRKTAKLIIDFLASVHNTONNKKLD 6482 2517 568 EPYSKVSGSRRKAGVFTANIESSGAVEKTPLIPFSTEEMSSHOLDC SYVRKVPQQILGGLUDVASGAMANAVPHASVCEKFQA ALALSRVELHKNDEKSPYKSKYSARALLEEVKALLGPAEDEDE RPSACHGENKFFKYTHNIYTLAGVYGLBMFFKAAHVCHSTL KRQLEHNAYIHIEWAINAATLSOPYINKLCPMERHCLSAANVI FGQTTKITSAFCDTPERSEGGVPELYMGRKGETARCWIKYCLTLMQ NAQLSMQDNIGELDLDKQSELRALRKKELDBEBSIRKKAVQFGT GELCDAISAVEEKVSYLRPLDFEBRERCHHKRITAMLE PLTVDLNPQYYLLVSRQLOFFLAHAYYMMDLKVALADRLROPD SHIVKKINNINSALKYOPJEDLSRDRECKMHKRIAMLE PLTVDLNPQYYLLVSRQLOFFLAHAYYMMDLKVALADRLROPD SHIVKKINNINSALKYOPJEDLSRDRECKMHKRIAMLE PLTVDLNPQYYLLVSRQLOFFLAHAYYMMPERCHMERCHHKRIAMLE PLTVDLNPQYYLLVSRQLOFFLAHAYYMMPERCHMERCHHKRIAMLE PLTVDLNPQYYLLVSRQLOFFLAHAYYMMPERCHMANARARGAGAGAGTTGKKARAPLSKRIGGLARFRAMKERAGALAAQP HAAQESEVELELSKEMVSLLPTMGRFRTKNALIT 6483 3 623 NSHLCGGLGRRARPISANGERRAMSGEGARFERARGRAGLAAQP PAASGGAGTTGSKARAAAATLKAAPGWLKRFLVWKPPRASARAQP GLVOGAAGPGSTSETFWATATATELPENTAL	1			PGVVTEKDASLUTOOUT CAUGUT HENGTHURDT HERET
DISESSANDICHLIEUENDRENTICERKALSHPRIJONTALIROI DISESSANDICHLIEUENDRENTICERKALSHPRIJONTALIROI YPSYSLQIQKNPAKSKURQAPNAAVVHHMRKLHMNLHSPGVRP EVENRPPETQASETSRPSSPEITITEAPVLDHSVALPALTOLDC QHGRRPTAPGGRSLINCLVNGSLHIASSPWGGSLAAPPGGCC SSCLNIGSKGKSSYCSEPTLIKKANKKONFKSEVMVPVKASGSS HCRAGTGGVCLIM 6479 3 949 SCROFGMHDAGGQAGAMELLSALSIGELALSFSRVPLFPVFDLS YFIVSILYLKYEPGAVELSRRIPIASHLCAMHLEGSVILLADLL LGBPLIDTFSNNSSILLASSAVMYLIFFVPLDLFYKCVCTPUVKL LIGHAMKEVVRVKAKTAVGIHHAHHHYHGGFVIHLATGWYKGSGVA LMSNFFGOLLGGWWRPFINTILHMSFFYKASLVGATLFFILOOTEN LPVSKASLIFIFTLFMVSCKVPLITATHSHSSPPDALGGYICPVIL FGSACGGDHHIDHNGGSHSGGGFGAQHSAMPAKSKKELSEGSRK KKAKKAD 6480 192 514 DFMSTYFPIHCPDYLRSAKMTEVMMNTQPMEEIGLSPRKDGLSY QIFPDFSDFDRCCKLKORLPSIVVEPFGGVESGGLRWPPEEFL VQEDEQDNCEETAKENKEQ KKARKAD 6481 110 1131 KSRNDLDVNNMFVLAGGTLAIPILAFVASFLLMFSALIRIYYWY WRRTLGMQVRYVHHEDYQPCYSFRGRGGKFSILMLIGFSAHDD MMLSVVKELFRINHLVCVDMRGHBGTTRSSLDDLSIDGQVKRIH QFVECLKLINKKPPHLUFSTMGGQVAGYAYPSDVSSLMLVCP AGLQYSTDNOFVQRLKELJGSAAVEKRPLIPSTPEEMSENLOLC SYVRFKYPQOILGGLUVBRIPHNFYRLFILVSEKSFYSLHQ NMKKKVPTQIIUGKQDQVLDVSGADMLAKSIANCQVELLENGG HSVVMERPKTAKLIIDFLASVINTINNIKKLD NHENKIKVPTQIIUGKQDQVLDVSGADMLAKSIANCQVELLENGG HSVWERPKTAKLIIDFLASVINTINNIKLCH NHENGERSGRFBKYYTHINIYTLAQVQRAVENLAVIEFHLOV NHIDTEELSAGEBHLVKCLRLLRYRLSHDCISLCIQAQNNIGI LWSERBEIFTAQAYLESSEALVINQYMKEVGSPPLDFERFLEE EKLITGGRRSGRFBKVYTHINIYTLAQVQNENMFRKAHATGHLE AKQLEHNAYHFIEMAINAATLSGPYINKLCFMERRHCLSAANVI FQGTGKISATEDTPERAGEGVPELYHORGGARVALAVIERHLOV NAQLSMQDNIGELDLDKQSELBALRKKELDEESIRKKAVQFGT GELCDAISAGTEDTPERAGEGVPELYHORGGARVALAVIPERLEBL EKLITGGRRSGRFBKVYTHINIYTLAQVQHKERFRKANKIANLE PLTVDLNFQYYLLVRRQQGFILHAYYDMMDLKVATADRLROPD SHIVKKINNIKSALKYQLFLDSLENDERCKMIKRIANLE PLTVDLNFQYYLLVRRQQGFILHAYYDMMDLKVATADRLROPD SHIVKKINNIKSALKYQLFLDSLENDERCKMIKRIANLE PLTVDLNFQYYLLVRRQQGFILHAYYDMMDLKVATADRLROPD SHIVKKINNINKSALKYQLFLDSLENGERFTKANVFPENTGEDVLRPA MAAKFRVARLYGRITADPKEELEKLARTSLEHYKFIVDYCEKHP RAAQSIEVBLELSKEMVSLLPTKMERFFTKNAUL GLUOZAAQGAQTTGEKARAAANTKARBFETKNAUL GLUOZAAQGAQTTGEKARAAARTKAGLAAQG	į.			ENSKIMITDEGLGVMPONGIMENS COMPONED POUR POUR POUR POUR POUR POUR POUR POUR
DDISESAKOFICHLLEKOPMENYTCEKALSHEN JONTALHRDI YPSYSLJOKNPASKYRKOAFNAAVUHHRKILHMILIS POWRR BVENRPPETQASETSRPSSPETTITEAPVLDHSVALPALTOLPC OHGRPPAPGGRSINCIJVNGSLHISSSLVWIGSLAAGPCGCC SSCLNIGSKGSSCSRPTLLKKANKKONKKSEVWPVVKASGSS HCRAGGTGVCLIM SCROFGWRPAGGGAGMELLSALSIGELALSPSRVPLFPVPDLS YFIVSILYLKYBPGAVELSRIPIASMLCAMHLGGSYILADLL LGPPLIDVSYNNSSILLASAVNYLIPDLDYYKCVCFLPVYLL LGPPLIDVSYNNSSILLASAVNYLIPDLDYYKCVCFLPVYLL LGPPLIDVSYNNSSILLASAVNYLIPDLDYYKCVCFLPVYLL LGPPLIDVSYSNSSILLASAVNYLIPDLDYYKCVCFLPVYLL LGPPLIDVSYSNSSILLASAVNYLIPDLDYYKCVCFLPVYLL LGPPLIDVSYSNSSILLASAVNYLIPDLGYYKCSGVA LMSNFEQLIRGVWRPETNSILHMSFPYKASLVGATLFTLOQTEN LMSNFEQLIRGVWRPETNSILHMSFPYKASLVGATLFTLOQTEN LGPPLOGRAMPAKSKEELSEGSRK KAKKAK LMSNFEQLIRGVWRPETNSILHMSFPYKASLVGATLFTLOQTEN KKAKKAD OFMSILFPTLHRVGCVCHPTSHSSPPDALGGYLIPDL FGSSACGGNHHIDNINGSCHSGGGGGGANSAMPAKSKEELSEGSRK KAKKAK OLIPPDSPDENCCKLKORLPSIVVEPTGESVESGELRWPPEEFL VOEDEQDNCEETAKENKEQ OLIPPDSPDENCCKLKORLPSIVVEPTGESVESGELRWPPEEFL VOEDEQDNCEETAKENKEQ OFFICELKINKEPHLUGVOPCVSFRGRGHRPSILMLHGFSAHKD MILSVVKFLPRINHLUCVDMPOHRGTTRSSLDDLSIDGQVKRTH OFFICELKINKEPHLUGVOPCVSFRGRGHRPSILMLHGFSAHKD MILSVVKFLPRINHLUCVDMPOHRGTTRSSLDDLSIDGQVKRTH OFFICELKINKEPHLUGVOPCVSFRGRGHRPSILMLHGFSAHKD MILSVVKFLPRINHLUCVDMPOHRGTTRSSLDDLSIDGQVKRTH OFFICELKINKEPHLUGVOPCVSFRGRGHRPSILMLHGFSAHKD MILSVVKFLPRINHLUCVDMPOHRGTTRSSLDDLSIDGQVKRTH OFFICELKINKEPHLUGVOLVSGAAVEKIPLIPSTPEEMSEMLUCC SYVRFKVPQQILIGUDVDVSGABAMANVPRABVCEKFQA ALALSRVSLHKNPEKEPYKSLYSARALLEEVKALLGPAPEDEDE RPPSKDGGGAGDHALGLDAFAVETNIESGGAVEKAMANVPRABVCEKFQA ALALSRVSLHKNPEKEPYKSLYSARALLEEVKALLGPAPEDEDE RPPSKDGGGAGDHALGLDAFAVETNICHMRHGLASANVI FGGTKKISAFGTFTTNITTLIKHTNITAGVYGHEMFKAHKVCHSTL KRQLSHNAYHIFIBMAINAATLSGYTINKLCFMERHCLSAANVI FGGTKKISAFGTFTTNITTLIKHTNITAGVYGHEMFKAHKVCHSTL KRQLSHNAYHIFIBMAINAATLSGYTINKLCFMERHCLSAANVI FGGTKKISAFGTFTTNITTLIKHTNITAGVYGHEMFKAHKVCHSTL KRQLSHNAYHIFIBMAINAATLSGYTINKLCFMERRECKHKRRI JAMLE PLTVDLNPGYYLLVSRQQGGFISHAYYMMCPFBHGBDVLRPA MAAKFRVARLYGKIITADPKGELBARAKRGGLAARQF MAAKFRVARLYGKIITADPKGELBARAKRGGLARAPG MAAKFRVARLYGKIITADPKGELBARAKRGGLARAPG PAANGLE		1		VDCWSIGVITVILLCOVDDEVPRTECVI PRINTED TO COME
PSYST_CIONFRAKSKRRQARANAAVVHIMIKLIHMILISPGVRP EVENRIPPETQASETSPESPEITTERPLUEDISVALPALTOLDPC OHGREPTAPGGSLINCLVUNGSLHISSSLVPHMQGSLAAGPCGCC SSCLNIGSKGKSSYCSPTSLKKANKKQMFKSEVWVPVKASGS HCRAGOTGVCLIM 5479 3 949 SCROFGHHARGGQAGAMELISALSGELALGFERVPLPFVFDLS YFIVSILIYLKYEPGAVELSRRIPIJFASWLCAMHCCGSYILADLL LGBELDYFSINSSILLASAWYLIFCCPLDLFYKCVCFLPVKL LGBELDYFSINSSILLASAWYLIFFCPLDLFYKCVCFLPVKL LFVAMKSUVRVRKIAVGIHHAHHHYHHGWFWHATGGVKOSGVA LMSNFFQLLRGWKRETNEILHMSPFTKASLYGALIFTLQOTRW LPVSKASLIFITTEMVSCKVFLTATHSHSSSPDALGGYICDPL FGSACGDHHHINHGSHSGGGFQAQHSAMPAKSKEELSEGSRK KKAKKAD 6480 192 514 DFMSITYPTHCDPYLRSAKWTEVMNTQPMEEIGLSPRKDGLSY QIPPDPSDPDRCCKIKDRLPSIVVBFTEGEVESGELRWPPEEFL VQEDEQDNCBETAKENREQ QIPPDSDPDRCCKIKDRLPSIVVBFTEGEVESGELRWPPEEFL VQEDEQDNCBETAKENREQ QIPPDSDPDRCCKIKDRLPSILVBFTEGEVESGELRWPPEEFL VQEDEQDNCBETAKENREQ QFVECLKLNKKPFHLVGTSMGGQVAGVYAAYYBDVSSLMLVCP AGLQYSTDNGFVQRLKELQGSAAVEKIPLIPSTFEEMSEMLQLC SYVFKYVPQOLIQGLUDVRIPHINNFYRKLFIETVSEKSFYSLMQ NMGKIKVPTQIIIGKUDVRIPHINNFYRKLFIETVSEKSFYSLMQ NMDKIKVPTQIIIGKUDVRIPHINNFYRKLFIETVSEKSFYSLMG NMDKIKVPTQOLIGGLUDVRIPHINNFYRKLFIETVSEKSFYSLMG NMDKIKVPTQOLIGGLUDVRIPHINNFYRKLFIETVSEKSFYSLMG NMDKIKVPTQIIIGKGDDVLDVRIPHINNFKLD SYVFKYVPQOLIQGLUDVRIPHINNFKLD SYVFKYVPQOLIGGLUDVRIPHINNFKLD SYVFKYVPQOLIGGLUDVRIPHINNFKLD SYVFKYVPQOLIGGLUDVRIPHINNFKLD NMDKIKVPTQOLIGGLUDVRIPHINNFKLD SYVFKYVPQOLIGGLUDVRIPHINGKELD SYVFKYSQSRRKAGVPTANIESGAVERAMANVPWAEVCEKFQA ALALSRVELHKNPEKETYKSKYSARALLEEVKALLGPAPEDEBDE RPEADEGGPGADGHALGIPAEVVEPGAVGRANLAVIFFHLGV NHIDTEBLSAGEBHLVKCLRLLRRYRLSHDCISLCIQAQNNLGI LWSERSETTAQAVEKYSVLRPLDFERSTIPLTETPEE EKLTEQERSKRFKKVTHRLYTLAQVVQHMEWEKKAAHVCHSTL KRQLEHNAYHEIBMAINAATLSGFYINKLCFMBARRICLSAANVI FGGTGKISATEDTPEAGEGVPBLIVFGKRSIARGWKYCLTIMQ MAQLSMGDNIGGLDLDKQSELRALRKKELDEESTIKKKAVQFGT GGILCATSAVEEKYSVLRPLDFEARRECHMEKRILADEPLAVFTANKFPQ IDGYVTDHIEVVQDHSALFKGLAFFETDMBERCKHKKRIAMLE PLTVDLWPQYYLLVNRQLOFFILABRYYDMMDLKVATADRILADPD SHIVKKINNINKSBALKYVQLIFILGRDVNRYPEHIGBDVLRPA MLAKFRVARLIYGKITTADPKKELENLATSLEHYKRIUTUGVCEKHP BAAQGBLYGETSSTFYNNTATILPLSGWODSILTNITTEKKLM	1			DDISESAKDFICHILEKDPNEDVTCEVALGUDULTGONTO
BVERRPETQASETSRPSSPEITTTERPULDISVALEPALTOLIC OHGREPTAPGGGSLANCLVINGSLHASSLYPMEQGSLAAGPCGCC SSCLNIGSKGKSSYCSEPTLLKKANKKQNFKSEVWFVVKASGSS HCRAGGTGVCLIM SCROFGMHEAGGGAGAMELISALSIGELALGFSRVPLPPVFDLS YFIVSILYLKYRPGAVELSRRIPTAGMICAMHACRGSYILADLL LGBLIDYFSNNSSILLASAWYLIFFCPJDLFYKCVCFLPVKL IFVAMKEVVRVRKIAVGIHAHHHYHMGWFMIATGWVKGSGVA LMSNFEQLLRGWWRETNEILHMSFPTKASLYGAILFTLQOTRW LPVSKASLIFIFTLFWGVKVPITAHSSPPTALGGYTCPVL FGSACGGDHHHNHGGSHSGGGPGAQHSAMPAKSKEELSEGSRK KKAKKAD 192 514 DFMSIYFPIHCPDYLRSAKWTEVMNNTQPMEEIGLSPRKDGLSY QIFPDPSDPDRCKIKDRLPSIVVEPTEGEVESGELRWPPEBFL VQEDEGDMCESTAKENKRQ VGENGDMCESTAKENKRQ KSRMDLDVVNMFVLAGGTLAIPTLAFVASFILWFSALTRIYYWY MRRTLGMQVRYVHHEDYGYSFRGFGHKPSILMHGFSAHKD MMLSVVKFLPKNILLLVCVDMPGHEGTTRSSLDDLSIGGQVKRIH QFVECLKLMKKFFHLVGTSMGGQVAGVYAAVYBDVSSLMLVCP AGGLYSTNOFVORLKELQGSAAVEKIPLIPSTPEERSEMLQLC SYVRFKVPQQILQGLVDVRIPHNNFYRKLPLBIVSEKSRYSLHQ NMDKIKVPTQIIMGKQDQVLDVSGADMLAKSIANCQVELLERGG HSVWERPRKTAKLIIDFLASVHINTNKKLD 6482 2517 568 EPVSKVSGSRRKAGVPTANIESGAVEAAMANVPWAEVCEKFQA AALASRAVEHNNENEEVYKSKYSARALLEPVARDEVCEKFQA MALLSREVEHTSALGHLVKCLRLLRRYRLSHDCISLCYQAONNIGI LWSERBETTAQAYLESSERLIVOKHSGSPLDTERFLPEE EKLTEOGESKRFEKVYTHNLTYLAQVYQHLEMFEKAAHYCHSTL KRQLEHNAYHPIEMAINAATLSGFYINKLCFMERHCHLSAANVI FGQTGKISATEDTFEAEGEVFELIVPRGKGIARCHIKVCLTIMQ NAQLSMQDNIGELDLDKQSELRALRKKELDEESIRKKAVQFGT GSLCDALSAVEKVSVIKRPLDFERSREVSSPLDTGRAKPCLTSAMVI FGQTGKISATEDTFEAEGEVFELIVPRGKGIARCHIKVCLTIMQ NAQLSMQDNIGELDLDKQSELRALRKKELDEESIRKKAVQFGT GSLCDALSAVEKVSVIKRPLDFERSREVSSPLDTFEAKFEP EKLTEOGRYKFFEKVYTHNLTYLAQVYQHLEMFEKAAHYCHSTL KRQLEHNAYHPIEWAINAATLSGFYINKCFPRESSTIKKAVQFGT GSLCDALSAVEKVSVIKRPLDFERSREJELGQHVYPERKEFER SHIVKKINNLMSALKYVQLFILDSLROPNNVPPEHIGSDVLRFA MAAKFRVARLYGKITTADPKKELENLATSLEHVKFIVDYCEKHP BAAGGAQTFGEKAEAAATLKAAPGWLKRFIVMKFIVDYCEKHP BAAGGAQTFGEKAEAAATLKAAPGWLKRFIVMKPPAASARAGP CLVOEAAQPQGSTSTETPNNTATPLIPSGWOOSFLTNITTEKVLM	1			YPSVSI-OTOKNEAKSKWPOAENAANGRUMBUL WART WART
OHGREYTAPGGRELMCLVNGSLHISSSLVPHMGGSLAAGPCGCC SSCLNIGSKKSSYSCSPTLLKKANKKOPKSEVMVPVKASGSS HCRAGOTGVCLIM SCRGPGWHPAGGGAAMELLSALSIGELALSFSRVPLPPVFDLS YFIVSILYLKYBPGAVELSRIBIPIASWLCAMLHCGSYILADLL LGBELIDYFSNNSSILLASAWWIJFFCPLDIFYKCVCFLPVKL IFVAMKEVVRVKRIAVGHHAHHNGFWMIATGAWKGSGVA LMSNFFOLLEGWKPETNEILHMSPFTKASLYGAILFTLQOTRW LPVSKASLIFIFTLFWVSCAVFLATHHSHSSPFDALGGYICPVL FGSACGGDHHHDNIGGSHSGGGFGAQHSAMPAKSKELSGSRK KKAKKAD 6480 192 514 DFMSITYFPHCPVYLRSAKWTEVMNNTOPMEBIGLSPRKOGLSY QIPPDPSDPDRCCKLKDRLPSIVVEPTEGEVESGELRWPPEBFL VQEDEQDNCEETAKENKEQ VQEDEQDNCEETAKENKEQ WRSTLGMOVRYWHEDVGFCYSFRGRPGHKPSILMLHGFSAHKD WMSJVVKPLPNRIHLHVCVDMPGHETTSSLDDLS 105QVKRIH OFVECLKLMKKPFHLVGTSMGGVAGVYAAYYPSDVSSLMLVCP AGLQYSTDNQFVQRLKELGGSAVEKIPLIPSTEEMSEMLGLC SYVRFKVPQQILQGLUDVRIPHNNTYRKLFJETVSEKSRYSLMQ NMDKIKVFTQIIGKCQDQVLDVSGADMLAKSIANCQVELLENCG HSVWERPRYRTAKLIDIFJASVHNTNKKLD FRYSKPRYRTAKLIDIFJASVHNTNKKLD FPWSKYSQSRRKAGVPTANIEESQAVEAAMANVPWAEVCEKFQA ALALSRVSLHKNPEKEPYKSKYSARALLEEVKALLGPRAEDEDE RPFAEBGGFGAODHALGIPAEVVEPGVAGAVRAVLSTFHLGV NHIDTEBLSAGEBHLVKCLRLLRRYRLSHDCISLCIQAQNNLIGI LWSERGETETAQAYLESSERLIVOWGRGIAACHIVETPILEE EKLTDOERSKSFEKVYTHNLYYLAQVYQHLEMEEKAAHYCHSTL KRQLEHNAYHPIEWAINAATLSGFYINKLCFMBARRCUSAANVI FGGTCKISATEDTPEAGEGVPELIVARGRIAACHIVCLTIMQ NAQLSMQDNIGELDLDKQSELRALRKKELDEESSIRKKAVQFGT GELCDAISAWEEKVSLYRPLDFERREINLATSLEHYKRLUTHTAM NAQLSMQDNIGELDLDKQSELRALRKKELDEESSIRKKAVQFGT GELCDAISAWEEKVSLYRPLDFERGENERCKHHKRIAMEP PLTVDLNPQYYLLVNRQLQFEIAHAYYDMMULKVAITADRIADPD SHIVKKINNINKSBLKYVQLFIDESDURPNVPPEHIGSDVLRPA MLAKFRVARLIYGKITTADPKKELENLATSLEHYKRIVDYCEKHP RAAGGEAVELELSKEWVSLLPTKMERFTTRMALT 6483 3 623 NSHLLCGLERRAPLSANGERAANLKREUWERPPASARAGG GLVCBAAQPQGSTSETETPNNTJELPLYSCWOSPITNITIELYLLW		j		EVENRPPETOASETSPRESERTITITED BUT DUCKAL BALTON DO
SSCINIGSKOKSSYCSBPTLLKKANKKONFKSEVMUPUKASGSS HCRAGOTGVCLIN SCROPGMIPAGGQAGAMELISALSIGELALSFSRVPLPPVFDLS YFIVSILYLKYBPGAVELISRRIIPIASMICAMIHCFGSYLLADLL LGBPLIDYFSNNSSILLASAUWYLIFFCPLDIFYKCCVELPVKL IFVAMKEVURVRIANGIHHAHHHYHHGWFWITATGAVKGSGVA LMSNFFQLLRGWKPFTNEILHMSPPPTKASLYGAILFTLQOTKM LPVSKASLIFIFTLFMVSCKVPLTATHHSSSPPDALEGYICCVL FGSACGGDHHHDNHGGSISGGGPGAQHSAMPAKSKEELSEGSRK KKAKKAD 192 514 DFMSIYFPHCPDYLRSAMMTEVMMNTQPMEEIGLSPRKDGLSY QIPPDPSDPDRCCKLKDRLPSIVVEPTEGSVESGELRWPPEFFL VQEDEQDNCEETAKENKEQ ALPONIC SEMBLE VOLUME VOLU	1			OHGRRPTAPGGRSLNCIJVNGSLHTSSSLVENHOGSLAACROOG
6479 3 949 SCROFGWHPAGGQAGAMELISALSIGELALSFSRVPLPPVFDLS SCROFGWHPAGGQAGAMELISALSIGELALSFSRVPLPPVFDLS YFIVSILYLKYEPGAVELSRRIPIASMLCAMLHCFGSYLLADLL LGBELIDYFSNNSSILLASAWYLIFFCPLDLFYKCVCFLPVKL IFVAMKEVUVRVRIAGTHAHHHGMFVMIATGWKGSGGA LMSNFEQLLRGWKPETNEILHMSPPTKASLYGAILFTLQQTRW LPVSKASLIFIFTLEWVSCKVFLTATHHHSSPPTDALEGYICDVL FGSACGGDHHHDNHGGSHISGGGAGHSAMPAKSKEELSEGSRK KKAKKAD 6480 192 514 DFMSIYPPHCPDYLRSAKMTEVMNNTQPMEEIGLSPRKDGLSY QIPPDPSDPDRCCKLKDRLPSIVVPPTEGEVESGELRWPPEEFL VQEDEQDNCEETAKBNKBQ 6481 110 1131 KSRMDLDVVNNFYLAGGTLAIPILAFVASFLLWFSALIRIYYWY WRRTLGMQVRYVHHEDYQFCYSFRGRPGHRPSILMHGFSAIKD MIMSVVKFLPKHLHLVCVDMFGHSTTRSSLDDLSIDGGVKRIH GFVECKLKHKKPFHVLGTSMGGVAYNAYYPSDVSGLMUCP AGLQYSTDNGFVQRLKELQGSAAVEKTPLIPSTPEEMSEMLQLC SYVRFKVPQQILQGLVDVRIPHNNFYRKHPLEIVGSKSFYSHQ NMDKIKVPTQIIWGKQDQVLDVSGADMLAKSIANCQVELLERNGG HSVVMERPRKTAKLIIDFLASVHNTONNKKLD 6482 2517 568 EPVSKVSGSRRAGYPTANIESGAVEAMMNVPWAEVCEKFQA ALALSRVELHKNPBKEPYKSKYSARALLEEVKALLGPAPEDEDE RPEAEDGGGAGDHALGLPAEVYPEGGVAGAVAVAVFBAEVCEKFQA ALALSRVELHKNPBKEPYKSKYSARALLEEVKALLGPAPEDEDE RPEAEDGGGAGDHALGLPAEVYPEGGVAGAVAVAVFBAEVCEKFQA ALALSRVEHRNPBKEPYKSKYSARALLEEVKALLGPAPEDEDE RPEAEDGGGAGDHALGLPAEVYPEGGVAGAVAVAVFBAEVCEKFQA ALALSRVEHRNPBKEPYKSKYSARALLEEVKALLGPAPEDEDE RPEAEDGGGAGDHALGLPAEVYPEGGVAGAVAVAVFBAEVCEKFQA ALALSRVEHRNPBKEPYKSKYSARALLEEVKALLGPAPEDEDE RPEAEDGGGAGDHALGLPAEVYPEGGVAGAVAVAVAVFBAEVCEKFQA ALALSRVEHRNPBKEPYKSKYSARALLEEVKALLGPAPEDEDE RPEAEDGGGAGDHALGLPAEVYPEGGVAGAVAVAVAVFBAEVCEKFQA ALALSRVEHRVPBKEPYKSKYSARALLEEVKALLGPAPEPEDE EKLTEGERSKAFEKVYTHNLYYLAQVYGHLEMFERAAHVCHSTL KRQLEHNAYHDEWALDHAGGAACHARGAANVI FGGTKKISATEDTERAGGEVPELLYHQRKGEIARCHIKVCHILGHG MAQLSMQDNIGELDLDKQSELRALRKKELDEESIRKAQVGFGT GELCDAISAVEEKVSYLRPLDFERAELFLLIGGVYVFFAKEFFQ IDGYVTDHIEVVQUHSALIFKGLAFFTEMALTIMLE PLIVULNPOYYLLUNRQIQFELAHAYYDMMDLKVAIADRLRDPL MAAKGRARTYGKITURQIQFELAHAYYDMMDLKVAIADRLRDPL MAAKGRARTYGKITURQIQFELAHAYYDMMDLKVAIADRLRDPL SHIVKKINNLNKSALKYYQLFLDSIRDPNKVPPEHIGGDVLRPA MAAKGRARTYGKITURGLOFFTHWMTATPLSVWKPRASARAQB PAASGGAGTORT	1			SSCLNIGSKGKSSYCSRPTLLKKANKKONEKSEUMUDUVA CCCC
SCRGPGWHPAGGQAGAMELLSALSGELALSFSRVPLPPVFDLS YFIVSILYKYEBGAVELSRRIPIASWLCAMIHCFGSYILADLL LGBPLIDYFSNNSSILLASSAWTIFCPLDLEYKCUCFLPVKL IFVAMKEUVRVRKIAVGIHAHHHYHHGWFVMIATGWVKGSGVA LMSNFEQLLRGVWKPETNSILHMSPPTKASLYGAILFTLQOTKW LPVSKASLIFIFTLFWJSCKUFULATHHSSPPTABLGGVICPVL FGSACGGDHHHDNHGGSHSGGGPGAQHSAMPAKSKEELSEGSRK KKAKKAD 6480 192 514 DFMSIYFPIHCPDYLRSAKMTEVMMNTQPMEEIGLSPRKDGLSY QIPPDBSDFDRCCKIKDRLPSIVVEPTEGEVESGELRWPPEFL VQEDEQDNCEETAKENKEQ VQEDEQDNCEETAKENKEQ WRRTLGMQVRYHHEDVQCFCYSFGGRPGHMSILMLHGFSAHKD MMLSVVKFLPKHLHLUCVDMPGHBGTTRSSLDDLSIDGVKRIH QFVECLKLNKKPFHLVGTSMGQVAGVYAAYYPSDVSSLMLVCP AGLQYSTDNQFVQRLKELQGSAAVEKIPLIPSTPEEMSSRMLQLC SYVRFKVPQQILQGLJOVDIFIHNYKKLPLEIVSHEKSRYSLHQ NMDKIKVPTQIIWGKQDQVLDVSGADMLAKSLANCQVELLENCG HSVWREPRKTAKLIIDFLASVINTIONIKLD 6482 2517 568 EPPSKVSGSRRAGVFTANIESSGAVEAANANVPMAEVCEKFQA ALALSRVEHKNPBKEPYKSKYSARALLEEVKALLGPAPEDEDE RPEAEDGPGAGDHALGLPARVVSPEGFVAQAVAVALAVIEFHLGV NHIDTEELSAGEBHLVKCLHLLRYRLSHDCISLCIQAQNNIGI LWSEREEIETAQAYLESSEALYNQYWKEVGSPPLDFTERFLPEE EKLTEGERSKRFEKVYTHNLYYLAQVYQHLEMFEKAAHVGHSTL KRQLEHNAYHFIEMAINAATLSGFYINKLCFMERAHCLSAANVI FGGTGKISATEDTFEARGEVPELIYHGKGEIARCHIKYCLTLMQ NAGLSMONIGGELDDLKQSSLRALRKEELDEEESIRKKAVQFGT GELCDAISAVEEKVSYLRPLDFEERSELJHLGGHVVFFAKKFFQ IDGYVTDHIEWQDHSALTKGLAFFETBMCKHANJADRLROPD SHIVKKINNLNKSALKYYQLFLDSLROPNKVFPEHIGEDVLRPA MLAKFRVARIYGKIITADFKKELEMIATSLEHYKFIUDYCEKHP SHIVKKINNLNKSALKYYQLFLDSLROPNKVFPEHIGEDVLRPA MLAKFRVARIYGKIITADFKKELEMIATSLEHYKFIUDYCEKHP BAAGGAQTTGEKARAAAAHAAAAHAAPGMLARFFTWMALT 6483 3 623 NSHLLCGLRARAPLSANGREARAMEQRLABFFTAARKRAGLAAQP PAASGGAQTTGEKARAAAAMEQRLABFFTAARKRAGLAAQP PAASGGAQTTGEKARAAAAMEQRLABFFTAARKRAGLAAQP PAASGGAQTTGEKARAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA				HCRAGOTGVCLIM
4 STYVSIIYLKYEPGAVELSRRIIPIASHLCMM.HCFGSYILADLL LGEBLIDYFSINSSILLASAVWYLIFFCPLDLFYKCVCFLPVKL LFVAMKEVVRVRIAVGIHRAHHHYHHGWFVMIATGWVKGSGVA LMSNFEGLLRGVWKPETNEILHNSFPTKASLYGAILFTLQOTRW LPVSKASLIFIFTLFTMYSCSLTJATHSHSSPPDALEGGYLCVL FGSACGGDHHDNHGGSHSGGGPGAQHSAMPAKSKEELSEGSRK KKAKKAD 6480 192 514 DFMSIYFPHCPDYLRSAKMTEVMNNTQPMEEIGLSPRKDGLSY QIFPDPSBPDRCCKLKDRLPSIVVEPTEGEVESGELRWPPEEFL VQEDEQDNCEETAKENKEQ 6481 110 1131 KSRMDLDVVMMFVIAGGTLAIPILAFVASFLLWFSALTRIYYWY WRRTLGMQVBYVHHEDYQFCYSFRGRPGHKPSILWHHGFSAHKD MWLSVVKFJRKHLHLVCVDMPGHEGTTRSSLDDLSIDGQVKRIH QFVECLKLNKKPFHLVGTSMGGQVAGVYAAYYPSDVSSLMLVCP AGLQYSTDNGFVQRLKELQGSAAVERIPLIPSTPEEMSEMLQLC SYVRFKYPQOILGGLVDVBIPINNFYRKLFLSVSKKSRYSLHQ NMDKIKVPTQIIWGKQDQVLDVSGADMLAKSIANCQVELLENCG HSVVMERPRKTAKLIIDTLASVHNTONNKKLD 6482 2517 568 EPVSKVSGSRRAGVFTANIESGAVEAMANVPRAEVCEKFQA ALALSRVEIHKMPEKEPYKSKYSARALLEEVKALLGPAPEDEDE RPEAEDGPGAGDHALGLPAEVVEPSGFVAQRAVRLAVIEFHLGV NHIDTEELSAGEEHLVKCLRLLRRYRLSHDCISLCIQANIGI LWSERBEISTAQAYLESSGALVNOYMKEVGSPPLDPTERFLPEE EKLTEQERSKRFEKVYTHNLYYLAQVYQHEMFEKAANYCHSTL KRQLEHNAYHPIEWAINAATLSGYYINKLCFMEARHCLSAANVI FGQTTKISATEDTFEAEGEVPSLYNORMGBIACCMHKYCLTLMQ NAQLSMONIGIBLDLDKQSELRALKKEBLDEESIRKKAVQFGT GELCDAISAVEEKVSYLRPLDFEBRAEBLFLLGGHYVPEAKEFFQ IDGYYTDHIEVVQDHSALFKGLAFFETDMERCCMHKRRIAMLE PLTVULNPGYVILLVNRQTQFEIJAHAYYDMMLKVAIADRIRDPD SHIVKKINNLNKSALKYYQLFLDSLRDPNKYPPEHIGEDVLRPA MLAKFRVARRLYGKIITADPKKELENLATSLEHKKFIVDYCEKHP BAAGGAGTEVELBLSKEMYSLLIVMRFPTEMARAT 6483 3 623 NSHLLCGLRARAPLSANGREARAMEQRLAEFFRAARKRAGLAAQP PAASGGATPGEKARAAPTLKARAPGWKKRFLVWKPPRASARAQG GLVQEAAQPQGSTEETHWINTAIPLPSCWDOSFTINTIFLKVLIM	6479	3	949	
IGBELIDYFSNNSSILLASAVWILIFCCIDLFYKCUCFLPVKL IFVAKKEVURVKIAVGIHAHHHYHHGWFVMIATGWVKGSGVA LMSNFEQLLRGVWKPETNEILHNSFPTKASLVGALIFTLQOTRW LPVSKASLIFIFTLFWSCKVFLTATHSHSSPPDALEGGICPVL FGSACGODHHIDNIGGSHSGGGFGAQHSAMPAKSKEELSEGSRK KKAKKAD 6480 192 514 DFMSIYFPIHCPDYLRSAKMTEVMNNTQPMEEIGLSPRKDGLSY QIFPDSDPDRCCKLKDRLPSIVVEPTEGGVESGELRWPPEEFL VQEDEQDNCEETAKENKEQ AUGUSTUNGFVAHEDVQPCYSFRGRPGHKPSILMLHGFSAHKD WRRTLGMOURYVHEDVQPCYSFRGRPGHKPSILMLHGFSAHKD WRLSVVKFLPKNLHLVCVDMPGHEGTTRSSLDDLSIDGQVKRIH QFVECLKLNKKFPHLVGTSMGGQVAGVYANYYPSDVSSIMLVCP AGGQYSTDNGFVQRIKELGGSAAVERIPLIPSTPEMSEMLQLC SYVRFKYPQQILQGLVDVRIPHNNFYRKLFLEIVSEKSRYSLHQ MNDKKKVPTQIIWGKQDQVLDVSGAMUMAKSIANCQVELLENCG HSVVMERPRKTAKLIIDFLASVHNTDNKKKLD 6482 2517 568 EPVSKVGGSRRAGVPTANIEESQAVEAMMNVPWAEVCEKFQA ALALSRVEHHKNPEKEPYKSKYSARALLEVKALLGPAPEDEDE RPEAEDGPGGGHALGLPBEVVEPSGPVAQRAVLAVIEFHLGV NHIDTEELSAGEEHLVKCLRLLRRYRLSHDCISLCIQAQNNLGI LWSEREBIETAQAVLESSEAUYNOYMKEVGSPPLDPTERFLPEE EKLITEGBRSKRFEKVYTHNIYYLAQVYCHLEMFEKRAHYCHSTL KRQLEHNAYHPIEWAINAATLSQFYINKLCFMEARHCLSAANVI FQQTGKISATEDTPEAEGEVPELHYGRGGIARCWIKYCLTLMQ NAQLSMONNIGELDLDKQSELRALRKKELDBEESIRKAVQCFGT GELCDAISAVEEKVSYLRPLDFEBARELFLLGQHYVFEAKEFFQ IDGYVTDHIEVVQDHSALFKGLAFFETDMERCCMHKRRIAME PLTVDLNPQYYLLVNRQQTGFIAHAYYDMMDLKVAVADRURDPD SHIVKKINNLWKSALKYYQLFLDSLRDPNKVPPEHIGEDVLRPA MLAKFRVARLYGKIITADPKKELENLATSLEHKKFITUPYCEKHP BAAQGIEVELELSKEMVSLLIFMERFETKMAUT 6483 3 623 NSHLLCGGRARAPLSANGREARAMEQRLAEFRAARKRAGLAQP PAASQGAQTPGEKARAAATLKARAPGWKKRIVKKPLNKKPLM	i			YFIVSILYLKYEPGAVELSRRIPTASWI.CAMI.HCEGGYTTADIT
IFVAMKEVURVRIKA TO THHAHHHYHHOMFUMI ATGWVIKGSGVA LMSNFEQLIRAGVMEPTME ILHMSPFTKASLYGAILFTLQOTRW LPVSKASLIFITTLFMVSCKVFLIATHSHSSPFDALEGYICPVL FGSACGGDHHHDNINGGSHSGGGFGAQHSAMPAKSKEELSEGSRK KKAKKAD 6480 192 514 DFMSIYFPIHCPDYLRSAKMTEVMMNTQPMEEIGLSPRKDGLSY QIFPDPSDPDRCCKIKDRLPSIVVEPTEGEVESGELRWPPEEFL VQEDEQDNCEETAKENKEQ 6481 110 1131 KSRMDLDVVNMFYIAGGTLATPILAFVASFILWFSALIRTYYWY WRRTLGMQVRYVHHEDVQFCYSFRGRPGHKPSILMLHGFSAHKD MWLSVVKFLPKNLHLVCVDMPGETTRSSLDDDISIDGQVKRIH QFVECLKLNKKPFHLVGTSMSGQVAGVYAAYYPSDVSSIMLVCP AGGQYSTDNQFVQRLKELQGSAAVEKIPLIPSTPEEMSEMLQLC SYVRFKVPQQILQGLVDVRIPHNNFKKLFLEIVSEKSRYSLHQ NMDKIKVPTQIIMGKQDQVLDVSGADMLAKSIANCQVELLENCG HSVVMRPPRKTAKLIIDFLASVHNTDNNKKLD 6482 2517 568 EPVSKVSGSRRKAGVPTANIESGGAVBAAMANVPMAEVCEKFQA ALALSRVELHKNPEKEPYKSKYSARALLEEVKALLGPAPEDEDE RPEAEDGPGAGDHALGLPAEVVEPEGFVAQRAVRLAVIEFHLGV NHIDTEELSAGEEHLVKCLRLLRRYRLSHDCISLCIQAQNNLGI LWSGEREIETADAYLESSEAUNOYMEWGSPLDPTERFLPEE EKLTEQERSKRPEKVYTHNLYYLAQVYQHLEMEEKAAHYCHSTL KRQLEHNAYHPIEWAINAATLSGFYINKLCFMBARHCLSAANVI FGGTKKISATEDTPEAEGEVPELYHQRKGBIARCWIKYCLITLMQ NAQLSMQDNIGELDLDKQSELRALRKKELDEESSIRKKAVQFGT GELCDAISAVEEKVSYLRPLDFEBARELFILLGGHYVFEAKEFFQ IDGYVTDHIEVVQDHSALPKGLAFFETDMERRCKMKRRIAMLE PLTVDLNPQYYLLVNRQLQFETAHAYYDMMDLKVATADRLROPD SHIVKKINNLNKSALKYYQLFLDSLRDPNKVPPEHIGEDVLRPA MLAKFRVARLYGKIITADPKKELENLATSLEHYKFIVDYCEKHP BAAQEIEVELELSKEMVSLLPTKMERFFRYMALIT 6483 3 623 NSHLLCGGRARAPLSANGREARAMEQRLASFRAARKRAGLAAQP PAASGGAQTPGEKAEAAATLKAAPGWIKRFILWKRPPASARAQP GLVQEAAQPQGSTSETPUNTATPLPSCWOOSFLITHITEKVLLW				LGEPLIDYFSNNSSILLASAVWYLIFFCPLDLFYKCYCFLDYKI
LMSNFEQLLRGVWKPETNEILLMSFPTKASLYGATLFTLQQTRW LPVSKASLIFITTLFMVSCKVFLTATHSHSSPFDALEGYICPVL FGSACGGDHHHDNHGGSHSGGFGAQHSAMPAKSKEELSEGSRK KKAKKAD 192 514 DFMSIYFPIHCPDYLRSAKMTEVMMNTQPMEEIGLSPRKDGLSY QIPPDPSDFDRCCKLKDRLPSIVVEPTBGEVESGELRWPPEEFL VQEDEQDNCEETAKENKEQ KSRMDLDVVMFVIAGGTLAIPILAFVASFLLWFSALTRIYYWY WRRTLGMQVRYVHHEDVQFCYSFRGRGHKPSILMLHGFSAHKD WRSJVVFLPKNHHLVCVDMPGHEGTTRSSLDDLSIDGQVKRIH QFVECLKLNKKPFFLLVGTAGGGVAGVYAAYYPSDVSSLHUVCP AGLQYSTDNQFVQRLKELQGSAAVEKIPLIPSTPEEMSEMLQLC SYVRFKVPQQILQGLVDVRIPHNNFYRKLFLEIVSEKSRYSLHQ NMKKIVPTQIIWGKQDQVLDVSGADMLAKSIANCQVELLENCG HSVVMERPRKTAKLIIDFLASVINTDNNKKLD 6482 2517 568 EPVSKVSGSRRKAGVPTANTEESQAVBAAMANUPMAEVCEKFQA ALALSRVELHKNPEKEPYKSKYSARALLEEVKALLGPAPEDEDE RPEAEDGPGAGDHALGLPAEVVSPEGGVAQRAVRLAVIEFHLGV NHIDTEELSAGEHLUKCLRLLRRYRLSHDCISLCIQAQNNLGI LWSERBEIFTAQAYLESSEALYNQYMKEVGSPPLDETERFLPEE EKLIEQERSKRFEKVYTHNLYYLAQVYQHLEMEFKAAHVCHSTL KRQLEHNAYHPIEWAINAATLSQFYINKLCFMEARHCLSAANVI FGQTGKISATEDTPEAEGEVPLYHQKRKGEIAKCMKYCLTLMQ NAQLSMQDNIGELDLDKQSELRALRKKELDEESSIRKKAVQFGT GELCDAISAVEEKVSYLRPLDPEARBELFILGGHYVFEAKEFPQ IDGYVTDHIEVVQDHSALPKGLAFFETDMERRCKMHKRRIAMLE PLITVDLNPQYYLLVNRQ LQFEIAHAYYDMDLKVATADRIRDDD SHIVKKINNLNKSALKYYQLFLDSLRDPNKVPPEHIGEDVLRPA MLAKFRVARLYGKIITADPKKELBLATSLEHYKFIVDYCEKHP BAAQSIEVELELSKEMVSLLPIKMERFETKMALT 6483 3 623 NSHLLCGGRARAPLSANGREARAMEQRLAEFRAARKRAGLAAQP PAASGGAQTPGEKARAAATLKAAPGWKRFIKWALT	ŀ			IFVAMKEVVRVRKIAVGIHHAHHHYHHGWFVMIATGWVKGSGVA
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6480 192 514 DFMS1YFPIHCPDYLRSAKMTEVMMNTQPMEEIGLSPRKDGLSY QIFPDPSDFDRCKLKDRLPSIVVEPTEGEVESGELRWPPEEFL VQEBEQDNCEETAKENKEQ 6481 110 1131 KSRMDLDVVNMFVIAGGTLAIPILAFVASFLLWFSALIRIYYWY WRRTLGMQVRVHHEDYQPCYSFRGRPGHKPSILMLHGFSAHKD MWLSVVKFLPKNLHLVCVDMPGHEGTTRSSLDDLSIDGQVKRIH QFVECLKLNKKPFHLVGTSMGGQVAGVYAAYYPSDVSSLMLVCP AGLQYSTTNQFVQRLKELQGSAAVEKIPLIPSTPEEMSEMLQLC SYVRFKVPQQILQGLVDVBIPHNNFYRKLPLEIVSEKSRYSLHQ NMDKIKVPTQIIWGKQDQVLDVSGADMLAKSIANCQVELLENCG HSVVMEPRKTAKLIIDFLASVHNTDNNKKLD 6482 2517 568 EPVSKVSQSRRKAGVPTANIESSQAVEXAMANVPWAEVCEKFQA ALALSRVELHKNPEKEPYKSKYSARALLEEVKALLGPAPEDEDE RPEAEDGPGAGDHALGLPAEVVPEGGFVAQRAVRLAVIEFHLGV NHIDTEELSAGEEHLVKCLRLRRYRLSHDGISLCIQAQNNLGI LWSEREEIETAQAYLESSEALYNQYMKEVGSPPLDPTERFLPPE EKLITEGERSKRFEKVYTHNLYYLAQVYQHLEMFEKAAHVCHSTL KRQLEINAYHPIEWAINAATLSQFYINKLCFMEARHCLSAANVI FGQTGKISATEDTPEAEGEVPBLYHGKKGEIARCWIKYCLITLMQ NAQLSMQDNIGELDLDKQSELRALRKKELDEESIRKKAVQFGT GELCDAISAVEEKVSYLRPJDFEARELFILGQHYVFEAKEFFQ IDGYYTDHIEVVQDHSALFKGLAFFETDMERGKMHKRIANLE PLTVDLNPQYYLLVNRQIQFEIAHAYYDMMDLKVAIADRLRDPD SHIVKKINNINKSALKYYQLEFILDSLRDPNKVPPEHIGGDVLRPA MLAKFRVARLIYGKIITADPKKELENLATSLEHYKFIVDYCEKHP EAAQEIEVELELSKEMVSLLPTKMERFRTKMALT 6483 3 623 NSHLLCGLRARAPISANGREARAMEGRLAAFRARKRRALAAQP PAASQGAQTPGEKAEAAAATLKAAPGWLKRFIVWKPRPASARAQP GLVQEAAQPQGSTSETFWNTAIPPLPSCWDOSFITNITFIKVLIM	1			FGSACGGDHHHDNHGGSHSGGGPGAQHSAMPAKSKEELSEGSRK
QIFDPSDFDRCKLKDRLPSIVVEPTEGEVESGELRWPPEEFL VQEDEQDNCETAKENKEQ 110 1131 KSRMDLDVVNMFVIAGGTLAIPILAFVASFLLWFSALTRIYYWY WRRTLGMQVRYVHEDYQPCYSFRGRPGHKPSILMLHGFSAHKD MWLSVVKFLPKNIHLUCUDMPGHEGTTRSSLDDLSIDGQVKRIH QFVECLKLNKKPFHLVGTSMGQVAGVYAAYYPSDVSSLMLVCP AGLQYSTDNGFVQRLKELQGSAAVEKIPLIPSTPEEMSEMLQLC SYVRFKVPQQILQGLVDVRIPHNNFYRKLFLEIVSEKSRYSLHQ NMDKIKVPTQIIWGKQDQVLDVSGADMLAKSIANCQVELLENCG HSVVMERPRKTAKLIIDFLASVHNTDNNKKLD 6482 2517 568 EPVSKVSQSRKAGVFTANIESGAVVZAAMANVPWAEVCEKFQA ALALSRVELHKNPEKEPYKSKYSARALLEEVKALLGPAPEDEDE RPEAEDGPGAGDHALGLPAEVVEPEGFVAQRAVRLAVIEFHLGV NHIDTEELSAGEEHLVKCLRLLRRYRLSHDCISLCIQAQNNLGI LWSEREEIETAQAYLESSEALINQYMKEVGSPPLDFTERFLPEE EKLITEGBRSKRFEKVYTHNLYYLAQVYQHLEMFEKAAHYCHSTL KRQLEHNAYHPIEWAINAATLSQFYINKLCFMEARHCLSAANVI FGQTGKISATEDTFEAEGGVPELYHQKKGEIARCWIKYCLTLMQ NAAQLSMQDNIGELDLDKQSELRALRKKELDEESIRKKAVQFGT GELCDAISAVEEKVSYLRPLDFEARSEPLFLIGGHVVFEAKEFFQ IDGYVTDHIEVVQDHSALFKGLAFFETDMERKCMHKRRIANLE PLTVDLNPQYYLLVNRQIQFEIAHAYYDMMDLKVAIADRLRDPD SHIVKKINNLNKSALKYYQLFLDSLARDPNKVPPEHIGEDVLRPA MLAKFRVARLYGKIITADPKKELENLATSLEHYKFIVDYCEKHP EAAQEIEVELELSKEMVSLLPTKMERFRTKMALT 6483 3 623 NSHLLCGLRARAPLSANGREARAMEGRLABFRAARKRGLAAQP PAASQGAQTPGEKKAEAAATLKAAPGWLKRFIVWKRPRASARAQP GLVQBAQPQGSTSETTWNTAIPLPSCWDOSFITNITFIKVLLW				KKAKKAD
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VQEDEQDNCEETAKENNEQ 1131 KSRMDLDVVNMFVIAGGTLAIPILAFVASFLLWFSALIRIYYWY WRRTLGMQVRYVHHEDVQPCYSFRGRPGHKPSILMLHGFSAHKD MWLSVVKFLPKNLHLVCVDMPGHEGTTRSSLDDLSIDGQVKRIH QFVECLKLNKKPFHLVGTSMGQQVAGVYANYVPSDVSSLWLVCP AGLQYSTDNQFVQRLKELQGSAAVEKIPLIPSTPEEMSENLQLC SYVRFKVPQQILQGLVDVRIPHNNFYRKLFLEIUSEKSRYSLHQ NMDKIKVPTQIIWGKQDQVLDVSGADMLAKSIANCQVELLENCG HSVVMENPRKTAKLIIDFLASVHNTINNKKLD 6482 2517 568 EPVSKVSQSRRKAGVFTANIEESQAVEAAMANVPWAEVCEKFQA ALALSRVELHKNPEKEPYKSKYSARALLEEVKALLGPAPEDEDE RPEAEDGPGAGDHALGLPAEVVEPEGPVAQRAVRLAVIEFHLGV NHIDTEELSAGEEHLVKCLRLIRRYRLSHDCISLCIQAQNNLGI LWSEREEIETAQAYLESSEALYNQYMKEVGSPPLDTERFLPEE EKLTEQBRSKRFEKVYTHNLYYLAQVYOHLEMFEKAAHVCHSTL KRQLEHNAYHPIEWAINAATLSQFYINKLCFMEARHCLSAANVI FGQTGKISATEDTFEAEGEVPELVHQRKGEIARCWIKVCLTLMQ NAQLSMQDNIGELDLDKQSELRALRKKELDEEESIRKKAVQFGT GELCDAISAVEEKVSYLRPLDFEEARELFLLGGHYVFEAKEFFQ IDGYVTDHIEVVQDHSALFKGLAFFETDMERRCKMHKRRIAMLE PLTVDLNPQTYLLVNRQIQFEIAHAYYDMDLKVAIADRLRDPD SHIVKKINNLNKSALKYSLIPLDSLEDDNKVPPEHIGEDVLRPA MLAKFVARLYGKIITADPKKELENLATSLEHYKFIUDYCEKHP EAAQEIEVELELSKEMVSLLPTKMERFRTKMALT 6483 3 623 NSHLLCGLRRAPLSANGREARAMEQRLAFFRAARKRAGLAAQP PAASQGAQTPGEKAEAAATLKAAPGWLKRFLVWKPPRASARAQP GLVQEAAQPPGGSTESTPWNTAIPLPSCWDOSFLTNTTFLKVLLM	1			QIFPDPSDFDRCCKLKDRLPSIVVEPTEGEVESGELRWPPERFI.
ASKMULDVVNMY LAGGTLAIP ILAFVASFILLMPSALIRIYYW WRRTLGMQVRYVHEDYQPCYSFRGPHKPSILMLHGFSAHKD MWLSVVKPLPKNLHLVCVDMPGHEGTTRSSLDDLSIDGQVKRIH QFVECLKLNKKPFHLVGTSMGGQVAGVYAAYYPSDVSSLWLVCP AGLQYSTDNQFVQRLKELQGSAAVEKIPLIPSTPEEMSEMLQLC SYVRFKVPQQILQGLVDVRIPHNNFYRKLFLEIVSEKSRYSLHQ NMDKIKVPTQIIUGKQDQVLDVSGADMLAKSIANCQVELLENCG HSVVMERPRKTAKLIIDFLASVHNTDNNKKLD 6482 2517 568 EPVSKVSQSRRKAGVPTANIEESQAVEAAMANVPWAEVCEKFQA ALALSRUHKNPEKEPYKSKYSARALLEEVKALLGPAPEDEDE RPPAEDGFGAGDHALGLPAEVVEPEGPVAQRAVRLAVIEFHLGV NHIDTEELSAGEEHLVKCLRLLRRYRLSHDCISLCIQAQNNLGI LWSEREEIETAQAYLESSEALYNQYMKEVGSPPLDPTERFLPEE EKLTEGBRSKRFEKVYTHNLYYLAQVVQHLEMFEKAAHYCHSTL KRQLEHNAYHPIEWAINAATLSQFYINKLCFMEARHCLSAANVI FGQTGKISATEDTPEAEGEVPELYHQRKGEIARCWIKYCLTLMQ NAQLSMQDNIGELDLDKQSELRALRKKELDEEESIRKKAVQFGT GELCDAISAVEKVSYLRPLDFEEARELFLLGQHYVFEAKEFFQ IDGYVTDHIEVVQDHSALFKGLAFFETDMERRCKMHKRRIAMLE PLTVDLNPQYYLLVNRQIQFEIAHAYYDMMDLKVAIADRLRDPD SHIVKKINNLNKSALKYYQLFLDSLRDPNKVPPEHIGEDVLRPA MLAKFRVARLYGKIITADPKKELENLATSLEHYKFIVDYCEKHP EAAQSIEVELELSKEMVSLLPTKMERFRTKMALT 6483 3 623 NSHLCGGRARAPLSANGERARAMEGILABFRAARKRAGLAAQP PAASQGAQTPGEKAEAAATLKAAPGWLKRPLVWKRPPASARAQP GLVQBAAQPGGSTEETPWNTAIPLFSCWDOSFLTNITFLKVLLW				VQEDEQDNCEETAKENKEO
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6487 352 863 SPLANERSWYTHATDUGDIKIEVFCERTPKTCENFLALCASN YYNGCIFHRNIKGFMUOTGDPTGTGRGGNSIWGKKEGEYSEYL KHNVRGVUSNANNGPBYTNGSQFFITYGKQPHLDMKYTVFGKVID GLETLDELEKL PUNEKTYPRENDVHIKDITIHANPFAQ 6488 878 241 TALQEFGTSGPPLSLRFALFSGTGRKPLPGGRGFSWPFSPRVP MEPPNLYPVKLYVYDLSKGLARRLSFINLGKQLEGIWHTSIVVH KDEFFFGSGGISSCPPGGTLLGPPDSVDVWGSTEVTEEIFLEYL SSLGESLFRGEAYNLFEHNCNTFSNEVAGFLTGRKLPSYITTLP SEVLSTPFGGALRFLLDSIQIPPGGSSVGRPNGQS KVARMATALGEBELDNEDVYSLLNVRREASSEELKAAYRRLCML YHPDKHRDPBLKSQAERLFNLVHQAYEVLSDPQTRAIVDIYGKR GLEMEGWEVVERRRTPAEIREFFERLQRERERERLQQRTNPKGT ISVGVDATOLLFDRYDEFYEDVSSFFPQLEINKHHISQSIEAPL TATDTAILGGSLSTQNGNGGGSINFALRRVTSAKGWGELEFGAG DLQGPLFGLKLFRNLTPRCFVTTNCALDFSSKGIRPGLTTVLAR NLDKNTVGYLQWHCSSPLLQVRGFRHTRACABPBFFRFFLIVD TWIDACGGARTPSTAWTSAAVKLREACLSGPGSGSHQLLLLTPR SKRRTGG 6490 3 1183 HERGCEVWLGYGFRAAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFHGRRWATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPERGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGIMLATCSADGIVRIYE APDVNNLSGWSLQHEISCKLSCSCISWNPSSRAHSPMIAVGSD DSSPNAMAKVQIFEVNENTRKYAKAETLMTVTDVPHDIAFAPNL GRSFHILAIATKDVRIFTLKFVPKELTSSGGPTKFEIHIVAGFD MINSQVWRVSWNITGTVLASSGDDCCVRLWKANYMDNWKCTGIL KGNGSPVNGSSQQOTENPSLGSNIPSLONSLNGSSAGRKHS HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG GSFHILAIATKDSRTSVTDVKFAPKHMGLMLAATCSADGIVRIYE APDVWNLSGWSQQOTENPSLGSNIPSLGSNDFSCGRKHS KDLIHDVSFDPHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSWWRVWSWNITGTVLASSGDDCCVRLWKANYMDNWKCTGIL KGNGSPVNGSSQQOTENPSLGSNIPSLGSNDFSCGRKHS KDLIHDVSFDPHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSWWRVWRWHAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLUBSRTSVTDVKFAPKHMGLMLAATCSADGIVRIYE APDVWNLSQWSQWITGSRTSVTDVKFAPKHMGLMLAATCSADGIVRIYE APDVWNLSQWSLQHEISCKLSCSCISWPSSSRAHSPMIAVGSD DSSPNAMAKVQIFPENENTRKYALGETLTMTVTDDVHJAFAPNL GRSFHILLAIATVDGVRIFTENTDVAVARDFFFEHIVARGD DSSPNAMAKVQIFPENENTRKYALGETLTMTVTDDVHJAFAPNL		l		ISETYNRLALEHIQQHPEEPLEGTTWTHSLKAQLLSLPFWVWTV
SFLKPLRGKMSVTLHTDVGDIKIEVFCERTPKTCENFLALCASN YYNGCIFHRNIKGFMVQTGDPTGTGRGGNSIWGKKFEDEYSEYL KHNVRGVVSMANNGPNTNOSQSPFITYGKQPHLDMKYTVFGKVID GLETLDELEKLPVNEKTYRPLNDVHIKDITHANDFAQ 6488 878 241 TALQEFGTGFPFLSLRPALPSGTGRFKPLFGARGFSWPFSPRVP MEPPNLYPVKLYVPULSKGLARLSFIMLGKQLEGIWHTSIVVH KDEFFFGSGGISSCPPGGTLLGPPDSVDVOGSTEVTEELFLEVL SSLGESLFRGEAVNLFHNCNTESNEVAGFLTGRKIPSYITDLP SEVLSTPFGGALRPHLDSTOLPPGGSSVGRPBGGS 6489 1457 375 KVAKMATALSEEELDNEDYYSILNVRREASSEELKAAYRRLCML YHPDKHRDBELKSQABRIPNLVHQAYEVLSDPQTRAIYDIYGKR GLEMEGWEVVERRTPAETEEFERLQREREERRLQRTNPKGT ISVGVDATDLFDRYDEEYEDVSGSSFPQIEINKMHISGSIEAPL TARDTAILSGSLSTONGNGGGSINFALRRVTSAKGWGELEFGAG DLGGPLFGKLKPRNLTPRGFVTTNCALQFSSRGIRPGLTVLAR NLDKNTVGYLQWHCSSPLLQVGRPHRNTRACAPEPSFRPFLHVP TWDACCSGARTPSTAWTSAAVKLREACLSGPGSGSHQLLLLTPR SKRRTGGG 6490 3 1183 HEAGCEVWLGYGPRAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSRDFHGRRWATGSSDOSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTILVDSRTSVTDVKFAPKHMGIMLATCSADGIVRIYE APDVWNLSGWSLOHBISCKLSCSCISWPSSSRAHSPMLAVGSD DSSPNAMAKVQIFEYNENTRKYAKABTLMTVTDVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVTKELTSSGGPTKFEIHIVAGFD NINSQVWRVSNNITGTVLASSGDDCVKLWKANYMDNRCTGIL KGMGSPVNGSSQQTSNPSLGSNIPSLQNSLNGSSAGRKHS HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG GSHWVKRTILUDSRTSVTDVKFAPKHMGIMLATCSADGIVRIYE APDVWNLSGWSLOHBISCKLSCSCISWPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDDVHDIAFAPNL GGSFHILAIATKDVRIFTLRSVKFAPKHMGIMLATCSADGIVRIYE APDVWNLSGWSLOHBISCKLSCSCISWPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDDVHDIAFAPNL GSSWWRVTHAHPEFGQVLASCSFDRTAAVWEETVGESNDKLRG GSHWVKRTILUDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVWNLSGWSLOHBISCKLSCSCISWPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDDVHDIAFAPNL GRSFHILAIATKDVRIFTLRVSTRAVEETVGESNDKLRG GSHWVKRTILUDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVWNLSGWSLOHBISCKLSCSCISWPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDDVHDIAFAPNL GRSFHILAIATVDVRIFTLRYAGAETLMTVTDDVHDIAFAPNL	1			1FLVPYLQMFLFLYSCTRADPKTVGYCIIPICLAVICNRHQAFV
YYNGCIPHRNIKGEMVOTGDPTGTGEGGSI MGKKPEDEYSEYL KHNVRGVVSMANNGPNTNGSQFPITYGKQPHLDMKYTVFGKVID GLETLDELEKLPVWEKTYRPLNDVHIKDITHANDFAQ GLETLDELEKLPVWEKTYRPLNDVHIKDITHANDFAQ TALQEFGTGGPPLSLRPABGTGRFKELPGARGPSWPPSDRVP MEPPNLYPVKLYVYDLSKGLARRLSPIMLGKQLEGIMHTSIVVH KDEFFFGSGISSCPPGGTLLGPPDSVVDVGSTEVTEEIFLEYL SSLGESLFRGEAYNLFEHRUTFSNEVAQFLTGRKIPSYITDLP SEVLSTPFGQALRPLLDSIQIQPPGGSSVGRPMGGS 6489 1457 375 KVARMATALSEEELDNEDYYSLLWNREASSEELKAAVRRLCML YHPDKHRDPBLKSQAERLFNLVHQAYEVLSDPQTRAIYDIYGKR GLEMEGWEVVERRRTPAEIREEFFRLQREREERRLQQRTNPKGT ISVGVDATDLFDRYDEEYSDVSGSSFPQIEINKHISQSIEAPL TATDTAILSGSLSTQNGNGGGSINFALRRVTSAKGWGELEFGAG DLQGPLFGLKLFRNLTPRCFVTTNCALOFSSRGIRPGLITVLAR NLDKNTVGYLQMHCSSPLLQVQRPHRNTRACAPEPSPRPFLHVP TWDAECSGARTPSTAWTSAAVKLREACLSGPGSGSHQLLLLTPR SKRRTGGG 6490 3 1183 HEAGCEWULGYGFRAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSPDFHGRRWATCSSDQSVKWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAWEELVGESDNLKG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVNNLSGWSLQHBISCKLSCSISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTKYKAKAETLMTVTDPVDIAPAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEHHIVAQFD NINNSQWRVSWNITGTVLASSGDDCCVRLWKANYMDNWKCTGIL KGNGSFVNGSQQGTGVPLASGSDDCCVRLWKANYMDNWKCTGIL KGNGSFVNGSQQGTTSVLASGSDCCVRLWKANYMDNWKCTGIL KGNGSFVNGSQQGTTSVLASGSDCCVRLWKANYMDNWKCTGIL KGNGSFVNGSQQGTTSVLASGSDCCVRLWKANYMDNWKCTGIL KGNGSFVNGSQQGTTSVLASGSDCCVRLWKANYMDNWKCTGIL KGNGSFVNGSQQGTTSVLASGSDCCVRLWKANYMDNWKCTGIL KGNGSFVNGSCQGTTSVLASGSDCCVRLWKANYMDNWKCTGIL KGNGSFVNGSVWRVWNNTGTSDGSVRWWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAWEEST VGESNOKLRG GSHWKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVNNLSQWSLQHBISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GSSWWRVTWAHPEFGQVLASCSFDRTAAWWEST VGESNOKLRG GSHWKRTTLUDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVNNLSQWSLQHBISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTIKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTIKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTIKYAKAETLMTVTDPVHDIAFAPNL GSSWWRVTHATHSTANAKTTARTATTRATATTARTORTITATATORTITATATATATATATATATATA	6487	253	260	
KHNYRGVVSMANNGPNTNGSQFFITYGKQPHLDMKYTVEGKVID GLETLDELEKLPVNEKTYPLNDVHIKDITIHANPFAQ GLETLDELEKLPVNEKTYPLNDVHIKDITIHANPFAQ TALQEFGTSGPPLSLRFALPSGTGRFKPLFGARGFSWPPSPRVP MEPPNLYPVKLYVYDLSKGLARRLSPIMLGKQLEGIWHTSIVVH KDBFFFGSGGISSCPPGGTLLGPPDSVVDVGSTEVTEEIFLEYL SSLGESLFRGBAYNLFBRINCNTFSNEVAQFLTGRKIPSYITDLP SSLUSTPFGQALRPLLDSIQIQPPGGSSVGRPMQQS 6489 1457 375 KVAMMATALSEELDNEDYYSLLTNVRREASSEELKAAVRRLCML YHPDKHRDPBLKSQABRIFNLVHQAZVEUSDPQTRAIVDIYGKR GLEMEGWEVVERRRTPAEIREEFERLQREREERRLQQRTNPKGT ISWGVDATDLFDRYDEEVEDVSGSSFPQLEINKMHISGSIEAPL TATDTAILSGSLSTQNGGGSINFALRRVTSAKGWGELEFGAG DLQGPLFGLKLFRNLTPRCFVTTNCALQFSSRGIRFGLITVLAR NLDKNTVGYLQWHCSSPLLQVQRPHRNTRACAPEPSRPFPFLHVP TWIBAECSGARTPSTAWTSAAVKLREACLSGPSGSSHQLLLLTPR SKRRTGGG 490 3 1183 HEAGGEWULGYGFRAAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSPDFHGRRMATCSSDQSVKVWDKSESGDHCTASWKT HSGSVWRVTVAAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVYDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLGHEISCKLSCSCISWBPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKABTLMTVTDPVHDIAPAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFFIHIVAQFD NINSQWRVSWNITGTVLASSGDDCCVRLWKANYMDNWKCTGIL KGNGSPVNGSQQGTSMPSLGSNIPSLQSNIPSLGSRKHS 6491 3 1183 HEAGCEVWLGYGFRAAAAAAATVLFGGAGPTETMFVARSITADH KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDTRTAAVWEEIVGESNDKLRG QSHWVKRTTLUDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVNNLSQWSQQGTENGFSQGTFTMFVARSITADH KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDHCTASWKT HSGSVWRVTWAHPEFFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLUDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVNNLSQWSQGTFTTMFVARSITADH KDLIHDVSFDFHGRRMATCSSDCSVKVWDKSESGDHCTASWKT HSGSVWRVTWAHPEFFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLUDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVNNLSQWSQGTFTTMFVTRYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTKKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTKKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTKKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTKKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTKKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTKKYAKAETLMTVTDPVHDIAFAPNL	0407	352	863	SFLKPLRGKMSVTLHTDVGDIKIEVFCERTPKTCENFLALCASN
GLETLDELEKLPVNEKTYRPLNDVHIKDITIHANDFAQ TALQEFGTSGPPLSLRFALPSGTGRFKFLFGARGPSWFPSDRVP MEPPNLYVKLYVYDLSKGLARRLSFIMLGKQLEGIWHTSIVVH KDEFFFGSGISSCPFGGTLLGPPDSVVDVGSTEVTEEIFLEYL SSLGSSLFRGEAYNLFEINCNTFSNEVAQFITGRKIPSYITDLP SEVLSTPFGOALPELLDSIQIPPGGSSVGRPMGQS 6489 1457 375 KVAKMATALSEELDNEDYYSLINVREASSEELKAAYRRLCML YHPDKHRDPBLKSQAERIFNLUHQAVEVLSDPQTRAIVDIYGKR GLEMEGWEVVERRRTPAEIREFERLQRERERRLQQRTNFKGT ISWGVDATDLFDRYDEEVEDVSGSSFPQIEINKMHISQSIEAPL TATDTAILSGSLSTQNGNGGGSINFALRRVTSAKGWGELEFGAG DLQGPLFGLKLFRNLTRECFYTTNCALQFSSRGIRPGLITTVLAR NLDKNTVGYLQWHCSSPLLOVQRPHRNTRACAPEPSFPPFLHVP TWDAŁCSGARTPSTAWTSAAVKLREACLSGPGSGSHOLLLITPR SKRRTGGG 6490 3 1183 HEAGCEVWLGYGPRAAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSPDFHGRRMATCSSDQSVKVWKSESGDWHCTASWKT HSGSVWRVTVAHPFFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGIMLATCSADGIVRIYE APDVNNLSOWSLOHEISCKLSCSCISWPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD NHNSQVWRVSWNITGTVLASSGDDCCVRLWKANYMDNWKCTGIL KONGSPVNGSSQQGTSMPSLGSNTPSLQNSLMGSSAGRKHS HEAGCEVWLGYGPRAAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSPDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGIMLATCSADGIVRIYE HEAGCEVWLGYGPRAAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSPDFHGRRMATCSSDGSVKVWDKSESGDHCTASWKT HSGSVWRVTWAHPEFFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGIMLATCSADGIVRIYE APDVNNLSQWSLGHEISCKLSCSCISWPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQPD DSSPNAMAKVQIFEYNENTRYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKKPAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKKPAKETHTVDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKKPAKETHTUDPVHDIAFAPNL				YYNGCIFHRNIKGFMVQTGDPTGTGRGGNSIWGKKFEDEYSEYL
TALQEFGTSGPPLSLRPALESGTGRFKPLFGARGPSWPPSPRVP MEPPNLYPVKLYVYDLSKGLARRLSS IHMGKQLEGIHHTSTVVH KDEFFFGSGGISSCPFGGTLLGPPDSVVDVGSTVTEEIFLEYL SSLGESLFRGEAYNLFBHNCNTFSNEVAQFLTGRKIPSYITDLP SEVLSTPFGGALRPLLDSIQIPPGSSVGRPMGQS KVAKMATALSEELDNEDYYSLLNVRREASSEELKAAYRRLCML YHPDKHRDPBLKSQAERLFNLVRQAYEVLSDPQTRATYDIYGKR GLEMEGWEVVERRRTPAEIREFERLQREREERRLQQRTMPKGT ISVGVDATDLFDRYDEEYPCVSGSSFPQIEINKHHISQSIEAPL TATDTALLSGSLSTONGNGGGSINFALRRVTSAKGWGELFFGAG DLGGPLFGLKLFRNLTPRCFVTINCALOFSSRGIRPGLTTVLAR NLDKNTVGYLQWHCSSPLLQVGPRHRNTRACAPEPSFRPFLHVP SKRRTGGG 6490 3 1183 HEAGCEVWLGYGPRAAAAAANTULFGGAGPTETMFVARSIAADH KOLIHDVSFDFHGRRMATCSSDGSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAWWEEIVGESNDKLRG QSHWVRRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMLAVGSD DSSPNAMAKVQIFFYNENTRKYAKAETIMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD NHNSQVWRVSWNITGTVLASSGDDGCVRLWKANYMDNWKCTGIL KONGSPVNGSSQOGTBSJGSNGSPGTTAAVWEEIVGSSAGRKHS KDLIHDVSFDFHGRRMATCSSDQSVKWWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGSSNDKLRG GSSPVNGSSQOGTBSJGSNGSTGSTAAVWEIVGSAGRKHS KOLIHDVSFDFHGRRMATCSSDQSVKWWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEIVGSDGNGKLGG GSSPVILGSCSCGSTGSTGSSGSTAASPSTAADH KDLIHDVSFDFHGRRMATCSSDQSVKWWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEIVGSDGNDKLRG QSHWKRTTLVDGRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVWNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFFYNENTAVKAKAETLMTVTDDVHDLAFAPNL GRSFWILAIATKDVRIFTILKPYKKELTSSGGPTKFEIHVVAOPD GRSFFIILAIATKDVRIFTILKPYKKELTSSGGPTKFEIHVVAOPD				KHNVRGVVSMANNGPNTNGSQFFITYGKQPHLDMKYTVFGKVID
MEPPILYPVKLYVJDISKGIARRISP IMLGKQLEGIHHTS IVVH KDEFFFGSGGISSCPPGGTLLGPPDSVVDVGSTEVTEEI FLEYL SSLGESLFRGEAYNLFEHNCHTFSNEVAQFLTGRKI BSYITDLP SEVLSTPGQALRPLDS IQLQPPGGSSVGRPMGQS KVAKMATALSEEELDNEDYYSLLNVRREASSEELKAAYRRLCML YHPDKHROPBLKSQASRLFNLVHQAYEVLSDPQTRAIYDI YGKR GLEMEGWEVVERRRTPAEI REEFERLQGRTHPKGT ISVGVDATDLFDRYDEEYEDVSGSSFPOIEINKMI SQSI EAPL TATDTAILSGSLSTQNGNGGGSINFALRRVTSAKGWGELEFGAG DLQGPLFGLKLFRNLTPRCFYTINCALQFSSRGI RPGLITTVLAR NLDKNTVGYLQWHCSSPLLQVGRPHRNTRACAPEPSFRPFLHVP TWDAECSGARTPSTAWTSAAVKLREACLSGPGSGSHQLLLLTPR SKRRTGGG 6490 3 1183 HEAGCEVWLGYGFRAAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFHGRRMATCSSDQSVKWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHNGLMLATCSADGIVRIYE APDVNNLSQNSLQHEISCKLSCSCISWNPSSSRAHSPMLAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVKRELTSSGGPTKFEIHIVAQPD NNNSQWRVSWNITGTVLASSGDDGCVRLWKANYMDNWRCTGIL KONGSPVNGSSQQOTSNPSLGSNIPSLQNSLMGSAGRKHS HEAGCEVWLGYGPRAAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFHGRRMATCSSDQSVKWWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHIGLMLATCSADGIVRIYE HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGSSNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHIGLMLATCSADGIVRIYE APDVVNLSQWSLQHEISCKLSCCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTILKPYKKELTSSGGPTKFEIHIVAQOPD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GSSWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGSSNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVVNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPYKKELTSSGGPTKFEIHIVAOPRD	6488	070	047	GLETLDELEKLPVNEKTYRPLNDVHIKDITIHANPFAQ
KDBFFFGSGISSCPPGGTLLGPPDSVVDVGSTEVTEEIFLEYL SSLGESLFRGAYNLFBHNCNTFSNEVAQFITGRKIPSYITDLP SSLUSTPFGQAINPLDSIQIQPPGGSSVGRPNGQS KVAKMATALSEELDNEDYYSLLNVRREASSELKAAYRRLCML YHPDKHRDPBLKSQABRIFNLVHQAYEVLSDPQTRAIYDIYGKR GLEMEGWEVVERRRTPAEIREFFERLQRERERRLQQRTMPKGT ISVGVDATDLFDRYDEEYEDVSGSSFPQIEINKMHISQSIEAPL TATDTAILSGSLSTQNGNGGGSINFALRRVTSAKGWGELFFGAG DLQGPLFGLKLFRNLTPRCFTTTNCALQFSSRGIRPGLTTVLAR NLDKNTVGYLQWHCSSPLLQVQRPHRNTRACAPEPSFRPFLHVP TWIDECSGARTPSTAWTSAAVKLREACLSGPGSGSHQLLLLTPR SKRRTGGG 6490 3 1183 HEAGCEWWLGYGPRAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFHGRRWATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMILSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTKYAKABETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQPD NHNSQVWRVSWNITGTVLASSGDDCCVRLWKANYMDNWKCTGIL KGNGSPVNGSSQQGTSNPSLGSNIPSLQNSLNGSSAGRKHS 6491 3 1183 HEAGCEVWLGYGPRAAAAAATVLFGGAGFTETMFVARSIAADH KDLIHDVSFDFHGRRWATCSSDDCVVRUWKANYMDNWKCTGIL KGNGSPVNGSSQQGTSNPSLGSNIPSLQNSLNGSSAGRKHS 6491 3 1183 HEAGCEVWLGYGPRAAAAAATVLFGGAGFTETMFVARSIAADH KDLIHDVSFDFHGRRWATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVWNLSQWSLQHEISCKLSCSCISWPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTKKYAKAETLMTVTDPVHDIAFAPNL GRSFIILAIATKDVRIFTIKPVRKYAKAETLMTVTDPVHDIAFAPNL GRSFIILAIATKDVRIFTIKPVRKELTSSGGPTKFEHHVAORD	0400	8/8	241	TALQEFGTSGPPLSLRFALPSGTGRFKPLPGARGPSWPPSPRVP
SSIGESLFRGEAVNLFBENCNTFSNEVAQFLTGRKIPSYITDLD SEVLSTPFGQALRPLLDSIQIQPPGGSSVGRPNGQS KVAKMATALSEELDNEDYYSLINVRREASSEELKAAYRRLCML YHPDKHRDPBLKSQAERLFNLVHQAYEVLSDPQTRAIYDIYGKR GLEMEGWEVVERRRTPAEIREFFERLQREREERRLQQRTNPKGT ISVGVDATDLFDRYDEEYEDVSGSSPPQIEINKMHISQSIEAPL TARDTAILSGSISTQNGNGGGSINFALRRVTSAKGWGELEFGAG DLQGPLFGLKLFRNLTPRCFVTTNCALQFSSRGIRPGLTTVLAR NLDKNTTGYLQWHCSSPLLQVQRPHRNTRACAPEPSFRPFLHVP TWDAECSGARTPSTAWTSAAVKLREACLSGPGSGSHQLLLLTPR SKRRTGGG 6490 3 1183 HEAGCEVWLGYGPRAAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFHGRRWATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMLAVGSD DSSPNAMAKVQIFEYNENTKKYAKABTLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD NINSQWWZSWNITGTVLASSGDDCCVRLWKANYMDNWKCTGIL KGNGSPVNGSSQQGTSNPSLGSNIPSLQNSLNGSSAGRKHS HEAGCEVWLGYGPRAAAAAATVLFGGAGFTETMFVARSIAADH KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVWNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTKKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKFYRKAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKFYRKAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKFYRKAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKFYRKAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKFYRKAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKFYRKAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKFYRKAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKFYRKAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKFYRKELTSSGGPTKFEHHVARGD				MEPPNLYPVKLYVYDLSKGLARRLSPIMLGKQLEGIWHTSIVVH
SEVISTPFGQALRPLLDSTQIQPFGGSSVGRPNGQS KVAKMATALSEEELDNEDYYSLINVRREASSEELKAAYRRLCML YHPDKHRDPBLKSQAERLFNLVHQAYEVLSDPQTRAIYDIYGKR GLEMEGWEVVERRRTPAEIREEFERLQRRREERRLQQRTNPKGT ISVGVDATDLFDRYDEEYEDVSGSSFPQIEINKMHISQSIEAPL TATDTAILSGSLSTQNGRGGSINFALRRVTSAKGWGELEFGAG DLQGPLFGLKLPRNLTPRCFVTTNCALQFSSRGIRPGLTVLAR NLDKNTVGYLQWHCSSPLLQVORPHRNTRACAPEPSFRPFLHVP TWDAECSGARTPSTAWTSAAVKLREACLSGPGSGSHQLLLLTPR SKRRTGGG 6490 3 1183 HEAGCEVWLGYGPRAAAAAATVLFGGAGPTETMFVARSIAADH KOLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLGHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD NHNSQVWRVSWNITGTVLASSGDDGCVRLWKANYMDNWKCTGIL KONGSPVNGSSQQGTSNPSLGSNIPSLQNSLNGSSAGRKHS 6491 3 1183 HEAGCEVWLGYGPRAAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDPHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWHPPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVWNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPYRKELTSSGGPTKFEIHIVAQFD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPYRKELTSSGGPTKFEIHIVAQFD	i			KDEFFFGSGGISSCPPGGTLLGPPDSVVDVGSTEVTEEIFLEYL
6499 1457 375 KVAKMATALSEEELDNEDYYSLLNVRREASSEELKAAYRRLCML YHPDKHRDPBLKSQABRIFNIJVHQAYEVLSDPQTRAIYDIYGKR GLEMEGWEVVERRRTPAEIREEFERLQREREERRLQQRTNPKGT ISWOVDATDLFDRYDEYEPDVSGSSFPQIEINKMHISQSIEAPL TATDTAILSGSLSTQNGNGGGSINFALRRVTSAKGWGELEFGAG DLQGPLFGLKLFRNLTPRCFVTTNCALQFSSRGIRPGLTTVLAR NLDKNTVGYLQWHCSSPLLQVGRPHRNTRACAPEPSFRPFLHVP TWDAECSGARTPSTAWTSAAVKLREACLSGPGSGSHQLLLLTPR SKRRTGGG 6490 3 1183 HEAGCEVWLGYGPRAAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFHGRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD NHNSQVWRVSWNITGTVLASSGDDCCVRLWKANYMDNWKCTGIL KGNGSPVNGSSQQGTSNPSLGSNIPSLGNSLNGSSAGRKHS HEAGCEVWLGYGPRAAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWLCIASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATRDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATTDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD				SSLGESLFRGEAYNLFEHNCNTFSNEVAQFLTGRKIPSYITDLP
YHPDKHRDPBLKSQABRLEFNLVHQAYEVLSDPQTRAIYDIYGKR GLEMEGWEVVERRTPAEIREEFERLQREREERRLQQRTNPKGT ISVGVDATDLFDRYDEEYEDVSGSSFPQIEINKMHISQSIEAPL TATDTAILSGSLSTQNGNGGGSINFALRRVTSAKGWGELEFGAG DLQGPLFGLKFRNLTPRCFVTTNCALQFSSRGIRPGLTTVLAR NLDKNTVGYLQWHCSSPLLQVQRPHRNTRACAPEPSFRPFLHVP TWDAECSGARTPSTAWTSAAVKLREACLSGPGSGSHQLLLLTPR SKRRTGGG 6490 3 1183 HEAGCEVWLGYGPRAAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKKTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSFMIAVGSD DSSPNAMAKVQIFFYNENTRKYAKABTLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRRELTSSGGPTKFETHIVAQFD NHNSQVWRVSWNITGTVLASSGDDCCVRLWKANYMDNWKCTGIL KGNGSPVNGSSQQGTSNPSLGSNIPSLQNSLNGSSAGRKHS HEAGCEVWLGYGFPRAAAAAATVLFGGAGFTETMFVARSIAADH KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVWNLSQWSLQHEISCKLSCSCISWNPSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATRDVRIFILKPVRKAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATRDVRIFTIKKPVRKELTSSGGPTKFEIHIVAOFD	6489	1457		SEVLSTPFGQALRPLLDSIQIQPPGGSSVGRPNGQS
GLEMEGWEVVERRTPAEIREEFERLQREREERRLQQRTNPKGT ISVGVDATDLFDRYDEEYEDVSGSSFPQIEINKMHISGSIEAPL TATDTAILSGSLSTQNGNGGGSINFALRRVTSAKGWGELEFGAG DLQGPLFGLKLFRNLTPRCFVTTNCALQFSSRGIRPGLTTVLAR NLDKNTVGYLQWHCSSPLLQVQRPHRNTRACAPEPSFRPFLHVP TWDAECSGARTPSTAWTSAAVKLREACLSGPGSGSHQLLLLTPR SKRRTGGG 1183 HEAGCEVWLGYGPRAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEBIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAKSPMIAVGSD DSSPNAMAKVQIFFYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKFVRKELTSSGGPTKFEIHIVAQFD NHNSQVWRVSWNITGTVLASSGDDGCVRLWKANYMDWKCTGIL KGNGSPVNGSSQQGTENPSLGSNIPSLQNSLNGSSAGRKHS KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFFYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKFVRKELTSSGGPTKFEIHIVAQFD DSSPNAMAKVQIFFYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKFVRKELTSSGGPTKFEIHIVAQFD	0405	145/	375	KVAKMATALSEEELDNEDYYSLLNVRREASSEELKAAYRRLCML
ISYGVDATDLFDRYDEEYEDVSGSSFPQIEINKMHISQSIEAPL TATDTAILSGSLSTQNGNGGGSINFALRRYTSAKGWGELEFGAG DLQGPLFGLKLFRNLTPRCFVTTNCALQFSSRGIRPGLTTVLAR NLDKNTVGYLQWHCSSPLLQVQRPHRNTRACAPEPSFRPFLHVP TWDAECSGARTPSTAWTSAAVKLREACLSGPGSSGHQLLLLTPR SKRRTGGG 1183 HERGCEWWLGYGPRAAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPPEFGQVLASCSFDRTAAVWEBIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVTIFTLKFVRKELTSSGGPTKFEIHIVAQFD NHNSQVWRVSWNITTTVLASSGDDGCVZHWKANTMDWKCTGIL KGMGSPVWGSQQGTENPSLGSNIPSLQNSLNGSSAGRKHS KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSRRHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKFVRKELTSSGGPTKFEIHIVAOFD GRSFHILAIATKDVRIFTLKFVRKELTSSGGPTKFEIHIVAOFD	1 1]		YHPDKHRDPELKSQAERLFNLVHQAYEVLSDPQTRAIYDIYGKR
TATDTAILSGSLSTQNGNGGGSINFALRRVTSAKGWGELEFGAG DLQGPLFGLKLFRNITPRCFYTTNCALQFSSRGIRPGLTTVLAR NLDKNTVGYLQWHCSSPLLQVQRPHRNTRACAPEPSFRPFLHVP TWDAECSGARTPSTAWTSAAVKLREACLSGPGSGSHQLLLLTPR SKRRTGGG 1183 HEAGCEVWLGYGPRAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFHGRRWATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEBIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWMPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD NHNSQVWRVSWNITGTVLASSGDDGCVRLWKANYMDWKCTGIL KGNGSPVNGSQQGTSNPSLGSNIPSLQNSLNGSSAGRKHS KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAOFD		·		GLEMEGWEVVERRRTPAEIREEFERLQREREERRLQQRTNPKGT
DLQGPLFGLKLFRNITFRCFVTTNCALQFSSRGIRPGLTTVLAR NLDKNTVGYLQMHCSSPLLQVQRPHRNTRACAPEPSFRPFLHVP TWDAECSGARTPSTAWTSAAVKLREACLSGPGSGSHQLLLLTPR SKRRTGGG 1183 HEAGCEVWLGYGPRAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFHGRRWATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD NHNSQVWRVSWNITGTVLASSGDDGCVRLWKANYMDNWKCTGIL KGNGSPVNGSSQQGTSNPSLGSNIPSLQNSLNGSSAGRKHS HEAGCEVWLGYGPRAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSRRHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAOFD	1 1	1		LSVGVDATDLFDRYDEEYEDVSGSSFPQIEINKMHISQSIEAPL
NLDKNTVGYLQWHCSSPLLQVQRPHRNTRACAPEPSFRPFLHVP TWDAECSGARTPSTAWTSAAVKLREACLSGPGSGSHQLLLLTPR SKRRTGGG 6490 3 1183 HEAGCEVWLGYGPRAAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEBIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD NHNSQVWRVSWNITGTVLASSGDDGCVRLWKANYMDNWKCTGIL KGNGSPVNGSSQQGTENPSLGSNIPSLQNSLNGSSAGRKHS 6491 3 1183 HEAGCEVWLGYGPRAAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLUDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAOFD	} I			TATUTALLEGELSTQNGNGGGSINFALRRVTSAKGWGELEFGAG
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SKRRTGGG HEAGCEVMLGYGPRAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSPDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT HEGSVWRVTWAHPEFGQVLASCSFDRTAAVWEBIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAPAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD NHNSQVWRVSWNITGTVLASSGDDGCVRLWKANYMDNWKCTGIL KGNGSPVNGSSQQGTENPSLGSNIPSLQNSLNGSSAGRKHS KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSRRHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAOFD	[[j		MILDANTVGYLQWHCSSPLLQVQRPHRNTRACAPEPSFRPFLHVP
6490 3 1183 HEAGCEVWLGYGPRAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWMPSSSRAKSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD NHNSQVWRVSWNITGTVLASSGDDGCVRLWKANYMDNWKCTGIL KGNGSPVNGSSQQGTSNPSLGSNIPSLQNSLNGSSAGRKHS HEAGCEVWLGYGPRAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVRRTTLUDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAOFD] [INDALCEGARTYSTAWTSAAVKLREACLSGPGSGSHQLLLLTPR
KDLIHDVSFDFHGRRMATGSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPERGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATGSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTREYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD NHNSQVWRVSWNITGTVLASSGDDGCVRLWKANYMDNWKCTGIL KGNGSPVNGSSQQGTENPSLGSNIPSLQNSLNGSSAGRKHS 6491 3 1183 HEAGCEVWLGYGPRAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAOFD	6490		17.03	
HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWMPSSSRAKSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD NHNSQVWRVSWNITGTVLASSGDDGCVRLWKANYMDNWKCTGIL KGNGSPVNGSSQQGTSNPSLGSNIPSLQNSLNGSSAGRKHS 6491 3 1183 HEAGCEVWLGYGPRAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAOFD		-	1103	newGCbvWLGYGPRAAAAAATVLFGGAGPTETMFVARSIAADH
QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD NHNSQVWRVSWNITGTVLASSGDDGCVRLWKANYMDNWKCTGIL KGNGSPVNGSSQQGTSNPSLGSNIPSLQNSLNGSSAGRKHS 6491 3 1183 HEAGCEVWLGYGPRAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLUDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAOFD				ADDITADVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT
APDVMNLSQWSLQHBISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETIMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD NHNSQVWRVSWNITGTVLASSGDDGCVRLWKANYMDNWKCTGIL KGNGSPVNGSSQQGTENPSLGSNIPSLQNSLNGSSAGRKHS 1183 HEAGCEVWLGYGPRAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAOFD]]			nsgsvwkvTwaHPEFGQVLASCSFDRTAAVWEBIVGESNDKLRG
DSSPNAMAKVQIFEYNENTRKYAKAETIMTVTDPVHDIAPAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD NHNSQVWRVSWNITGTVLASSGDDGCVRLWKANYMDNWKCTGIL KGNGSPVNGSSQQGTENPSLGSNIPSLQNSLNGSSAGRKHS HEAGCEVWLGYGPRAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSGRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAOFD	[]	}		VSHWVARTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE
GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD NHNSQVWRVSWNITGTULASSGDDGCVRLWKANYMDNWKCTGIL KGNGSPVNGSSQQGTSNPSLGSNIPSLQNSLNGSSAGRKHS 6491 3 1183 HEAGCEVWLGYGPRAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAOFD]			APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD
NHNSQVWRVSWNITGTVLASSGDDGCVRLWKANYMDNWKCTGIL KGNGSPVNGSSQQOTSNPSLGSNIPSLQNSLNGSSAGRKHS HEAGCEVWLGYGPRAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAOFD				DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL
KGNGSPVNGSSQQGTSNPSLGSNIPSLQNSLNGSSAGRKHS 6491 3 1183 HEAGCEVWLGYGPRAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDGRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAOFD	[[1	i	GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD
HEAGCEVWLGYGPRAAAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFHGRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDGRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAOFD				NHNSQVWRVSWNITGTVLASSGDDGCVRLWKANYMDNWKCTGIL
KDLIHDVSFDFHGRAMAAAATVLFGGAGPTETMFVARSIAADH KDLIHDVSFDFHGRAMATCSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMMLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAOFD	6491			KGNGSPVNGSSQQGT6NPSLGSNIPSLQNSLNGSSAGRKHS
KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAOFD	"""	3	1183	HEAGCEVWLGYGPRAAAAAATVLFGGAGPTETMFVARSIAADH
HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPYKFEIHIVAOFD	l Í		İ	KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT
QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAOFD]		HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG
APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAOFD		1	ļ	QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIVE
DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAOFD		1	ļ	APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD
GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAOFD				DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNI.
NHNSQVWRVSWNITGTVLASSGDDGCVRLWKANYMDNWKCTGIL	ļ		i	GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAOFD
				NHNSQVWRVSWNITGTVLASSGDDGCVRLWKANYMDNWKCIGIL

SEQ Predicted Predicted end Amino acid second	
1 2 deliced cha Amilio acid segi	ment containing signal peptide
""	Ysteine, D=Aspartic Acid, E=
Joede Ton Gidealite Acid,	F=Phenylalanine, G=Glycine,
derresponding in-hiscidine, is	Isoleucine, K=Lysine,
	thionine, N=Asparagine,
	utamine, R=Arginine,
I sectifie, Island	reonine, V-Valine,
	<pre>%=Tyrosine, X=Unknown, *=Stop</pre>
- - - - - - - - - -	ole nucleotide deletion,
sequence \=possible nucl	eotide insertion)
KGNGSPVNGSSQQGT	SNPSLGSNIPSLQNSLNGSSAGRKHS
6492 34 2573 IPFLKSCCCCCLFDF	PPPPLDQVQEEECEVERVTEHGTPKPFRK
FDSVAFGESQSEDEQ	PENDLETDPPNWOOLVSREVILIGIKPCET
KRQEVINELFYTERA	HVRTLKVLDQVFYQRVSREGILSPSELRK
IFSNLEDILQLHIGI	NEOMKAVRKRNETSVIDQIGEDLLTWFSG
PGEEKLKHAAATFCS	NOPFALEMIKSROKKDSRFQTFVQDAESN
PLCRRLQLKDIIPTQ	MORLTKYPLLLDNIATYTEWPTEREKVKK
AADHCRQILNYVNQA	VKEAENKQRLEDYQRRLDTSSLKLSEYPN
VEELRNLDLTKRKMI	HEGPLVWKVNRDKTIDLYTLLEDILVLL
QKQDDRLVLRCHSKI	LASTADSKHTFSPVIKLSTVLVROVATDN
KALFVISMSDNGAQI	YELVAQTVSEKTVWODLICRMAASVKEOS
TKPIPLPQSTPGEGD	NDEEDPSKLKEEOHGISVTGLOSPDRDIG
LESTLISSKPOSHSL	STSGKSEVRDLFVAERQFAKEQHTDGTLK
EVGEDYQIAIPDSHL	PVSEERWALDALRNLGLLKQLLVQQLGLT
EKSVQEDWQHFPRYR	TASQGPQTDSVIONSENIKAYHSGEGHMP
FRTGTGDIATCYSPR	TSTESFAPRDSVGLAPODSOASNILVMDH
MIMTPEMPTMEPEGG	LDDSGEHFFDAREAHSDENPSEGDGAVNK
EEKDVNLRISGNYLI	LDGYDPVQESSTDEEVASSLTLOPMTGIP
AVESTHOQQHSPONT	HSDGAISPFTPEFLVOORWGAMEYSCFET
QSPSSCADSQSQIME	YIHKIEADLEHLKKVEESYTILCORLAGS
ALTDKHSDKS	
6493 557 1147 TPARMAYQGSSTSDC	MSKTLDSASAHFAASAVVSAPVPSRSEVA
KEQNTGHNNINGVVQ	PSGTSKTLYSTNMALSSSPGISAVOLVRT
VGHTTNHLIPALCT	SSPOTLPMNNSCLTNAVHLNNVSVVSPVN
VHINTRTSAPSPTAL	KLATVAASMDRVPKVTPSSAISSIARENH
EPERLGLNGIAETTV	AMEVT
6494 2425 1052 AVAGGARPCSTPSSP	HRRCRRHRPRPLPRPPAAIMSASAVYVLD
LKGKVLICRNYRGDVI	DMSEVEHFMPILMEKEEEGMLSPILAHGG
VRFMWIKHNNLYLVA:	TSKKNACVSLVFSFLYKVVQVFSEYFKEL
EEESIRDNFVIIYELI	LDELMDFGYPOTTDSKILORYITOEGHKI.
ETGAPRPPATVTNAVS	SWRSEGIKYRKNEVFLDVIBSVNLLVSAN
GNVLRSEIVGSIKMR	/FLSGMPELRLGLNDKVLFDNTGRGKSKS
VELEDVKFHQCVRLSF	RFENDRTISFIPPDGEFELMSYRLNTHVK
PLIWIESVIEKHSHS	RIEYMIKAKSQFKRRSTANNVEIHIPVPN
DADSPKFKTTVGSVKV	vpenseivwsiksfpggkeylmrahfgl
PSVEAEDKEGKPPISV	KFEIPYFTTSGIQVRYLKIIEKSGYQAL
PWVRYITQNGDYQLRT	
1032 AVAGGARPCSTPSSPF	RRCRRHRPRPLPRPPAAIMSASAVYVLD
LKGKVLICRNYRGDVI	MSEVEHFMPILMEKEEEGMLSPILAHGG
VRFMWIKHNNLYLVAT	SKKNACVSLVFSFLYKVVQVFSEYFKEL
EEESIRDNFVIIYELI	DELMDFGYPQTTDSKILQEYITQEGHKL
ETGAPRPPATVTNAVS	WRSEGIKYRKNEVPLDVIESVNLLVSAN
GNVLRSEIVGSIKMRV	FLSGMPELRLGLNDKVLFDNTGRGKSKS
VELEDVKFHQCVRLSR	FENDRTISFIPPDGEFELMSYRLNTHVK
PLIWIESVIEKHSHSR	IEYMIKAKSQFKRRSTANNVEIHIPVPN
DADSPKFKTTVGSVKW	VPENSEIVWSIKSFPGGKEYLMRAHFGL
PSVEAEDKEGKPPISV	KFEIPYFTTSGIQVRYLKIIEKSGYQAL
6496 247 559 LPAVSLIDIOLUL PRV	
DYAGDDE TO THE TOTAL TOT	SIHSLFCIMFLCAQEWLTLGLNVPLLFY
HFWRYFHCPADSSELA	YDPPVVMNADTLSYCQKEAWCKLAFYLL
SFFYYLYCMIYTLVSS	
ANIQUERICPRENTINE	PCGAKMGNGTEEDYNFVFKVVLIGESGV
GKTNLLSRFTRNEFSH	DSRTTIGVEFSTRTVMLGTAAVKAQIWD
TAGLERYRAITSAYYR	GAVGALLVFDLTKHQTYAVVERWLKELY
	ATTENDED TO THE ATTENDED TO
DHAEATIVVMLVGNKS	DLSQAREVPTEEARMFAENNGLLFLETS EIFAKVSKQRQNSIRTNAITLGSAQAGQ

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F-Phenylalanine, G-Glycine,
1.0.	location	corresponding	U-Victidine T-Yesleveine, V. Zarafas
	corresponding	to first	HaHistidine, Ialsoleucine, Kabysine,
	to first		L=Leucine, M=Methionine, N=Asparagine,
		amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			EPGPGEKRACCISL
6498	2636	272	SLRLCPWGTHLAGPTTMRLSSLLALLRPALPLILGLSLGCSLSL
		•	LRVSWIGGEGEDPCVEAVGERGGPQNPDSRARLDQSDEDFKPRI
1			VPYYRDPNKPYKKVLRTRYIQTELGSRERLLVAVLTSRATLSTL
	1		AVAVNRTVAHHFPRLLYFTGQRGARAPAGMQVVSHGDERPAWLM
ł			SETLRHLHTHFGADYDWFFIMQDDTYVQAPRLAALAGHLSINQD
1	1		LYLGRAEEFIGAGEQARYCHGGFGYLLSRSLLLRLRPHLDGCRG
1			DILSARPDEWLGRCLIDSLGVGCVSQHQGQQYRSFELAKNRDPE
1	{		
1	1		KEGSSAFLSAFAVHPVSEGTLMYRLHKRFSALELERAYSEIEQL
1			QAQIRNLTVLTPEGEAGLSWPVGLPAPFTFHSRFEVLGWDYFTE
1			QHTFSCADGAPKCPLQGASRADVGDALETALEQLNRRYQPRLRF
1	[QKQRLLNGYRRFDPARGMEYTLDLLLECVTQRGHRRALARRVSL
			LRPLSRVEILPMPYVTEATRVQLVLPLLVAEAAAAPAFLEAFAA
	·		NVLEPREHALLTLLLVYGPREGGRGAPDPFLGVKAAAAELERRY
			PGTRLAWLAVRAEAPSQVRLMDVVSKKHPVDTLFFLTTVWTRPG
1	1		PEVLNRCRMNAISGWQAFFPVHFQEFNPALSPQRSPPGPPGAGP
I	l i	•	DPPSPPGADPSRGAPIGGRFDRQASAEGCFYNADYLAARARLAG
!	Į ;		ELAGQEEEEALEGLEVMDVFLRFSGLHLFRAVEPGLVQKFSLRD
1	i l		CSPRLSEELYHRCRLSNLEGLGGRAQLAMALFEQEQANST
6499	3	2040	SCSADTRPSGQAWPTVGLRAAAGAFRTGSPLALGPETPQVACLP
		•	GHPPVRPQVSGGPGAMPDPAAHLPFFYGSISRAEAEEHLKLAGM
		•	ADGLFLLRQCLRSLGGYVLSLVHDVRFHHFFIERQLNGTYAIAG
			GKAHCGPAELCEFYSRDPDGLPCNLRKPCNRPSGLEPOPGVFDC
			LRDAMVRDYVRQTWKLEGEALEQAIISQAPQVEKLIATTAHERM
	,		PWYHSSLTREEAERKLYSGAQTDGKFLLRPRKEQGTYALSLIYG
			KTVYHYLISQDKAGKYCIPEGTKFDTLWQLVEYLKLKADGLIYC
Į.]		LKEACPNSSASNASGAAAPTLPAHPSTLTHPQRRIDTLNSDGYT
			PEPARITSPDKPRPMPMDTSVYESPYSDPEELKDKKLFLKRDNL
ļ	1		LIADIELGCGNFGSVRQGVYRMRKKQIDVAIKVLKQGTEKADTE
			EMMREAQIMHQLDNPYIVRLIGVCQAEALMLVMEMAGGGPLHKF
ļ.			LVGKREEIPVSNVAELLHQVSMGMKYLEEKNFVHRDLAARNVLL
1			VNRHYAKISDFGLSKALGADDSYYTARSAGKWALKWYAPECINF
<u>t</u>	}		RKFSSRSDVWSYGVTMWEALSYGQKPYKKMKGPEVMAFIEQGKR
	}		MECPPECPPELYALMSDCWIYKWEDRPDFLTVEQRMRACYYSLA
<u> </u>			SKVEGPPGSTQKAEAACA
6500	1773	726	TGPTHASADAWGLVRSVTEWCANVRGNPCAAALSCPQAVLDAGK
	 		MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHBHHHL
			QAPNKEDILKISEDERMELSKSFRVYCIILVKPKDVSLWAAVKE
		•	TWTKHCDKAEFFSSENVKVFESINMDTNDMWLMMRKAYKYAFDK
			YRDQYNWFFLARPTTFALIENLKYFLLKKDPSQPFYLGHTIKSG
		•	DLEYVGMEGGIVLSVESMKRLNSLLNIPEKCPEQGGMIWKISED
	1		KQLAVCLKYAGVFAENAEDADGKDVFNTKSVGLSIKEAMTYHPN
Į l	1		QVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGPYFQ
6501	1	570	LVGMSGGGTETPVGCEAAPGGGSKKRDSLGTAGSAHLIIKDLGE
1 1	1		IHSRLLDHRPVIQGETRYFVKEFEEKRGLREMRVLENLKNMIHE
			TNEHTLPKCRDTMRDSLSQVLQRLQAANDSVCRLQQREOERKKI
	1		HSDHLVASEKQHMLQWDNFMKEQPNKRAEVDEEHRKAMERLKEO
			YAEMEKDLAKPSTF
6502	213	1650	
		1020	AGNKPDPWAGRNRTAVLPDVSVFHREDVGWNRSWLQQSYQAVKE
			KSSEALEFMKRDLTEFTQVVQHDTACTIAATASVVKEKLATEGS
	i		SGATEKMKKGLSDFLGVISDTFAPSPDKTIDCDVITLMGTPSGT
			AEPYDGTKARLYSLQSDPATYCNEPDGPPELFDAWLSQFCLEEK
	Ì	•	KGEISELLVGSPSIRALYTKMVPAAVSHSEFWHRYFYKVHQLEQ
			EQARRDALKQRAEQSISEEPGWEEEEERLMGISPISPKRAKVPV
	ł		AKISTFPEGEPGPQSPCEENLVTSVEPPAEVTPSESSESISLVT
Ll			QIANPATAPEARVLPKDLSQKLLEASLEEQGLAVDVGETGPSPP

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
ľ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
į	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	5542555	\=possible nucleotide insertion)
	 	<u> </u>	IHSKPLTPAGHTGGPEPRPPARVETLREEAPTDLRVFELNSDSG
1		Í	KSTPSNNGKKGSSTDISEDWEKDFDLDMTEEEVQMALSKVDASG
,	}		EVSGPGGSEGSEPNGPGCESSPQPAQLSPQEGPCSCLR
6503	213	1650	AGNKPDPWAGRNRTAVLPDVSVFHREDVGWWRSWLQQSYQAVKE
1			KSSEALEFMKRDLTEPTQVVQHDTACTIAATASVVKEKLATEGS
Į.			SGATEKMKKGLSDFLGVISDTFAPSPDKTIDCDVITLMGTPSGT
ļ			AEPYDGTKARLYSLQSDPATYCNEPDGPPELFDAWLSQFCLEEK
1			KGEISELLVGSPSIRALYTKMVPAAVSHSEFWHRYFYKVHQLEQ
ſ			EQARRDALKQRAEQSISEEPGWEEEEELLMGISPISPKEAKVPV
1			AKISTFFEGEPGPQSPCRENLVTSVEPPAEVTPSESSESISLVT
			QIANPATAPEARVLPKDLSQKLLEASLEEQGLAVDVGETGPSPP
l l			IHSKPLTPAGHTGGPEPRPPARVETLREEAPTDLRVFELNSDSG
			KSTPSNNGKKGSSTDISEDWEKDFDLDMTBEEVQMALSKVDASG
			EVSGPGGSEGSEPNGPGCESSPQPAQLSPQEGPCSCLR
6504	2131	1294	GKVCLVAHWVCLSILSPPPAGMKTPNAQEAEGQQTRAAAGRATG
i i			SANMTKKKVSQKKQRGRPSSQPCRNIVGCRISHGWKEGDEPITQ
			WKGTVLDQVPINPSLYLVKYDGIDCVYGLELHRDERVLSLKILS
			DRVASSHISDANLANTIIGKAVEHMFEGEHGSKDEWRGMVLAQA
1 1			PIMKAWFYITYEKDPVLYMYQLLDDYKEGDLRIMPESSESPPTE
1 1			REPGGVVDGLIGKHVEYTKEDGSKRIGMVIHQVEAKPSVYFIKF
			DDDFHIYVYDLVKKS
6505	2131	1294	GKVCLVAHWVCLSILSPPPAGMKTPNAQEAEGQQTRAAAGRATG
]			SANMTKKKVSQKKQRGRPSSQPCRNIVGCRISHGWKEGDEPITQ
1 1			WKGTVLDQVPINPSLYLVKYDGIDCVYGLELHRDERVLSLKILS
1			DRVASSHISDANLANTIIGKAVEHMFEGEHGSKDEWRGMVLAOA
1 1			PIMKAWFYITYEKDPVLYMYQLLDDYKEGDLRIMPESSESPPTE
1 1			REPGGVVDGLIGKHVEYTKEDGSKRIGMVIHQVEAKPSVYFIKF
			DDDFHIYVYDLVKKS
6506	1	1350	EVSPPTSCCLTVAVADPGVSEGFRGFGAGCEMPGRGRCPDCGST
] .]	1		ELVEDSHYSQSQLVCSDCGCVVTEGVLTTTFSDEGNLREVTYSR
1	1		STGENEQVSRSQQRGLRRVRDLCRVLQLPPTFEDTAVAYYOOAY
i I			RHSGIRAARLOKKEVLVGCCVLITCROHNWPLTMGAICTLLYAD
1 [LDVPSSTYMQIVKLLGLDVPSLCLAELVKTYCSSFKLFOASPSV
1 1	1		PAKYVEDKEKMLSRTMQLVELANETWLVTGRHPLPVITAATFLA
1 1	-		WQSLQPADRLSCSLARFCKLANVDLPYPASSRLQELLAVLLRMA
}			EQLAWLRVLRLDKRSVVKHIGDLLQHRQSLVRSAFRDGTABVET
1 1			REKEPPGWGQGGGGEVGNNSLGLPQGKRPASPALLLPPCMLKS
1 1			PKRICPYPPVSTVTGDENISDSEIEQYLRTPQEVRDFQRAQAAR
6507	1878	020	QAATSVPNPP
550,	10/0	929	RSHASRLPELPSGCLVLQVQELVQMSGMEATVTIPIWQNKPHGA
]]	1		ARSVVRRIGTNLPLKPCARASFETLPNISD_CLRDVPPVPTLAD
			IAWIAADEEETYARVRSDTRPLRHTWKPSPLIVMQRNASVPNLR
			GSEERLLALKKPALPALSRTTELQDELSHLRSQIAKIVAADAAS
}]		ASLTPDFLSPGSSNVSSPLPCFGSSFHSTTSFVISDITEETEVE
ļ .]	VPELPSVPLLCSASPECCKPEHKAACSSSEEDDCVSLSKASSFA
ŀ ŀ	[İ	DMMGILKDFHRMKQSQDLNRSLLKEEDPAVLISEVLRRKFALKE
6508	862	342	EDISRKGN
		344	WEARKRPQRWPSERREVRVPPPHLQRGRSGLEPGTFRKMAAARP
	ł	•	SLGRVLPGSSVLFLCDMQEKFRHNIAYFPQIVSVAARMLKNTTL
	ļ	ļ	DLLDRGLQVHVVVDACSSRSQVDRLVALARMRQSGAFLSTSEGL
6509	2	1053	ILQLVGDAVHPQFKEIQKLIKEPAPDSGLLGLFQGQNSLLH
	-	T023	FVWNPRGGRKRRQAAVTQAATRASGTPSPRDGTMTQGKLSVAN
	Ì		KAPGTEGQQQVHGEKKEAPAVPSAPPSYBEATSGEGMKAGAFPP
1			APTAVPLHPSWAYVDPSSSSSYDNGFPTGDHELFTTPSWDDQKV
			RRVFVRKVYTILLIQLLVTLAVVALFTFCDPVKDYVQANPGWYW
			ASYAVFFATYLTLACCSGPRRHPPWNLILLTVFTLSMAYLTGML

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A-Alanine, C-Cysteine, D-Aspartic Acid, E-
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
- {	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
- 1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W-Trantonine, V=valine,
1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	begannee	Codon, /=possible nucleotide deletion,
		 	\=possible nucleotide insertion)
ļ			SSYYNTTSVLLCLGITALVCLSVTVFSFQTKFDFTSCQGVLFVL
			LMTLFFSGLILAILLPFQYVPWLHAVYAALGAGVFTLFLALDTQ
6510	37	1156	LLMGNRRHSLSPEEYIFGALNIYLDIIYIFTFFLQLFGTNRE
		1	PCALDGCPQRGAVHPLLSSAMGLLAFLKTQFVLHLLVGFVFVVS
	1		GLVINFVQLCTLALWPVSKQLYRRLNCRLAYSLWSQLVMLLEWW
J		j	SCTECTLFTDQATVERFGKBHAVIILNHNFEIDFLCGWTMCERF GVLGSSKVLAKKBLLYVPLIGWTWYFLEIVFCKRKWEEDRDTVV
1	1]	EGLRRLSDYPEYMWFLLYCEGTRFTETKHRVSMEVAAAKGLPVL
1			KYHLLPRTKGFTTAVKCLRGTVAAVYDVTLNFRGNKNPSLLGIL
	J		YGKKYEADMCVRRFPLEDIPLDEKEAAQWLHKLYQEKDALQEIY
1	İ		NQKGMPPGEQFKPARRPWTLLNFLSWATILLSPLFSFVLGVFAS
L	ł		GSPLLILTFLGFVGAGNGHCR
6511	2541	1425	GEEQPLAAAPTECLEQVIGGAGDPGTWASFPSPLPGPAPLKGGK
			TMATNFSDIVKQGYVKMKSRKLGIYRRCWLVFRKSSSKGPQRLE
1			KYPDEKSVCLRGCPKVTEISNVKCVTRLPKETKRQAVAIIFTDD
	İ .		SARTFTCDSELEAEEWYKTLSVECLGSRINDISLGEPDLLAPGV
1			QCEQTDRFNVFLLPCPNLDVYGECKLQITHENIYLWDIHNPRVK
1	1		LVSWPLCSLRRYGRDATRFTFEAGRMCDAGEGLYTFQTQEGEQI
			YQRVHSATLAIAEQHKRVLLEMEKNVRLLNKGTEHYSYDCTDTT
l.		•	MLPRSAYWHHITGSQNIAEASSYAGEGYGAAQASSETDLLNRFI
6512			LLKPKPSQGDSSEAKTPSQ
6512	159	807	FGKKSTWFPLSRSLRVASGRSCKLGHGGYTGSGPGFGBPRDSGA
1	1		EVPSGSGRATGCERGGVRGARQGRAPGSSIWRKEPRMVCTRKTK
1			TLVSTCVILSGMTNIICLLYVGWVTNYIASVYVRGOEPAPDKKT.
l			EEDKGDTLKIIERLDHLENVIKQHIQEAPAKPEEAEAEPFTDSS
6513	2		LFAHWGQELSPEGRRVALKQFQYYGYNAYLSDRLPLDRP
1 0323	'	756	FVSPEPGFSLAQLNLIWQLTDTKQLVHSFAEGQDQGSAYANRTA
			LFPDLLAQGNASLRLQRVRVADEGSFTCFVSIRDFGSAAVSLQV
l			AAPYSKPSMTLEPNKDLRPGDTVTITCSSYQGYPEAEVFWQDGQ
1			GVPLTGNVTTSQMANEQGLFDVHSILRVVLGANGTYSCLVRNPV
1	1		LOQDAHSSVTITPQRSPTGAVEVQVPEDPVVALVGTDATLRCSF
t			SPEPGFSLAQLNLIWQLTDTKQLVHSFAEGQDQGSAYANRTALF
			PDLLAQGNASLRLQRVRVADEGSFTCFVSIRDFGSAAVSLQVAA PYSKPSMTLEPNKDLRPGDTVTITCSSYQGYPEAEVFWQDGQGV
1			PLTGNVTTSQMANEQGLFDVHS1LRVVLGANGTYSCLVRNPVLQ
1	}		QDAHSSVTITPQRSPTGAVEVQVPEDPVVALVGTDATLRCSFSP
			EPGFSLAQLNLIWQLTDTRQLVHSFTEGR
6514	985	302	VGIPGPTISSAAEMEDLLDLDEELRYSLATSRAKMGRRAQQESA
	j f	1	QAENHLNGKNSSLTLTGETSSAKLPRCRQGGWAGDSVKASKFRR
1 '		1	KASEBIEDFRLRPQSLNGSDYGGDIPIIPDLEEVQEEDFVLQVA
].		APPSIQIKRVMTYRDLDNDLMKYSAIOTLDGEIDLKIJTKVI.Ap
-]		EHEVRERNPSWQDDVGWDWDHLFTEVSSEVLTEWDPLQTEKEDP
- CE - E			AGQARHT
6515	1345	305	GRVGSRRRGAAVPGGCGAGSTQLEVSASASCGALGSADMNPIVV
l i	}		VHGGGAGPISKDRKERVHQGMVRAATVGYGILREGGSAVDAVEG
	[1	AVVALEDDPEFNAGCGSVLNTNGEVEMDASIMDGKDLSAGAVSA
		į	VQCIANPIKLARLVMEKTPHCFLTDQGAAOFAAAMGVPEIPGEK
]	- 1	LVTERNKKRLEKEKHEKGAQKTDCQKNLGTVGAVALDCKGNVAY
j			ATSTGGIVNKMVGRVGDSPCLGAGGYADNDIGAVSTTGHGESII.
1		į	KVNLARLTLFHIEQGKTVEEAADLSLGYMKSRVKGLGGLIVVSK
6516			TGDWVAKWTSTSMPWAAAKDGKLHFGIDPDDTTITDLP
1 0270	1	1402	FRRLRYLGQDATAAARDLRTRGLQGYCPSATAROOVLVSALOOL
]		i	KGRRSEHRNENQEMPYSTNKELILGIMVGTAGISLLLLWYHKVR
			KPGIAMKLPEFLSLGNTFNSITLQDEIHDDOGTTVIFOEROLOI
		1	LEKLNELLTNMEELKEEIRFLKEAIPKLEEYIODELGGKITVHK
<u> </u>			ISPQHRARKRRLPTIQSSATSNSSEEAESEGGYITANTDTEEQS

SEQ	Predicted	Predicted end	1 hms and
ID	beginning	nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
]	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
[residue of	amino acid	Watronton Variation V. V.
J	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
1	sequence	•	\=possible nucleotide insertion)
		<u> </u>	FPVPKAFNTRVEELNLDVLLQKVDHLRMSESGKSESFELLRDHK
1		1	EXPRDEIEFMWRFARAYGDMYELSTNTQEKKHYANIGKTLSERA
l l			INRAPMNGHCHLWYAVLCGYVSEFEGLQNKINYGHLFKEHLDIA
			IKLLPEEPFLYYLKGRYCYTVSKLSWIEKKMAATLFGKIFSSTV
ł		Í	QEALHNFLKAEELCPGYSNPNYMYLAKCYTDLEENQNALKFCNL
	L		ALLLPTVTKEDKEAQKEMQKIMTSLKR
6517	3	1414	GRVWGGSSSLNAMVYVRGHAEDYERWOROGARGWDYAHCLDVFP
1	ł		KAQGHELGASRYRGADGPLRVSRGKTNHPLHCAFLEATOOAGVD
			LIEDMNGFQQEGFGWMDMTIHEGKRWSAACAYLHPALSRTNI.KA
]			EAETLVSRVLFEGTRAVGVEYVKNGOSHRAYASKEVILSGGAIN
		İ	SPQLLMLSGIGNADDLKKLGIPVVCHLPGVGONLODHLETVIOO
1	}	1	ACTRPITLHSAQKPLRKVCIGLEWLWKFTGEGATAHI.ETGGPTD
	1		SQPGVPHPDIQFHFLPSQVIDHGRVPTOOEAYOVHVGPMRGTSV
İ		İ	GWLKLRSANPQDHPVIQPNYLSTETDIEDFRICVKITPRIFACE
ł			ALAPFRGKELQPGSHIQSDKEIDAFVRAKADSAYHPSCTCKMGQ
}			PSDPTAVVDPQTRVLGVENLRVVDASIMPSMVSGNLNAPTIMIA
6518	242	1098	EKAADIIKGQPALWDKDVPVYKPRTLATQR
J		****	PAWNPGSEPRTRVRPRARSFPLPPPRAPRRRHRLLRAVPGPSR
1			RHRCRRAPPPPSTMGDAGSERSKAPSLPPRCPCGFWGSSKTMN
			LCSKCPADFQKKQPDDDSAPSTSNSQSDLFSEETTSDNNNTSIT TPTLSPSQQPLPTELNVTSPSKEECGPCTDTAHVSLITPTKRSC
1	Į.		GTDSQSENEASPVKRPRLLENTERSEBTSRSKQKSRRRCFQCQT
1 :			KLELVQQELGSCRCGYVFCMLHRLPEQHDCTFDHMGRGREEAIM
			KMVKLDRKVGRSCQRIGEGCS
6519	3	1113	ERKMAEPPSPVHCVAAAAPTATVSEKEPFGKLQLSSRDPPGSLS
f i			AKKVRTEEKKAPRRVNGEGGSGGNSROLOPPAAPSPOGVGGDAG
			WSFAPLSAAPSPSSSRSSFSFSAGTAVPSSASASISODGPPVII.
			VPPTLLHAQPHHLLLPAAAAASANAKSRRPKEKREKERRRUGI.
1 1			GGAREAGGASREENGEVKPLPRDKIKDKIKERDKEKEPRKKKUK
1			VMNEIKKENGEVKILLKSGKEKPKTNIEDLOIKKVKKKKKKKKKH
1	}		ENEKRKRPKMYSKSIQTICSGLLTDVEDOAAKGILNDNIKDVVC
l j			KNLDTKNYDSKIPENSEFPFVSLKEPRVQNNLKRLDTLEFKQLI
6520	3	1113	HIEHQPNGGASVIHCLQ
	1	**13	ERKMAEPPSPVHCVAAAAPTATVSEKEPFGKLQLSSRDPPGSLS
l i			AKKVRTEEKKAPRRVNGEGGSGGNSRQLQPPAAFSPQSYGSPAS
i I			WSFAPLSAAPSPSSSRSSFSFSAGTAVPSSASASLSOPGPRKLL
l 1			VPPTLLHAQPHHLLLPAAAAASANAKSRRPKEKREKERRRHGL GGAREAGGASREENGEVKPLPRDKIKDKIKERDKEKEREKKKHK
i			VMNEIKKENGEVKILLKSGKEKPKTNIEDLQIKKVKKKKKKKKK
1	1		ENEKRKRPKMYSKSIQTICSGLLTDVBDQAAKGILNDNIKDYVG
	ł		KNLDTKNYDSKIPENSEFPFVSLKEPRVQNNLKRLDTLEFKQLI
			HIEHQPNGGASVIHCLQ
6521	. 184	1798	KLFKMATDTSQGELVHPKALPLIVGAQLIHADKLGEKVEDSTMP
		ſ	IRRTVNSTRETPPKSKLAEGEEEKPBPDISSEESVSTVEEQENE
İ	1		TPPATSSEAEQPKGEPENEEKEENKSSEETKKDEKDOSKEKEVE
j	i	,	VKKTIPSWATLSASQLARAQKQTPMASSPRPKMDAILTEATKAC
		ŀ	FQXSGASVVAIRKYIIHKYPSLELERRGYLLKOALKREINPGUT
ļ	ĺ		KQVKGKGASGSFVVVQKSRKTPOKSRNRKNRSSAVDPEPOVKLE
1	!	1	DVLPLAFTRLCEPKEASYSLIRKYVSOYYPKLRVDIRPOLLKNA
	1	Ţ	LQRAVERGQLEQITGKGASGTFOLKKSGEKPLLGGSLMEYATLG
	1	1	ALAAMNEPKTCSTTALKKYVLENHPGTNSNYOMHLLKKTLOKCR
	į		KNGWMEQISGKGFSGTFQLCFPYYPSPGVLFPKKEPDDSRDEDR
1			DEDESSEEDSEDEEPPPKRRLQKKTPAKSPGKAASVKORGSKPA
j			PKVSAAQRGKARPLPKKAPPKAKTPAKKTRPSSTVIKKPSGGSS
6522	1042		KKPATSARKE
			NKWLRPSPRSHRTPESGRVLSLFRLPPPGMALSGSTPAPCWEED

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Deginning No: Unclected Location Corresponding to first amino acid amino acid residue of amino acid amino acid sequence Peroline, October Pe	SEO	Predicted	Predicted end	Amino agid cognost
Incation Corresponding to first Samino acid residue of residue of residue of amino acid residue of amino acid residue of amino acid residue of amino acid sequence Serine, T-Threonine, V-Valine, Serine, T-Threonine, V-Valine, Serine, T-Threonine, V-Valine, Very Codon, /-possible nucleotide deletion, V-Valine, REMANDER V-Valine, V-Val	ID	l .	1	Amino acid segment containing signal peptide
Totach corresponding to first amino acid aible nucleotide deletion, Vaposaible nucleotide	NO:	nucleotide	location	Glutamic Acid. F=Phenylalanine G-Glycina
LeLeucine, Membethionine, NeAsparagine, baino acid residue of amino acid residue of amino acid sequence sequenc	1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine
amino acid residue of amino acid sequences sequences seq	1		to first	L=Leucine, M=Methionine, N=Asparagine.
saino acid residue of amino acid sequence Seguence	1			P=Proline, Q=Glutamine, R=Arginine
### Tryptophan, Y=Dyrosine, X=Unknown, *=Stop doon, /=posaible nuclectide deletion,	1			S=Serine, T=Threonine, V=Valine.
sequence sequence Codon, /=possible nuclectide insertion	ł			W=Tryptophan, Y=Tyrosine, X=Unknown, *=Ston
### Sequence ### Characteristic A-possible nucleotide insertion ### BCLDYGNISLINEMPEVWGGQUTESULLADDERPGRAGG \$## SARSGLAKLLELBERGQCDESNLRLLGQLLAVLAREDLLDHAR RKRRPVSPBRYSTSSSKKTEGGCRERGSCRAGGSSSANGGGSP PTKRGRRSGRSGGARRRRGDPHPSSSGSPPDLDLAXK RKRRPVSPBRYSTGTSSKKTEGGCRERGSSSANGGGSP PTKRGRRSGGARRRRGDPHPSSSGSPPDLDLAXK ### SARGGLARCHARCHARCHARCHARCHARCHARCHARCHARCHARCH		1	sequence	Codon, /=possible nucleotide deletion
SRARSGLKLLLELERRGCCESNIKLIGGLEVLAKHLELHHLA RKRRRPUSPERYSYGTSSSKEKTEGSCRRRGSSSSANSOGGS PTKRGRRGRGRFGGGARRRRGGDPHPSSSGSPDDLLAKAK RSKLGJFRRCMLVFKKASSKGPRLLKFPDBKAAVFRNPHKVT ELNIKNITELPETKKHAVA I FPIDETSKFAVDLKGGVKK RSKLGJFRRCMLVFKKASSKGPRLLKFPDBKAAVFRNPHKVT ELNIKNITELPETKKHAVA I FPIDETSKFAVA KRORD LDIJGECTMOITENITUMDIHNAKVKLUMMPLSISRKGDBT WFTFESGIMCDTGEGJFTGTTREGEMIYGKVHASTLAIAEGHER HALGMEGKARLGTSELTPMTLSKSISLPRSAYMHHTTRGNSVGE TYSLGGNHERRHSDLTGKSCKTSERRFLEBANVYGGTHHLF MDTSTCKVVIDLE 6524 2 1097 ASCYTRRFTAALBSGERIAGRRSPIALAMASNFNDIVKGGVVKI RSKKLGIFRRCMLVFKKASSKGPRRLEKFPDEKAAYFRHKVT ELHINKNITELPETSKHAVATIFPDTTSKFAVAFGTHKVT ELHINKNITELPETSKHAVATIFPDTTSKFACESELBABEWC KHLCMECLGTRINDISLGSEDDLAAGGGVEGNBEFRVVLMFTDN LDIJGECTMGITHENIYLMDIHNAKVKLVMMPLSKRRYGDBT WFTFESGRMCDTGGGLFTGTTEGEMIYGKVHSATLAIAEGHER KHLCMECLGTRINDISLGSEDDLAAGGGVEGNBEFRVVLMFTDN LDIJGECTMGITHENIYLMDIHNAKVKLVMMPLSKRRYGDBT WFTFESGRMCDTGGGLFTGTTEGEMIYGKVHSATLAIAEGHER KHLCMECLGTRINDISLGSEDDLAAGGGVEGNBEFRVVLMFTDN LDIJGECTMGITHENIYLMDIHNAKVELVMPLTRQSSEGUSP WFTFSGRMCDTGGGLFTGTTEGEMIYGKVHSATLAIAEGHER LMLEMEQKAALDTSLFTGTTEGEMIYGKVHSATLAIAEGHER LMLEMEQKAALDTSLFTTGTTEGEMIYGKVHSATLAIAEGHER LMLEMEQKAALDTSLFTTGTTEGEMIYGKVHSATLAIAEGHER LMLEMEQKAALDTSLFTTGTTEGEMIYGKVHSATLAIAEGHER LMLEMEQKAALDTSLFTTGTTEGEMIYGKVHSATLAIAEGHER LMLEMEQKAALDTSLFTTGTTEGEMIYGKVHSATLAIAEGHER LMLEMEQKAALDTSLFTTGTTEGEMIYGKVHSATLAIAEGHER LMLEMEQKAALDTSLFTTGTTEGEMIYGKVHSATLAIAEGHER LMLEMEQKAALDTSLFTTGTTEGEMIYGKVHSATLAIAEGHER LMLEMEQKAALDTSLFTTGTTEGEMIYGKVHSATLAIAEGHER LMLEMEQKAALDTSLTTGTTTGTTTTGTTTTGTTTTTGTTTTTGTTTTTTGTTTT	ļ	sequence		\=possible nucleotide insertion)
6523 2 1097 ASCOTTRETANDISGERIAGRESPIALAMASSYPDITYGGVYKI RSRKGJIPRKGHAVEKASKERSPIALAMASSYPDITYGGVYKI RSRKGJIPRKGHAVEKASKERSPIALAMASSYPDITYGGVYKI RSRKGJIPRKGHAVEKASKERSPIALAMASSYPDITYGGVYKI RSRKGJIPRKGHAVEKASKERSPIALAMASSYPDITYGGVYKI RSRKGJIPRKGHAVEKASKERPRIKEVPDEKAYPRHEVYT LLINIKHITELPRETKKHAVAIIPRDETSKTFACESELEAREWC KHLCMELGGTRICHDITAGUTHENIYLMDINNAKVELVMWELSURRYGRDET WFITESGRMCDTORGLIFTGTREGEMIYGKVHASATLAIACHER MILEWEGKARLGTSITEPRTLEKSISIPRANDLAVNYGITHHLF MOSTICKVVUBLE 6524 2 1097 ASCOTTRETALDSGERIAGRESPIALAMASNYFDITYGGVYKI RSRKGJIPRKGHVYKKASKKOPRRLEKPRDEKAYFRNYHKVT LLINIKHITELPRETKHAVAIIPRDETSKTPACESELEAREWC KHLCHELGTRINISIGGEDLAAGVGEROMEFRVYLMFTEN LDIYGECTMQITHENIYLMDINNAKVELVMWELSSLRRYGRDET WFTESGRMCDTORGLIFTGTREGEMIYGKVHATALAGNER KHLCHELGTRINISIGGEDLAAGVGEROMEFRVYLMFTEN LDIYGECTMQITHENIYLMDINNAKVELVMWELSSLRRYGRDST WFTESGRMCDTORGCLFTTGTREGEMIYGKVHATALAGDER LMLENEGKARLGTSLTEPHTLCKS ISLPRSAYWHHITAGNSVGE IYSLGAMHERINSDLTKKS CKTSENFLEENAPLWYGITHLEF LMLENEGKARLGTSLTEPHTLCKS ISLPRSAYWHHITAGNSVGE IYSLGAMHERINSDLTKS CKTSENFLEENAPLWYGITHLEF ROMSTCKVVUBLE GESPFSEERSIEFNFSSGRSRATVSSNSFCSDUTWFSSGUSVS PVKTFSDAGNSFIGFCPGSDEGPTRKKCTIGMVGEGSIQSSRY KESKSGUVKFGSEADFSSSSTGS ISAFEVIMITAGSKRSSSSR NRGPHGRSMGASSKHKPGSSPSSPEREKOLLSHLOLEPWSSGUSVS PVKTFSDAGNSFIGFCPGSDEGPTRKKCTIGMVGEGSIQSSRY KESKSGUVKFGSEADFSSSSTGS ISAFEVIMITAGSKRSSSSR NRGPHGRSMGASSKHKPGSSPSSPEREKOLLSHLOLEPWINSSGLADD KGIGNYFVUNINGNKLESLLGGVUGKGFRGVIWGERGSVV ERANGTOVVPYSPAISELIGSVUGKLGBERGHVWRGERGSVV ERANGTOVVPYSPAISELIGSVUGKLGDCPSSLADDESPPS MSSPFSELSALVVOLFREPRRSALLSPUTTEVLKKSGLAR MEDDIEEECHVPROJALKEARREIKGLKGVVETMSSLADD KGIGNYFVUNINGNKLESLLGGVTGARDELLUMPCGEGSVV ERANGTOVVPYSPAISELIGSVUGKCTWFYKGKON NEYVPYSBFSGGARCHTVKKGUSHGERGVVNAPHSUNINGHUMP LEPELVTATTTESGOBLUNINGSTGANVENTUNAPULARIR PHVATHPOTATOLIGERGVVYVNAPSSELVBLLAVAR PVVPYPULARAFTGORGTDPVYNIGALLGCCVVALHSLRRTAFR IXT 6526 2034 SGRAGEPEEWRGGCLIFFFSUNGCORGTPTVKGCUNGERGSVV ERANGTOVVPYSPAISELIGSVUGKCORFRTYKKGVBINGHUMP LIMPELGRARHLELERGULTRINBPLANVALLEPWVFYSIGHTHIN KHUPPYTHERDLKKLQLGEFFFFT PANDRESTVLLVV GULMGGRIDTVUGE	ł		1	ECLDYYGMLSLHRMFEVVGGQLTECELELLAFLLDEAPGAAGGL
6523 2 1097 ASCOTRENTALDSCENTAGERSPILAMANSPILVAGGVVKI RSKKJIFRRCHLVPKKASSKOPRILEKPPDEKAAYERSPIKVG ELINIKNITELRETKKHAVA I IPPDETSKIFFACESELEAEWEM KHLCMECLGTRINDISLGEPDILAAGVORGONERFRVYLMFIEN LDIYGECTMOITHENIYLMDIHNAKVILVMWELSSURKYGGDT WFIFESGRMCDTGECHTFOTREGEMIYQKVHAVGITHLIP MISHEGKARLOTSSITEPMILSKSISLPRSAYWHHITRQNSVCE IYSLGGNHERRHSDLTKSGKSKESERRLEEMSVHYGITHLIP MOTSTCKVVHDLE 6524 2 1097 ASCOTRENTALDSGERIAGRESPIALAMASNFNDIVKGGVVKI RSKKLGIFRRCHLVPKKASSKOPRRLEKFPDEKAAYFRHKUT ELINIKNITELPERTKHAVAI IFPDETSKIFACESELPAEWEM KHLCMECLGTRINDISLGEPDILAAGGVBCOMERFRVYLMPTEN LDIYGECTMOITHENIYLMDIHNAKVKLVMWPLSSLRRYGGDT WFFFSGRMCDTGEGFFTVYLMFTEN WFFFSGRMCDTGEGFFTVYLWWPLSSLRRYGGDST WFFFSGRMCDTGEGFFTVYLWWIPLSLRRYGGDST WFFFSGRMCDTGEGFFTVYLWWIPLSSLRRYGGDST WFFFSGRMCDTGEGFFTVYLWWIPLSLRRYGGDST WFFFSGRMCDTGEGFFTVYLSKSISLPRSAYWHHITRQNSVCE IYSLGGNHERRHSDLTGSKSKSRRFLEEMSHVVIJVITHLIP MOTSTCKVVHDLE 6525 1 1859 GESPFSEESSISFFSSKGRARTVSSNSFCSDDTGWFSSGSVS PVXTPSDAGNSPIGFCPGSDEGFFTKKCTIGMVGGSTGSSVK KESKAGLVKPGSEADFSSSSTSGISAPSVIMSTGASKRSSSSR NROPHIGRSNASSSIKFGSSSPSSNPEKKLLSHLCKNOLGFVAVHIP SVAPSSPSSNSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS				SRARSGLKLLLELERRGQCDESNLRLLGQLLRVLARHDLLPHLA
ASCQTRRETAALDSGERTAGRESPIALAMASSYRDIVKGGVVKI RSRKGJIFRCKUVYKKASKGPRILKKYPDEKYKRPRIKKYP ELHNIKNITELPRETKKHAVAIIFRDETSKTFACGSELREEM KHLCMELGGFRINDISLGEBELDLAAGVQREGORPHYVLMPIPN LDIYGECTMOITHENIYLMDINNAKVKLVMWPLSSLRRYGRDST WFFTESGRMCTOTGGELFTPOTTEGEMIYQKVHSATLAIAEQHER LMLEMSGKARLOTSLTEPMILSKS ISLPRSAYMVHJETPINL MIDSTCKVVIDLD 6524 2 1097 ASCQTRRETAALDSGERIAGRESPIALAMASNENDIVKGGVVKI RSRKGJIFRCHUVFKKASSKGPRRLEKPAPLWYGITHHLF MDTSTCKVVIDLE RSRKGJIFRCHUVFKKASSKGPRRLEKPAPLWYGITHHLF LEHNIKNITELPRETKHAVAIIFHDETSKFFACESELBAEBKC KHLCHELGFRINDISLGEBULAAGVGREGHSVVLMPTIN LDIYGECTMOITHENIYLMDIHNAKVKLVMWPLSSLRRYGRDST WFFTSGRMCDTGGGLFTFOTTEGEMIYQKVKHAVTAIADGHER LMLEMEGKARLOTSLTEPMILSKS ISLPRSAYWHHITRONSVGE IYSLGANHERRISDLTGKSKGKPSRFLEKPPDEWVLMPTIN LDIYGECTMOITHENIYLMDIHNAKVKLVMWPLSSLRRYGRDST WFFTSGRMCDTGGGLFTFOTTEGEMIYGKVHATAIADGHER LMLEMEGKARLOTSLTEPMILSKS ISLPRSAYWHHITRONSVGE IYSLGANHERRISDLTGKSKGKTSERFFLBENAPLVMYGITHHLP MOTSTCKVVUDLE GESPFSERESIENDSSGRARTVSSNSFCSDDTGWFSSGSUS PVKTPBJAGNSPIGPCFGSDEGPTRKKCTIGMVEGESIQSSRVK KESNGJUKFGSBADFSSSSTRSISAFVINSTAGSKRSSSSR NRGPHGRSNGASSHKPGSSPSSPERENLISHLCHMCAMALDFWIHP SVAPSSSSSNSGSYKSSDCSPIRRSGRYNSGSENHOVRPPNP EQYLITPLQQGEVTVHHLKTKLKSEBERLHHERSULLAMOLEDJPCOS PREMSITLINPPLDTMADGLSLEEQVTGEGADRELLVAUDGIANSTD LEPEIVTATTTSGDJELVHSTGAANLLSDUFTSVELKSGLAR MEDDIEBECHVPROJALAKGARREIKQLKGVTETMRSSLADD KOIQKYEVUNINGKKLESLLGGVTGGADRELLVAUDGIANSTD LEPEIVTATTTSGDJELVHSTGAANLLLSDVETFYUNGEGEGSVV ERAVOTDVVPYSPAISELIGSVUQKLQDCPSSLASDDEESPDS MSSPFSELSALVVULFTRYNBPSALLLSDVETFYNDAPHVANTEFR LYT GGRAGFPERWRGGTIDSKETWITFNAVENGEGSVRCTWFYKGGKD NKYVPYSBSFSQVLESTTWILAVILDEWKKLESPNBEILIHNP LLYMPTGGGROVVVULFTRYNSPITAGNULLSPUNTEFYNDETHLAVILLEW KNAWNOPVAGROSTDWSTTMSGCRFTVYKROWENSFITAPI KMWNOPVAGRANDWSTTMSGCRFTVYKROWENSFITAPI KMWNOPVAGRANDWSTTMSGORPRTVKROUNTLIPSNIKHH KNAWNYOPVAGRADDWSTTMSGORPRTVKROUNTLIPSNIKHH KNAWNYOPVAGRADDWSTTMSGORPRTVKROUNTLIPSNIKHH KNAWNYOPVAGRADDWSTTMSGORPRTVKROUNTLIPSNIKHH KNAWNYOPVAGRADDWSTTMSGORPRTVKROUNTLIPSNIKHH KNAWNYOPVAGRADDWSTTMSGORPRTVKROUNTLIPSNIKHH KNAWNYOPVAGRADDWSTTMSGORPRTVKROUNTLIPSN	Į.	1	ļ	RKRRPVSPERYSYGTSSSSKRTEGSCRRRRQSSSSANSQQGSP
RSRKGJI PRKOMLVPKRASSKOPRILKEVPDEKAAYERNPHKVT ELINI KRINTKLEPRETKKIAVA I I PIDETSKYPACSSELABEMO KHLCMECLGYRINDI SIGGED LAAGGVQEROBEPAVYLMETPM LD1YGGCTMQI THENI LYMDI HINAKVKLIVMPLESSLRKYGRDST WFIFESGRMCOTORGELIFFOTTERGEMI YQKVKATA I ALECHER LMLEMEGKARLOTISLTEPMTLEKSI SILPRSAYWHHITRQNSVGE I YSLQONNEWRINSDLTGKSKI SERRFELENAPLVMYGI THHLIP MDTSTCKKVVIDLE 6524 2 1097 ASCCYRRETA ALLOSGER I AGRESP I ALLAMASNIPOTVKQGYVKI RSKLIGI FRRCMLVFKKASSKOPRRLEKFP DEKAAYTRNPHKVT ELMILKNI TILPRETKIGHVAI I FHDETSKYFACESELEABEMC KHLCHECLGYRLINDI SIGGED DILAAGGVGEORFROVILMETDN LDI YGGCTMQITHENI I LIMDI HINAKVKLIVMPELSSLRRYGRDST WFIFESGRMCOTGRECHTYCKYRESEMPLEKEP DEKAAYTRNPHKVT LDI YGGCTMQITHENI I LIMDI HINAKVKLIVMPUSLSLRRYGRDST WFIFESGRMCOTGRECHTYCKYRESINFILEBRAPLWYGI THHLIP HDTSTCKKVVIDLE LMEMEGKARLOTISLTEPMTLSKS I SILPRSAYWHHI TRQNSVGE I YSLOGNHEBRISDLITAKSK KYRSINFILEBRAPLWYGI THHLIP MOTSTCKVVIDLE FYRTPSGRMCOTGRECHTYCKYRSINFILEBRAPLWYGI THHLIP MOTSTCKVVIDLE FYRTSGRANDI SILPRSSGRSARTVSSINFTCSDDTGWFSSGSUS PVXTFSDAGNSI I IPPDSSGRSARTVSSINFTCSDDTGWFSSGSUS NROPHIGRINGASSHKPOSS PSERCOLLSHLCRNOLSFWIK KERSGILVKRGSEADFRSSSSTROSI SAPEVHIMATAGSSSSR NROPHIGRINGASSHKPOSS PSERCOLLSHLCRNOLSFWIK KERSGILVKRGSEADFRSSSSTROSI SAPEVHIMATAGSSSSR NROPHIGRINGASSHKPOSS PSERCOLLSHLCRNOLSFWIK KERSGILVKRGSCAPTSHORT HINTOKACKER WEED HER SILTEN PHILTS BERCHIT SILTEN FROM KINGVEVININ INKKLESLLGGGENGELLIVODS I ANSTOL LPDEL VTATITTES GOLLEVERS PROBLITURE SILDED MSSPFESLSALLVOLLTPRINDSALLISPVETPIVLKSGLAR MEDDI I LEDEL VTATITES GOLLEVER FRANTUNDE HANGEGSVVV ERAVOTDVVYSPAISSLLGGVVQKGSSFLVDLLAWA PUVPYVLMAPSTORGOTDPVVNIGALLISPVETPIVLAGECOV ERAVOTDVVYSPAISSLLGGVVQKGSSFLVDLLAWA PUVPYVLMAPSTORGOTDPVVNIGALLISPVETPIVLSQRCTV ERAVOTDVVYSPAISSLLGGVVQKGSSFLVDLLAWA PUVPYVLMAPSTORGOTDPVVNIGALLISPVETPIVLSQRCTV KREDDPAACVERLIGOVY PLARGGVVRYNSSVLSILLIVND GOLDHLYVFYOTGOTDPAVNIGSLIGHDIST KRESKLNIVMOGG NCTYPTIGGSTDACHTRANT STROPPOK GOVSTAGHSLISS LILED ILTONGOSLIGHDIST SKESKINIVMOGG TTTLEBOLKKLOGSEF FOI FEKKKVDKSALALCTORDOR TILLIND LLINDYFYNDSTICKER FROM TERSTVAPLOF FOR THE TILLIND LLI	6523		1007	PTKRQRRSRGRPSGGARRRRRGPQPHPSSSQSPPDLPLKAK
ELINI KNITRLIPETKKHAVAI I PHDETSKTPACESEIJABEWK KHLCMECLOFILMAJOVAGENDER PRVYLMPTDN LDIYGECTMQITHEN YLMDIHMAKVKLVMPPLSJERKYGEDST WFFFESGEMCOTTEGLEN FYOTREGENT VJOKASTLA I AEOHER LAMEMEGICARLOTSLITEPMILSKI SISLPRSAYMHHITAQNSVCE I YSLQUNHENRHSDLTGKSCKTSENRFLEENAPLWYYGITHHLF MDTSICKVUHDLE 6524 2 1097 ASCQTRRRTAALDSGERIAGRSPI ILAMASNFNDI VKQGVKI RESKKLGI FRKCMUV FKKASSKGPRILEK PDEKAAYFENPHKVT ELMIKNATRLIPESTKHIAVAI I PHDETSKTPACESELEAEEWC KHLCMELGYFILMDI SIGLEPPLLAAGAVGRERMVYLMPTDN LDIYGECTMQITHEN YLMDIHMAKVKLUMMPLSSLRYGRDST WFFFESGRMCDTOGELPFTLAGTRER PROVERNYLMPTDN LDIYGECTMQITHEN YLMDIHMAKVKLUMMPLSSLRYGRDST WFFFESGRMCDTOGELFTFQTTREGENIYQKVHSATHAIAZQHER LMLEMEKKARLOTSLITEMTLSKS I SLIPESAPEWNYTHHITAQNSVEB I YSLQGNIERRHSDLTGKSCKTSENRFLEENAPLWNYGITHHLP MOTSTCKVVIDLE 6525 1 1859 GESPFSEESI IENNPSSGRSARTVSNSYCSDDTKMPSSGSVS VKSKSGGLVKHGERADFSSSSTGSRARTVSNSYCSDDTKMPSSGSVS VKSSKSGLVKHGERADFSSSSTGSSTARFUHMSTAGSKRSSSR NROPHGRNAGASSHKPQSSPSPRKOLLSMLCHGJSVNIH SKAPSSPSSSNSGSVKGSDCSPTHKKTGTGMVGRGSIQSSRYK KESKSGLVKHGERADFSSSSSTGSSTARFUHMSTAGSKRSSSRS NROPHGRNAGASSHKPQSSPSPRKOLLSMLCHGJSVNIH SKAPSSPSSSNSGSVKGSDCSPIHMRSGRMGVKGSNHOWRPNP EQYLTPLQQKEVTVHLKTTLKESSRIHBRESSIVELKSQLAR MEEDHIGECHRVRAQLALKEARRSKIKGKVYETMSSSLANDK KGIGKYFVDINTQINKLESLLGSMMAHSGSIRDELCLIPPCOG PEKSILTINPPLDTMADGLISERGYTSGRANVLELLIPUNGGCGSVVV ERAVQTDVTJVSPASTSSLLGSMMAHSGSIRDELCLIPPCOG PEKSILTINPPLDTMADGLISERGYVGSGRANVLELLIPUNGGCGSVVV ERAVQTDVTJVSPASTSSLLGSMVGVKGVYGSSFLDUGGCSVVV ERAVQTDVTJVAGALBERVFTVAJVDAEVHANR LMRELDPAACVERLDGVI PLANGGVVVRGVSSFLDULLAVAA PVVPTVLMAFSTQRGGTDVVTJGALLGFVCVVALHSLRRTAFR IKT	0323	_	1097	ASCUTRRATAALDSGERIAGRRSPIALAMASNFNDIVKQGYVKI
KHICMECLGTRIADISLICEPPILLAGVQREONERFNYTIMETEN LDITGETUDITTENTYLUM HINAKVKUMPLSSLRRYGDET WFTESGRNCDTOGGLFTFOTREGENITOKVHAATLAIAEQHER LMMEMBCARLOTSITEPMTISKSISLPRSAYWHITTKONSVGE IYSLQGNHENRHSDLTGKSCKTSENRFLEENAELWYNGITHHLF MOTSTCKVVHDLE 6524 2 1097 ASCQTRRATALDSGERIAGRRSPIALAMASNFNDIVKQGYVKI RSKKLGIFRKCHLVYKKASSKGPRILEKFPDEKAYYRHYTHHLF KSKKLGIFRKCHLVYKKASSKGPRILEKFPDEKAYYRHYTHHT LDIYGGCTMQITHENIYLMDIHMARVKLVWHDLSSLEAGEWC KHLCWECLGTRIADISLEEPDLLAAGVQREQNERFNYTLWPTIN LDIYGGCTMQITHENIYLMDIHMARVKLVWHDLSSLEAGEWC KHLCWECLGTRIADISLEEPDLLAAGVQREQNERFNYTLWPTIN LDIYGGCTMQITHENIYLMDIHMARVKLVWHDLSSLEAGEWC KHLCWECKGRALOTSITEMTISKSISLPRGAYWHHITRQNSVGE IVSLQGNHERMREDLTGKSCKTSENRFLERNAPLWYGITHHLP MOTSTCKVVIDLE GESPFSEESSISENSCKSTENRFLERNAPLWYGITHHLP MOTSTCKVVIDLE GESPFSEESSISENSCKSTENRFLERNAPLWYGITHHLP MOTSTCKVVIDLE GESPFSEESSISENSCSYKSDCSPIMRSGRYMSCGENRIVAN KESKSGLVKPGSEADFSSSSTGSSTSAPEVHMSTASSKSSSSS NRGPHGRSNGASSHKPGSSSSTSSPRKOLLSHLCRRONLSPVNIH SVAPSSPSSNSGSYKGSDCSPIMRSGRYMSCGENKVXPNIH SVAPSSPSSNSGSYKGSDCSPIMRSGRYMSCGENKVXPNIH SVAPSSPSSNSGSYKGSDCSPIMRSGRYMSCGENGUSPVNIH SVAPSSPSSNSGSYKGSDCSPIMRSGRYMSCGENGUSPVNIH SVAPSSPSSNSGSYKGSDCSPIMRSGRYMSCGENGUSPPNIH SVAPSSPSSNSGSYKGSDCSPIMRSGRYMSCGENGUSPPNIH SVAPSSPSSNSGSYKGSDCSPIMRSGRYMSCGENGUSPPNIH SVAPSSPSSNSGSYKGSDCSPIMRSGRYMSCGENGUSPPNIH SVAPSSPSSNSGSYKGSDCSPIMRSGRYMSCGENGUSPPNIH SVAPSSPSSNSGSYKGSDCSPIMRSGRAPHSEBETUELKSQLAR MEEDHIEEECHRVERQLALKERSRESH KOLKQVIPTMSSLADMC KGIOKYPVINIONICKUELSLOSMMANSCBELCLIPPCDS PEKSLTLINPLDTIMMAGLSLCMSMANSCBECHVXPPDDE EQVIPTLOGESTVUTVANAERSTROCHSSINDLEDFUNG MESPFELSALVVDLTPRNNSAILLSPVETYPANVLEHLIPPCBG BERSTLINPLOPTUPTAGSTCATAGT MEEDDFAACVERELDGVIPTLAAGGVVQPCDPSSLASPDEEEPDS MSSPFESLSALVVDLTPRNNSAILLSPVETYPANVLEHNAR LLEREDFAACVEREDGVIPTLAAGGVVQPCOPPSSLASPDEEPDS MSSPFESLSALVVDLTRNNSSHRITILINP KLMYHYPSPSTYGGTDPVVNIGALLGGPRPVXRGGENSVV BERNQTVPTBEDGRYDVYNIGALLRGGRYNFKYGDKD NKYYPYSESFSVUEETYMLATTLDEKKKLKLESPNRSIILLINP KLMYHYPPTVHOPTNSTYCTOTTVTVASERNTITTLIPLQRNPDFK GONTOTTVDTVAGGRAPSTVACKGENDLTITTLIPL LGPRKLLAHYPRFPTVKGFGTDTVTTVTASERMANTATTUPTY PHICKGRRYHLEG	1			FLUNTUMITED DESCRIPTION OF THE PROPERTY OF THE
LDIYGECTMQITHENIYLMDIHARKVKLVMMPLSSLRYGEDST WFFFESGRMCDTGEGLFTYGTREEMIYLMSATLAIAEDHER LMLEMEGKARLOTSLTERMTLSKSISLERSAYMHHITRQNSVGE IYSLQANNEWRHSDLTGKSKTSENRFLEENAPLVMYGITHHLF MDTSTCKVVHDLE 2 1097 ASCQTRRFTAALDSGERIAGRRSPIALMASNFNDIVKQGYVKI SKRKGIFRKGWLVFKKASSKGFRLLEFFDEKAAYFRNPHKYT ELHNIKNITHLPRETKKHAVAIIFHDETSKTFACESELBAEBEK KHLCMECLGFIRLMDISLGEPDLLAAGVURGONSRRNVYLMPTN LDIYGGCTMGITHENIYLMDIHARKVKLVMMPLSSLRRYGRDST WFFFSSGMKOTOTGELFTFOTREGSMIYOKANTAIAEQHER LMLEMEGKARLOTSLTEPMTLSKSISLPRSAYMHHITRQNSVGE IYSLQANHERRHSDLTKKSCKTSBNRFLEENAPLWNYGITHHLP MOTSTCKVVIDLE 6525 1 1859 GESPFSEESIEFNPSSSGRSARTVSSNSYCSDDTGWFSSGSVS VKFSSAGGLVKRGSEADFSSSSTASISLAFEVHMSTAGSKRSSSSN NRGPHGRNAGASSHKOGSSFSPSRKDLLERONLEFNIYHD SVAPSSPSSSNSGSVKGSCCSPIMRSGRYMSCGENHGVRPNP EQYLTPLOGKETVEHLKTKLKESERRLHRRSBSIVELKSQLAR MREDWIEEECHRVERQLALKERRSIKQUETMRSSLANDD KGIQKYFVDINTQNKKLESLLGSMMRHSGSLRDELCLDPFODS PEKSILLINPFDITMADGLSLEGVYGGSGALUGGSICJSNSTM KRGLDFAACVERLDGVI GLARGGVVRQVMSSFJUDLLAVAA PUVPTUMAFSTQRGGTDPVNIGALLEGVVRGWSSFJUDLLAVAA PUVPTUMAFSTQRGGTDPVNIGALLEGVCVVALHSLRRTAFR IKT 6526 2 2034 SGRAGEPEEWRGRQIIDSKETWIFFNSEDGQLEEAVSSGKCCN GRVVPTDGGRYDVHLGERMRYAVVWDELASEVRRTYFKGDKD NSYPYSSSFSQVLEETYMAUTDLEWKKLESPMREIILLHNP KLMMYNQPVAGSDDWGSTPMEGGRRTVKRGGVENISUDIHCGEP LOIPHLYFVYMGIGGACDLERASYSGKCCN GRVVPTDGGRYDVHLGERMRYAVVWDELASEVRRTYFKGDKD NSYPYSSSFSQVLEETYMAUTDLEWKLESENTRIILHNP KLMMYNQPVAGSDDWGSTPMEGGRRTVKRGGVENISUDIHCGEP LOIPHLYFYNGIGGACDLERASYSGKACN GRVVPTDGGRYDVHLGERMRYAVVWDELASEVRRTYFKGDKD NSYPYSSSFSQVLEETYMAUTDLEWKKLESPMREIIILHNP KLMMYNQPVAGSDDWGSTPMEGGRRTVKRGGVENISUDIHCGEP LOIPHLYFYNGIGGACDLERASYSGKACN GRVPTTDGTILDVPFYNSTGRSTUPTCHGYNDFICHTURGL KAQENQOIGRVEFLDVNWSPLHSTGVOVDLQRIIFSNIKHRH FINDTILDVPFYNSTFSTKNSMGLKRPAPPQPASAGNIFKSSECSSSN TRNGDYLDVGIGQVGVKYPRLIYKPEIFFAGSSIGMTFTURGL KRIDPNRFFTCKFFRINJENGLKRPAPPQPASAGNIFKSSECSSSN TRNGDYLDVGIGQVGVKYPRLIYKPEIFFAGSSIGMTFTURGL KRIDPNRFFTCKFFRINJENICHTYPDEVAKTEREPTIVAVKEEBECSSSN TRNGDYLDVGIGQGVTVLOEKPIESTREVLFALGSHLCWESSEDTVLLUV GMLNGGQRIDVLOEKPIESTREVLFALGSHLCWESSEDTVLLUV LKELYGTGGIFLDDPLO	1			KHI CMECL CERLINDISI CERRI LA ROMOR DE LA
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IMMEMBOKARLOTSLTERMTLSKSISLPRSAVMHHITTQNSVGE IYSLQGNIENHSBLDIKSKSKTSENRFLEENAPLVMYGITHHLP MDTSTCKVVHDLE ASCOTRRITAALDSGERIAGRSPIALAMASNIFNDIVKQGYVKI RSRKLGIFRRCWLVFKKASSKOPRRLEKFPDEKAAYFRNHKVT ELHNIKNITRLPRETKKHAVAIIFHDETSKTFACESELEBEBC KHLCMEGLGTILNDISLGEPDILLAGVGERGERTNYLHPTDN LDIYGECTMQITHENIYLMDIHNAKVXLVMWPLSSLRRYGRDST WFFFSGRMCDTGGGLFFTQTREGEMIYQKVUHPTDN LDIYGECTMQITHENIYLMDIHNAKVXLVMWPLSSLRRYGRDST WFFFSGRMCDTGGGLFFTQTREGEMIYQKVUHPTDN LDIYGECTMQITHENIYLMDIHNAKVXLVMWPLSSLRRYGRDST WFFFSGRMCDTGGGLFFTQTREGEMIYQKVUHPTDN LDIYGECTMQITHENIYLMDIHNAKVXLVMWPLSSLRRYGRDST WFFSGRMCDTGGLFFTQTREGEMIYQGGGSGSGSUS LMLENGQXARLOTSLTEPMTLSKSISLPRSAVMHHITQNSVGE IYSLGGNIENRHSDLTGKSCKTSENRFLEENAPLWYGITHHLP MDTSTCKVVHOLE GESPFSERESIEFNPSSGGRSARTVSSNSFCSDDTGMPSGSDSVS PVKTPSDAGNSPJGGLFGDSDCSTPKKKCTIGNVGGGSIQSSRYK KESKSGLVKPGSEADFSSSSTGSISRFVSHNSTGSKRSSSR NRGPHGRSNGASSHKPGSSSSSTGSISRFVSHNSTGSKRSSSRN NRGPHGRSNGASSHKPGSSSPSSTGSISRFVSHNSTGGSKRSSSSR NRGPHGRSNGASSHKPGSSPSSPEKOLLSMLCROLSPVNIHP SYAPSSPSSSNSGSYRGSDCSPIMRRGSMYMGCGNIGVFPND EQYLTPLQQKSVYVRHLKTKLKLGSERRLHERSSIEVELKSQLAR MEEDDIEGECHRVEAQLALKRAREEILAGVUJETMASSLADKD KGIQKYFVDINIQHALKRAREILAGVUJETMASSLADKD KGIQKYFVDINIQHADGLSLEEQVTGEGADRELLUGSILANSTD LPDELVTATTTSSGDLELUHSTPGANVLGUSITMSSLADKD KGIQKYFVDINIGHENRYAVUMBLELDFIVMGGESVVV ERAVOTDVVPYSBAISELIQSVLQKLQDPCPSSLASPBSSEDDS MSSPFSELSSLAVVDLTPRINNSAILLSPVFTYANDLABEVHANR LMRELDPAACVERRLDGVIPLARGGVVRQYWSSSFLVDLLAVAA PVVPYVLMAFSTQRGGTDPVNIGALLRGCVVVALHSLRRTAFR IKT SGRAGGEPEWRGRQIIDSKETWIPNSAILLSPVFTYANDLABEVHANR LNRHLDPAACVERRLDGVIPLARGGVVRQYWSSFLVDLLAVAA PVVPYVLMAFSTQRGGTDDVNIGEMRXAVYMBLASEVRCTWFKKQDKD NKYVPYSGSSFSQVLEETWILAVILDBWKKKLESPNREIIILHN KLMMYYOPAGSDDWGSTPMEQGRPRTVKRGVENIVOHTER KAQENQGIGRVSFLPVNMHSPLUSASVRCTWFKKGDKD NKYVPYSGSSFSGVLETWILAVILDBWKKKLESPNREIIILHN KLMMYYOPAGSDDWGSTPMEQGRPRTVKRGVENIVOHTER KAQENQGIGRUSFLUNMHSPLUSTVDUDLQRITLPSINNIH FINDTILLDVFYNNSTCQTIVDTVASERNYTTHLERINGRIPH FONDTLLDVFYNSSTCGTTWYFOTGFTWITTLFLENNIH FINDTILLDVFYNSSTCQTTIVTTVASERNYTTHLEFONNIH REFRENTERINGFTARFYPTKGFFFTAFTYPHYFOTGFFTHYTTYFLEFTARFYPHYFOTG	1			WETFESGRMCDTGRGLETFOTPRGEMIYOVUUGARUATA POVER
1YSLQONHENHASDLTGKSCKTSENRFLEENAPLVMYGITHLIP MDTSTCKVVHDLE ASCQTRRFTAALDSGERIAGRESPIALAMASNFNDIVKQGYVKT RSKKLGIFRCMLVFKKASSKGPRRLEKFPDKKAAYFRNFHKVT ELHNIKNITRLPRETKKHAVAIIFDETSKTFACESLLEAEBEC KHLCMECLGTRIANDISLGEFDLLAAGVQREQMERRNYLMPTEN LDIYGECTMQITHENIYLMDINNAKVMPLISSLRTYGROBT WFFFESGMCDTGEGFFFOTREGEMIYOKVISAATLAIAAQHER LMLEMQKARIOTSLTEMTLKSK ISLPAVWHITTRQNSVGE IYSLQGNHENRHSDLTGKSCKTSENRFLEENAPLWMIGITHHLP MDTSTCKVVHDLB GESPFSEERSIEFNPSSGRSARTVSSNSFCSDDTGWPSSQSVS PVKTFSDAGNSPIGFCPGSDEGFTRKKCTIGMVGGGSIQSSRYK KESKSGLVKYGSBADTSSSSTGSISHARYSNSFCSDDTGWPSSQSVS PVKTFSDAGNSPIGFCPGSDEGFTRKKCTIGMVGGGSIQSSRYK KESKSGLVKYGSBADTSSSSTGSISHANTSGENGLSPNYNIHP SYAPSSPSSSSTSSSTSSTSSTSSTSSTSSSSSSSS NRGPHGRSNGASSHKPGSSPSSPEKDLLSMLCRNQLSPVNIHP SYAPSSPSSSNGSYKGSDCSPIMRRSGRYMSGGENGVPPNNP EQYLTPLQQKEVTVRHLKTKLKBEBERLHERSSEIVELKSQLAR MEEDWIEEECHRVEAQLALKBARREIKQLKQVIETMSSGLADKD KGIQKYFVDINIONKLUSLLGANEWHASGSLEDELLDPFCDS FEKSITINPPLDTMADGLSLEEQUTGEGADRELLUGSIANSTD LEPBLVVATTTSESGDLEULHSTPGANVCRYWSSFLVELDSIANSTD LEPBLVVATTTSESGDLEULHSTPGANVCRYWSSFLVELDAVAA PVVPTVLWARSTQRGGTDPVYNIGALLRGCCVVALHSLRRTAFR IKT LKT LKT SGRAGEPEEMRGROIIDSKETWIPFNSSLLSVCVVALWSSFLVULAVAA PVVPTVLWARSTQRGGTDPVYNIGALLRGCCCVVALHSLRRTAFR IKT SGRAGEPEEMRGROIIDSKETWIPFNSSUSVINLTHSVALVAA PVVPYVMGIGBACDLERRSIVQCVONDPRSVISINLIGHTHK KAQENQCIGRVFILPVNNHSPLHSTGVDVDQLGRTHFKVGKGNINGNIHK KAQENQCIGRVFILPVNNHSPLHSTGVDVDQLGRTHFSVDHCGEP LQIPHLYPVNGIGBACDLERRSIVQCVONDPRSVISINLIGHTHK FINDTILLDVFYNNSTYCGTIVDTVASBCVRTWFYTGDLQFIGIP LGPRKKLLNYFSTRKNSMGIKRPAVQPASGANIPKSSEGSSN TRNGDYLDVGIGQVSVYPRLIYKREIFFPASGSIIGMFLTVRGL KRIDPNVFFTCKGFFRIVHPFPOKGARAIYTLFPLAGSHIMFILTURGL KRIDPNVFFTCKGFFRIVHPFPOKGARAIYTLFPLAGSHIMFILTURGL KRIDPNVFFTCKGFFRIVHPFPOKGARAIYTLFPLAVHEEVLFINIF PHKGRRWHLBLERGLTRNSMGIKRPAVQPASGANIPKSSEGSSN TRNGDYLDVGIGLDGVGVSVYPRLIYKREIFFFALGSHUKHEVEEPMLI PHKGRRWHLBLERGLTRNSMGIKNNLLGSLRMAWKSFTRAPY PALQASETPEETEABPESTSKPSDVNTETSTAAVEEVLEIVLIV LKEIYQTGGIFLDOPLO GWPLLSSTLEFBACKTYKGGINIRLDTTUIDTFDMKKORGDLS	1			LMLEMEOKARLOTSI.TEPMTI.SKSISI.DDCAVWUULTDOAGGE
6524 2 1097 ASCOTRETRALDISGERIAGRESPIALAMASNENDIVKQGTVKT RSKKJGIFERCMLVFKKASSKGPRLEKFFDEKAAYFRNHKVT ELHNIKNITELBETKKHAVAIITHDETSKTFACESLLEAEBEK KHLCMECLGFTELMDISLGFDLLAAGVGEQMERNVYLMPTIN LDIYGECTMQITHENIYLMDIHNAKVKLVMWPLISSLRRYGRDST WFFFSEGMENDTTGGGFTFFOTREGEMISLSLRRYGRDST WFFFSEGMENDTTGGGFTFFOTREGEMISLARAGHER LMLEMEQKARLOTSLTEPMTLSKSISLPRSAYWHHITRONSVGE IYSLOGNHENRHSDLTGKSCKTSENRFLEENAPLWMYGITHHLP MOTSTCKVVHDLB 6525 1 1859 GESPFSEESIEFNPSSGGRARTVSSNSFCSDDTGWFSSGSUS PVKTFSDAGMSPSGOFCOSDEGFTFKKCTIGMVGGGSIGSSRYK KESKSGLVKPGSBADFSSSSTSGISAPEVHMSTAGSKRSSSR NRGPHGRSNAGNSPGSFOFSDEGTFKKCTIGMVGGGSIGSSRYK KESKSGLVKPGSBADFSSSSTSGISAPEVHMSTAGSKRSSSR NRGPHGRSNAGNSPGSPSSPSREKDLLSHLCRDLSPVNTHP SYLPSSPSSNSGSYKGSDCSPIMRRSGYMSCGENIGWPSPOP EGYLTPLQGKEVTVRHLKTKLKESERRLHERSSIVELKSGLAR MEEDDIEGECHRVPAGLALKEAREE KOLKQVISTMRSSLADKD KGIOKYFVDINIGNKLESLLQGMEMAHSGSLRDELLDFPCDS PEKSLTLIPPLDTMADGISLEEQVTGGAADREIDELLDFPCDS PEKSLTLIPPLDTMADGISLEEQVTGGAADREIDELLDFPCDS PEKSLTLIPPLDTMADGISLEEQVTGGAADREIDELLDFPCDS PEKSLTLIPPLDTMADGISLEEQVTGGAADREIDELLDFPCDS PERSUTURPPLDTMADGISLEEQVTGGAADREIDELLDFPCDS PRESSTENSSLAVVDLTPRINNPSAILLSPVETPYANVDABEVHANR LMREIDPAACVEERLIGGSVVQKYGSSSFLUDLLAVAA PVVPYVLMAFSTQRGTDPVYNIGALLRGCVVVALHSLRATAFR IKT SGRAGEFEEWRGRQIIDSKETWIFFNSEDSQOLERSYSSKOCN NKYVPYSESSFSQVLBETYMLAVILDEWKKKLESPNREIIILIHNP KLMMYYOPVAGSDDMGSTPMEQGRPTVKROVENISVDIHCGGP LQIDHLVFVVKGIGPACDLRFRSIVQCVNDPRSVSLNLLQTHFK KAQENQCIGRVEFLEVNMHSPLHSTGVDVDLQRITLPSINNLRH FYNNTILDVFYNNSFIVCGTIVDTVASRIVITLFLGNRPPFK GGVSIAGHSLGSLLIFDILTNOKDSLIGDIDSEKSILNIVMOQGD TPTLEEDLKALGLSEFFD IFFEKVDERAGNITFKTEGESSIN TRNGDVLDUGIGQVSVKYPRLIYKKEIFFAGSSIGMKLTVRGGI KRIDPNYRFTCKGFFRIVHFPPPVAKIFTITLFLGNRPPFK GGVSIAGHSLGSLLIFDILTNOKDSLIGDIDSEKSILNIVMOQGG TPTLEEDLKALLGLGEGTTMSMDLKNNLLGSLRMAWASFTEAPY PALQASETFEFTEAPPSTSEKPSDVNTERSTVAVKEEVLPINV GMLNGGQRIDVVLQEKPIESFREVLFFALQSHLCYWESEDTVLLU LKEIYQTQGIFIDDPLO GMULDSGUTLPSDACKTYKGGINIRLDTTLIDTFDMKCORGDLS		[IYSLOGNHENRHSDLTGKSCKTSFNDFT.FFNADIJMYCTTIRIT P
ASCOTERRITAALDSGERIAGRRSPIALAMASNFNDIUKQGYVKI RSRKLGIFRRCWLVFKKASSKGFRALEKFPDEKAYFRRHYKT EHNIKNITRIPRETKHAWAIIFDETSKFFACESSLEAEBEK KHLCMECLGTRINDISLGEBDLLAAGVOREONEFNYUMPTPN LDIYGECFMQTTHENIVLMDINHAKYKLUMMPLSSLRRYGRDST WFFFESGRMCDTGEGLFTFOTREGEMIYOKVHSATLAIAEQHER LMLEMEQKARLOTSLTEPMILGKSLSLERBAYBHITTRONSVGE 17SLQGANEENHASDLTKKSKCHTSBRYFLEENAPLVMYGITHHLF MOTSTCKVVHOLB GSEPFESESIEFNESSGRSARTVSSNSFCSDDTGWFSSQSVS PVKTPSDAGNSPIGFCPGSDEGFTRKKCTIGMVGEGSIGSRYK KESKSGLVKPGSEADFSSSSTGSISAPEVHMSTAGSKRSSSSR NRGPHGRSNASSHKNGSSPSSPRFKOLLSHLCHOLSPVNTHP SVAPSSPSSNSGSYKGSDCSPIMRRSGRYMSCGEHHGVRPPNP EQYLTPLQQKEVTVENHLKYLKESERLHERESEIVELKSQLAR MREDWIEEECHRVEAQLALKEARREIKQLKQVIETKRSSLADKD KGIQKFFOLINIONKALESLLGSMMMARSGSLRDELCLDFPCDS FEKSLTLMPPLDTMADGLSLEEQVTGADVELLPITVMGGEGSVVV ERAVGTDVVPYSPALSELJGSVLQXLQDPCPSSLASPDESEPDS MESPPESLSALVVDLTPRNPNSALLLSPVETPYANVDAEVHANR LMRELDPAACVERLDGVIPLARGGVVRQVWSSSFLVULLAVAA PVVPTVLWAFSTORGGTDPVNIGGLLRGCCVVALHSLRRTAFR IKT SGRAGEPEEWRGRQIIDSKETWIPFNSEDSQQLEEAYSSGKGCN RVVPTDGGRYDVHLGERMRYAVWDELLSEVRCCTWFKGDKD NKYVPYSESFSQVLEETYMLAUTLDEWKKALESPNEEIIILHNP KLMMYRQVPAGSDDMSGTMPSGGRPKTLGCVVALPSLLRTH FINDTILDVPFYNSPTYCGTVDTVASEMMRIYTTLFLQRNDFK GGVSIAGHSLGSLILFDILTNOKDSLGDIDSREGSINIVMOGGD TPTLEEDLKKLOLSEFFDIFFEKENVKALALCTORDLGBIGIP LGJDHLVPVVNGIGPACDLRYRSIVQCUNDFRSVSLNLLQTHFK KAQENQQIGVVEFLPVNMSPLHSTGVDVDLGTLPSINKHRH FINDTILDVFFYNSPTYCGTVDTVASEMMRIYTTLFLQRNDFK GGVSIAGHSLGSLILFDILTNOKDSLGDIDSREGSINIVMOGGD TPTLEEDLKKLOLSEFFDIFFEKENVKALALCTORDLGBIGIP LGPRKKLLNYFSTRKNSMGIKRPAPQPASGANIPKESEFCSSSN TRNGDYLDVGIGQVSVKYPRIFFIFFERSPUNGERILACTORDLGBIGIP LGPRKKLLNYFSTRKNSMGIKRPAPQPASGANIPKESEFCSSSN TRNGDYLDVGIGQVSVKYPRIFFIFFERSPUNGERSFERML PHHKGRRWHLELBEGLTRMSMDLKNNLLGSLRMAWSSFTRAPY PALGASSTPFFTRABFETSERSPETSERSPSDIGMLTVTRGL KRIDPNYRFFTCKGFFNIYHFPDVAYRTEEPVVVGCWFEEMLI PHHKGRRWHLELBREGLTRMSMDLKNNLLGSLRMAWSSFTRAPY PALGASSTPFFTRABFETSSRSPETSERSPSTUMERSTVAVKEEVLPINV GMLNGGQRIDVVLQEKPIESFNEYLFALGSHCVWKEEVLPINV GMLNGGGRIDVVLQEKPIESFNEYLFALGSHCVWKEEVLPINV LKELYQTGQIFILDQPLQ GWPLLSFRIFTBOACKTYKGGINIRLDTTLIDFTMKCORGDLS	L			MDTSTCKVVHDLE
RSSKLGIFRRCMLVFKKASSKGFRRLEKFPDEKAAYFRNFHKVT ELHNIKNITRIPRBTIKRHAVAI I FIDETSKTFACESELEAEEWC KHLCMECLGTRINDISLGBPDLLAAGVOREONERFNYTLMPTIN LDIYGECTMQITHENIYLMDIHNAKVKLVMMPLSSLRRYGRDST WFTFSSGRNCDTGEGELFTQTTBEGEMIYOKVHSATLAIAEOHER LMLEMEQKARLOTSLTFPMTLGKSISLPRSAYWHHITRQNSVGE IYSLOGNHENRHSDLTKSKCKTSENRFLEERAPLVMYGITHHLF MOTSTCKVVHOLB 6525 1 1859 GESPFSERSIEFNPSSSGRARTVSNNSFCSDDTGWPSSOGUS PVKTPSDAGNSPIGFOGSDEGFTKKCTIGMVGGGSIQSRYK KESKSGLVKPGSEADFSSSSTGSIRPEVHMSTAGSKRSSSRR NRGPHGRSNGASSHKPGSSDSSFRKKCLIGMVGGGSIQSRYK KESKSGLVKPGSEADFSSSSTGSIRPEVHMSTAGSKRSSSRR NRGPHGRSNGASSHKPGSSPSSFRKKLLSHLCRNOLSPVNTHP SYAPSSPSSNSGSYKSSOCSPIRMSGRWNSGGSHNGVFNPNP EQYLTPLOQKSVTVRHLKTKLKESERRHFRESIVELKSQLAR MREDMIEEBCHRVEAQLALKEARKEIKQLKQVIETMRSSLADKD KOIQXYFVDINIONKKLESLLQSMMMARSGSLRDELCLDFPCDS FEKSITLNPPLDTMADGLSLEEQVTGGGADRELLVGDSIANSTD LEPBLVTATTTESSGLEUWHSTPGAAGVRGWSSFLVDLAVAA PUVPTVLMAFSTQRGGTDPVYNIGALLESPVTPANVDAEVHANR LMRELDPAACVERLDGVIPLSHSPYGHAUELDIPVMGGEGSVVV ERAVQTDVPYSPAISELIQSVLQKLQDPCPSSLASPDESEPDS MESPFELSJALVUDLTPRNPNSAILLSPVETPYANVDAEVHANR LMRELDPAACVERLDGVIPLSVHSTELHSTVLAVHUBLELDIPVMGGEGSVVV ERAVQTTDGRYDVHLGERMYVAVWDELASEVERCTWFYKGDKD NRVYPYSESFSQVLEETVMLAVTLDSKKZLESPNREIILHNP KLMVHYQPVAGSDDWGSTPMEQGRPRTVKRGVENISVDIHGGEP LQIDHLVFVVHGIGBACDLRFRSIVQCVNDFRSVSLNLLQTHFFK KAQENQGIGKVETLPVMNISPLHASTGVDVDLGRITLPSINRLRH FINDTILDVFYMSPTYCGTTVDTVASEMRRIYTLPFLQRNPDFK GGVSIAGHSLGSLILFDILTNCKDSLGDIDSKEGSINIVMDQGD TPTLEEDLKKLOLSEFFFIFEKEKVDKALALCTDRDLGFIGHEI LGPRKKLINTFSTRNSMGIKRPAPQPASGANIPKESBFCSSSN TRNGGYLDVGIGGGVEVPNIPHPFDFVAYRIEPMVVPGVEFFERMLI PHHKGRRRHLELREGLTRMSMDLKNNLLGSLRMAWKSFTRAPY PALDASSTPPETRABEFETSSKPSTRSTSVANKESPLFVRGL KRIDPNYRFPTCKGFFNIYHPFDPVAYRIEPMVVPGVEFFERMLI PHHKGRRRHHELLREGLTRMSMDLKNNLLGSLRMAWKSFTTAPY PALDASSTPPETRABEFETSSKPSTESTSVANKESTEVAVKEREVLPINV GMLMGGQRIDYVLQEKPIESFINSLYFBLQSHLCYWESEDTVLLV LKEIYTTGIFLDQFLQ GWVELLSFLIPSDACKKYNGGINIRLDFTTLIDFTDMKCORGDLS	6524	2	1097	ASCQTRRRTAALDSGERIAGRRSPIALAMASNENDTUKOGVUKT
ELHNIKNITR-PREITKHAVAIIFHDETSKTFACESELEAEBKO KHLOMECLETRINDISLGEPULAAGVQREQNERFNYVLMPTPN LDIYGECTMQITHENIYLMDIHNAKVXLVMWPLSSLRRYGRST WETFESGRMCDTGEGLFTFQTREGEMIYQKVHSATLAIAEQHER LMLEWBQXARLOTSSTJEMMILSKSISLPRSAYWHHITRQNSVGB IYSLQGNHENRHSDLTGKSCKTSENRFLBENAPLVMYGITHHLP MDTSTCKVVHDLB: GESPFSEEESIEFNPSSSGRSARTVSSNSFCSDDTGWPSSQSVS PVKTFSDAGNSPIGFCPGSDEGFTRKKCTIGMVGEGSIQSRYK KESKSGLVKFGSEADFSSSSSTAGSISAPEVHMSTAGSKRSSSR NRGPHGRSNGASHKPGSSPSSPREKDLLSMLCRNQLSPVNIHP SYAPSPSSSNSGSYKGSDCSPIMRRSGRMSGGENHGVRPPNP GYLTTPLQQKSVTVRHLKTKLKESERRLHERSESITELKSQLAR MEDMIEEEGIRVERQLALKEARREIKQLKQVIETMRSSLADKD KIQKYFDINIONKKLESLLGAWHANGSLEDELLUDDSIANSTD LFDEIVTATTESGDLELVHSTFGANVLEILLIVWGGEEGSVVV BERAVQTDVVFYSPAJISELIGGVLQKLQDPCPSSLASPDESSPDS MESPPESLSALVVDLTPRNPNSAILLSPVETPYANVDABVHANR LMRELDPAACVEERLIGVIPLARGGVVRQYWSSSFLVDLLAVAA PVVPTVLWAPSTQRGCTDEVVNTGALLRCCCVVALHSLRRTAFFR IKT IKT SGRAGEPBEWRGRQIIDSKETWIPFNSEDSQQLEERAYSSGKGCN GRVVPTDGGRYDVHIGRERMFYAVYWDELASEVRCTWFYKODKD NKYVPYSESFSQVLEETYMLAVTLDEWKKLESPNREILILHING KLMVHYQPVAGSDDWGSTPMCGGRPRTVKRGVENISVDIHGGEP LQIDHLVFVVHGIGPACDLEFFRSIVQCVDDFRSVSLNLLOTHFK KAGENQCIGRVETI-DVWHSPSTRATOVDVDLORITLPSINRRH FINDTILDVPFYNSPTYCQTIVDTVASEMNRIYTLPFLQRNPDFK GGVSIAGHSLGSLILEPILITNQKDSLGDIDSEKGSLMIVMDQGD TPTLEEDLKKLQLSGFFDIFFEKKDERALALTDDLQEIGIP LGPRKKILNYFSTRKNSMGIKPPAPQPASGANIFKESFCSSSN TRNGDYLDVGIGQVSVKYPRLIYKPEIPFAFGSPIGMFLTVRGL KRILDPNYRFPTCKGFFNIYHPFDVAYRIERMVGGEFFENLI PHHKGRRMHLELREGLTMSMDLKNHLLGSLRNAWKSFTRAPFY PALQAS TPEETERAFPESTSERFSDSVNTERFSSVAVKEEVLPINV GMLNGGQRIDYVLQEKPIESFNUTPFTLAGSHCWKESVIPLIV LKEIYQTQGIFLDQPLU GGWLASCTPETPTBERSDONTTERTSVAVKEEVLPINV GMLNGGQRIDYVLQEKPIESFNEYLFALQSHLCWBSEDTVLLU- LKEIYQTGGIFLDQPLU GGWLASCTIPEDGENGLAGHDAGHLERDETTLERGEDTTNANDLKNALKESULFINV GMLNGGQRIDYVLQEKPIESFNEYLFALQSHLCWBSEDTVLLU- LKEIYQTGGIFLDQPLU GGWLASGUPBLOGREDAGENTSTARPCTHANGCARGDLS				RSRKLGIFRRCWLVFKKASSKGPRRLEKFPDEKAAYFRNFHKVT
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LDIYGECTMQITHENIYLMDIHNAKVIKLWMPLSSLRRYGENST WFFFESGMCOTGGELFFFQTREGEMIYQKVHSATLAIAEQHER LMLEMEQKARLQTSLTEPMTLSKSISLPRSAYMHHTTRONSVGE IYSLQGNHENRHSDLTGKSCKTSENRFLBENAPLVMYGITHHLF MOTSTCKVVHOLB. 6525 1 1 1859 GESPFSEBESIEFNPSSGRSARTVSSNSFCSDDTGWFSSQSVS PVKTFSDAGNSPIGFCPGSDEGFTRKKCTIGMVGEGSIQSRYK KESKSGLVKFGGSADFSSSSSTAGSISAPEVHMSTAGSKRSSSR NRGPHGRSNGASHKPGSSPSSPREKDLLSMLCRNQLSPVNIHP SYAPSSPSSNSGSYKEGDCSPIMRRSGRYMSGGENHGVRPPNP EQYLTFLQQKSVTVRHLKTKIKRSEBRRLHERSESIVELKSQLAR MREDMIEEGCIRVERQLALKEARREIKQLKQVIFTMRSSLADKD KGIQKYFVDINIQNKKLESLLQSMENHAFGSLWDELCLDFPCDS PEKSITLMPPLDTMADGLSLEGQVTGEGADRELLVDSFIANSTD LFDEIVTATTTESGDLELVHSTFGANVLBLLPIVMGQEEGSVV BRAVQTDVPYSPAISELIQSVIQKLQDPCPSSLASPBESEDS MESPPESLSALVVDLTFRNENSAILLSPVETTYANVDAEVHANR LMRELDFRACVERELDGVIPLARGGVVRGVMSSSFLVDLLAVAA PVVPYVLMAFSTQRGTDPVVNIGALLRGCVVALHSLRRTAFR IKT 6526 2 2034 SGRAGEPEEWRRQIIDSKETWIPFNSEDSQQLEEAYSSGKGCN GRVVPTDGGRYDVALGERMYRYWDELASEVRRCTWFYKGDKD NKYVPYSESFSQVLEETYMLAVTLDEWKKKLESPRREIILHNP KLMWHYQPVAGSDDWGSTTPMCGCRPRTVKRGGENISVDIHGGEP LQIDHLVPVVHGIGPACDLRFRISQUNDFRSVEINLLQTHFK KAQENQQIGRVEFLPVNWHSPLHSTGVDVDLQRITLPSINRLRH FINDTILLDVFYMSPTYCGTIVDTVASEMRIYTTLFLQRNPDFK GGVSIAGHSIGSLILFPIITNOKDSLGDIDSKGSLIVVMOGGD TPTLEBDLKKLQLSEFFDIFEKEKVDKSALALCTDRDLQEIGIP LGPRKLILMFSTRKNSMGIKPRAPQPASGANIPKESEFCSSSN TRNGDYLDVGIGGVVSKYPRLIYMFEIFFAGSSIGMELTURGL KRIDPNYRFFTCKGFRNIYHPFDPVAYRIEPMVVPGVEFEPMLI PHKGRKRMHLELREGLTRMSNDLKNNLLGSLRNAWKSFTRAPY PALQASSTPEETRAPEFSTSEKPSDVNTEETSVAYKESULPINV GMLNGGGRIDVULQEKPISSFNEYLFALQSHLCYWESEDTVLLV LKEIYQTGGIFLDQPILQ LKEIYQTGGIFLDQPILG LKEIYGTGGIFLDQPILG GWPLLSRIUPDQPLC CKUPLLSRIUPDGRIC				KHLCMECLGTRLNDISLGEPDLLAAGVQREONERFNVYLMPTPN
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SYAPSSPSSSMIGSYKGSDCSPIMRRSGRYMSCGENHGVRPPNP EQYLTPLQQKEVTVRHLKTKLKESERRHERESEIVELKSQLAR MREDMIEEECHRVEAQLALKEARREIKQLKQVIETMRSSLADKD KGIQKYFVDINIQNKKLESLLQSMEMAHSGSLRDELCLDFPCDS PEKSLTLNPPLDTMADGLSLEEQVTGEGADRELLVGDSIANSTD LFDEIVTATTTESGDLELVHSTPGANVLELLPIUMGCEGGSVVV ERAVOTDVVPYSPAISELIQSVLQKLQDPCPSSLASPDESEPDS MESFPESLSALVVDLTPRNPNSAILLSPVETPYANVDAEVHANR LMRELDFAACVEERLDGVIPLARGGVVRQYWSSSFLVDLLAVAA PVVPTVLWAPSTQRGGTDPVYNIGALLRGCCVVALHSLRRTAFR IKT GSZ66 2 2034 SGRAGEPEEWRGRQIIDSKETWIPFNSEDSQQLEEAYSSGKGCN GRVVPTDGGRYDVHLGERMRYAVYWDELASEVRRCTWFYKGDKD NKYVPYSESFSQVLEETYMLAVTLDEWKKKLESPNREIIILHNP KLMVHYQPVAGSDDWGSTPMEQGRPTVKRGVENISVDIHCGEP LQIDHLVFVVHGIGPACDLRFRSIVQCVNDFRSVSLMLLQTHFK KAQENQQIGRVEFLPVNNHSPLHSTGVDVDLQRITLPSINRLRH FTNDTILDVFFYNSPTYCQTIVDTVASEMNRIYTLFLQRNPDFK GGGVSIAGHSLGSLILFDILTNQKDSLGDIDSEKGSLNIVMDQGD TPTLEEDLKKLQLSEFFDIFEKEKVDKEALALCTDRDLQEIGIP LGPRKKLLMYFSTRKNSMGIKRPAPQPASGANIPKESEFCSSSN TRNGGYLDVGIGQVSVKYPRLIYKPEIFFAFGSPIGMFLTVRGL KRIDPNYRFPTCKGFFNIYHPFDPVAYRIEPMVVPGVEFEPMLI PHKKGRKRMHLELREGLTRMSMDLKNNLLGSLRMAWKSFTRAPY PALQASETPEETEAEPESTSEKPSDVNTEETSVAVKEEVLPINV GMLNGGGRIDVYLQEKPIESFFEYLFALQSHLCYWESEDTVLLV LKEIYQTGGIFLDQPLQ 6527 1 922 GWVPLESRILFSDACKTYKQGINIRLDTTLIDFTDMKCORGDLS	i . I			NPGPHGPENGAGEHVPGGGPGGPDEVDLIGHT GPUOL
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MREDWIEEECIRVEAQLALKEAREIKQLKQVIETMRSSLADKD KGIQKYFVDINIQNKKLESLLQSMEMAHSGSIRDELCLDFPCDS PEKSLTINPPLDTMADGLSLEEQVTGEGADRELLVGDSIANSTD LFDEIVTATTTESGDLELVHSTPGANVLELLPIVMGQEEGSVVV ERAVQTDVVPYSPAISELIQSVLQKLQDPCPSSLASPDESEPDS MESFPESLSALVVDLTPRINPNSAILLSPVETPYANVDAEVHANR LMRELDFAACVEERLDGVIPLARGGVVRQYWSSSFLVDLLAVAA PVVPTVLWAFSTQRGGTDPVYNIGALLRGCCVVALHSLRRTAFR IKT 6526 2 2034 SGRAGEPEEWRGRQIIDSKETWIPFNSEDSQQLEEAYSSGKGCN GRVVPTDGGRYDVHLGERMRYAVYWDELASSURGCWFCTWFYKGDKD NKYVPYSESFSQVLEETYMLAVTLDEWKKKLESPNREIIILHNP KLMVHYQPVAGSDDWGSTFMEQGRPRTVKRGVENISVDIHCGEP LQIDHLVFVVHGIGPACDLRFRSIVQCVNDFRSVSLNLLQTHFK KAQENQQIGRVEFLPVNWHSPLHSTGVDVDLQRITLPSINRLRH FTNDTILDVPFYNSPTYCQTIVDTVASEMNRIYTLFLQRNPDFK GGVSIAGHSLGSLTLFDILTNQKDSLGDIDSEKGSLNIVMDQGD TPTLEEDLKKLQLSEFFDIFEKEKVDKEALALCTDRDLQEIGIP LGPRKKILNYFSTRKNSMGIKRPAPQPASGANIPKESEFCSSN TRNGDYLDVGIGQVSVKYPRLIYKPEIFFAFGSPIGMFLTVRGL KRIDPNYRFPTCKGFFNIVHFDPVAYRIEPMVVPGVEFEFMLI PHKGRKRMHLELREGLTRMSMDLKNNLLGSLRNAWKSFTRAPY PALQASETPEETBAEPESTSEKPSDVNTEETSVAVKEEVLPINV GMLNGGQRIDYVLQEKPIESFNEYLFALQSHLCYWESEDTVLLV LKEIYQTGGIFLDQPLQ 6527 1 922 GWVPLESRILPSDACKIYKQGINIRLDTTLIDFTDMKCORGDLS	1 1			EOYLTPLOOKEVTVRHIKTKI KESERPI HEDEGETURI VOOL DE
KGIQKYFVDINIQNKKLESLLQSMEMAHSGSLRDELCLDFPCDS PEKSLTLNPPLDTMADGLSLEEQVTGEGADRELLVGDSIANSTD LFDEIVTATTTESGDLELVHSTPGANVLELLPIVMGQEEGSVVV ERAVQTDVVPYSPAISELIQSVLQKLQDPCPSSLASPDESEPDS MESFPESLSALVVDLTPRNPNSAILLSPVETPYANVDAEVHANR LMRELDFAACVEERLDGVIPLARGGVVRQYWSSSFLVDLLAVAA PVVPTVLWAFSTQRGGTDPVYNIGALLRGCCVVALHSLRRTAFR IKT GSRAGEPEEWRGRQIIDSKETWIPFNSEDSQQLEEAYSSGKGCN GRVVPTDGGRYDVHLGERMRYAVYWDELASEVRRCTWFYKGDKD NKYVPYSESFSQVLEETYMLAVTLDEWKKKLESPNREIIILHNP KLMVHYQPVAGSDDWGSTPMEQGRPRTVKRGVENISVDIHCGEP LQIDHLVFVVHGIGPACDLRFRSIVQCVNDFRSVSLNLLQTHFK KAQENQQIGRVEFLPVNWHSPLHSTGVDVDLQRITLPSINRLRH FINDTILDVFFYNSPTYCQTIVDTVASEMWRIYTLPFLQRNPDFK GGVSIAGHSLGSLILFDILTNQKDSLGDIDSEKGSLNIVMDQGD TPTLEEDLKKLQLSEFFDIFEKEKVDKEALALCTDRDLQEIGIP LGPRKKILNYFSTRKNSMGIKRPAPQPASGANIPKESSFCSSN TRNGDYLDVGIGQVSVKYPRLIYKPEIFFAFGSPIGMFLTVRGL KRIDPNYRFPTCKGFFNIYHPFDPVAYRIEPMVVPGVEFEPMLI PHHKGRKRMHLELREGLTRMSMDLKNNLLGSLRMAWKSFTRAPY PALQASETPEETRAEPESTSEKPSDVNTEETSVAVKEEVLPINV GMLNGGQRIDYVLQEKPIESFNEYLFALQSHLCYWESEDTVLLV LKEIYQTGGIFLDOPLQ GSVPLLSRILPSDACKIYKQGINIRLDTTLIDFTDMKCORGDLS				MREDWIEEECHRVEAOLALKEARKEIKOLKOVIETMRSSLADKD
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LFDEI TTATTTESGDLELVHSTPGANVLBLLP IVMGQEEGSVVV ERAVQTDVVPYSPAISELI QSVLQKLQDPCPSSLAS PDESEPDS MESFPESLSALVVDLTPRNPNSAILLSPVETPYANVDAEVHANR LMRELDFAACVEERLDGVI PLARGGVVRQYWSSSFLVDLLAVAA PVVPTVLWAFSTQRGGTDPVYNIGALLRGCCVVALHSLRRTAFR IKT 6526 2 2034 SGRAGEPEEWRGRQI IDSKETWI PFNSEDSQQLEEAYSSGKGCN GRVVPTDGGRYDVHLGERMRYAVYWDELASEVRRCTWFYKGDKD NKYVPYSESFSQVLEETYMLAVTLDEWKKKLESPNREII ILHNP KLMWHYQPVAGSDDWGSTPMEQGRPRTVKRGVENISVDI HCGEP LQIDHLVFVVHGIGPACDLRFRSI VQCVNDFRSVSLNLLQTHFK KAQENQQIGRVEFLPVNWHSPLHSTGVDVDLQRITLPSINRLRH FTNDTILDVFFYNSPTYCQTIVDTVASEMNRI YTLFLQRNPDFK GGVSIAGHSLGSLILFDILTNQKDSLGDI DSEKGSLNIVMDQGD TPTLEBDLKKLQLSEFFDI FEKEKVDKEALALCTDRDLQEIGIP LGPRKKILNYSSTRKNSMGI KRPAPQPASGANI PKESEFCSSSN TRNGDYLDVGIGQVSVKYPRLIYNPEIFFAFGSPIGMFLTVRGL KRIDPNYRFPTCKGFFNIYHPFDPVAYRIEPMVVPGVEFEPMLI PHHKGRKRMHLELREGLTRMSMDLKNNLLGSLRMAWKSFTRAPY PALQASETPEETEABPESTSEKFSDVNTEETSVAVKEEVLPINV GMLNGGQRI DYVLQEKPIESFNEYLFALQSHLCYWESEDTVLLV LKEIYQTQGIFLDQPLQ 6527 1 922 GWVPLLSRILPSDACKIYKQGINIRLDTTLIDFTDMKCORGDLS]]			PEKSLTLNPPLDTMADGLSLEEOVTGEGADRELLVGDSIANSTD
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MESFPESLSALVVDLTPRNPNSAILLSPVETPYANVDAEVHANR LMRELDPAACVERLDGVIPLARGGVVRQYMSSSFLVDLLAVAA PVVPTVLWAFSTQRGGTDPVYNIGALLRGCCVVALHSLRRTAFR IKT 6526 2 2034 SGRAGEPEEWRGRQIIDSKETWIPFNSEDSQQLEEAYSSGKGCN GRVVPTDGGRYDVHLGERMRYAVYWDELASEVRRCTWFYKGDKD NKYVPYSESFSQVLEETYMLAVTLDEWKKKLESPNREIIILHNP KLMVHYQPVAGSDDWGSTPMEQGRPRTVKRGVENISVDIHCGEP LQIDHLVFVVHGIGPACDLRFRSIVQCVNDFRSVSLNLLQTHFK KAQENQQIGRVEFLPVNWHSPLHSTGVDVDLQRITLPSINRLRH FTNDTILDVFFYNSPTYCQTIVDTVASEMNRIYTLFLQRNPDFK GGVSIAGHSLGSLILFDILTNQKDSLGDIDSEKGSLNIVMDQGD TPTLEEDLKKLQLSEFFDIFEKEKVDKEALALCTDRDLQEIGIP LGPRKKLLNYFSTRKNSMGIKRPAPQPASGANIPKESEFCSSSN TRNGDYLDVGIGQVSVKYPRLIYKPEIFFAFGSPIGMFLTVRGL KRIDPNYRFPTCKGFFNIYHPFDPVAYRIEPMVVPGVEFEPMLI PHHKGRKRMHLELREGLTRMSMDLKNNLLGSLRMAWKSFTRAPY PALQASETPEETBAEPESTSEKPSDVNTEETSVAVKEEVLPINV GMLNGGQRIDYVLQEKPIESFNEYLFALQSHLCYWESEDTVLLV LKEIYQTQGIFLDQPLQ 6527 1 922 GWVPLLSRILPSDACKYYKQGINIRLDTTLIDFTDMKCORGDLS]]			ERAVQTDVVPYSPAISELIQSVLQKLQDPCPSSLASPDESEPDS
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G526 2 2034 SGRAGEPEEWRGRQIIDSKETWIPFNSEDSQQLEEAYSSGKGCN GRVVPTDGGRYDVHLGERMRYAVYWDELASEVRRCTWFYKGDKD NKYVPYSESFSQVLEETYMLAVTLDEWKKKLESPNREIIILHNP KLMVHYQPVAGSDDWGSTPMEQGRPRTVKRGVENISVDIHCGEP LQIDHLVPVVHGIGPACDLRFRSIVQCVNDFRSVSLNLLQTHFK KAQENQQIGRVEFLPVNWHSPLHSTGVDVDLQRITLPSINRLRH FTNDTILDVPFYNSPTYCQTIVDTVASEMWRIYTLFLQRNPDFK GGVSIAGHSLGSILFDILTNOKDSLGDIDSEKGSLNIVMDQGD TPTLEEDLKKLQLSEFFDIFEKBKVDKEALALCTDRDLQEIGIP LGPRKKILNYFSTRKNSMGIKRPAPQPASGANIPKESEFCSSSN TRNGDYLDVGIGQVSVKYPRLIYKPEIFFAFGSPIGMFLTVRGL KRIDPNYRFPTCKGFFNIYHPFDPVAYRIEPMVVPGVEFEPMLI PHHKGRKRMHLELREGLTRMSMDLKNNLLGSLRMAWKSFTRAPY PALQASETPEETEAPESTSEKPSDVNTEETSVAVKEEVLPINV GMLNGGQRIDYVLQEKPIESFNEYLFALQSHLCYWESEDTVLLV LKEIYQTQGIFLDQPLQ 6527 1 922 GWVPLLSRILPSDACKIYKQGINIRLDTTLIDFTDMKCORGDLS	1 1			LMRELDFAACVEERLDGVIPLARGGVVRQYWSSSFLVDLLAVAA
GRAGEPEEWRGRQIIDSKETWIPFNSEDSQQLEEAYSSGKGCN GRVVPTDGGRYDVHLGERMRYAVYWDELASEVRRCTWFYKGDKD NKYVPYSESFSQVLEETYMLAVTLDEWKKKLESPNREIIILHNP KLMVHYQPVAGSDDWGSTPMEQGRPRTVKRGVENISVDIHCGEP LQIDHLVPVVHGIGPACDLRFRSIVQCVNDFRSVSLNLLQTHFK KAQENQQIGRVEFLPVNWHSPLHSTGVDVDLQRITLESINRLRH FTNDTILDVPFYNSPTYCQTIVDTVASEMNRIYTLFLQRNPDFK GGVSIAGHSLGSLILFDILTNQKDSLGDIDSEKGSLNIVMDQGD TPTLEEDLKKLQLSEFFDIFEKEKVDKEALALCTDRDLQEIGIP LGPRKKILNYFSTRKNSMGIKRPAPQPASGANIPKESEFCSSSN TRNGDYLDVGIGQVSVKYPRLIYKPEIFFAFGSPIGMFLTVRGL KRIDPNYRFPTCKGFFNIYHPFDPVAYRIEPMVVPGVEFEPMLI PHKGRKRMHLELREGLTRMSMDLKNNLLGSLRMSWFSTRAPY PALQASETPEETEAEPESTSEKPSDVNTEETSVAVKEEVLPJINV GMLNGGQRIDYVLQEKPIESFNEYLFALQSHLCYWESEDTVLLV LKEIYQTQGIFLDQPLQ 6527 1 922 GWVPLLSRILPSDACKTYKQGINIRLDTTLIDFTDMKCORGDLS	1 1	Í		PVVPTVLWAFSTQRGGTDPVYNIGALLRGCCVVALHSLRRTAFR
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KLMVHYQPVAGSDDWGSTPMEQGRPRTVKRGVENISVDIHCGEP LQIDHLVFVVHGIGPACDLRFRSIVQCVNDFRSVSLNLLQTHFK KAQENQQIGRVEFLPVNWHSPLHSTGVDVDLQRITLBSINRLRH FTNDTILDVFFYNSPTYCQTIVDTVASEMNRIYTLFLQRNPDFK GGVSIAGHSLGSLILFDILTNQKDSLGDIDSEKGSLNIVMDQGD TPTLEEDLKKLQLSEFFDIFEKEKVDKEALALCTDRDLQEIGIP LGPRKKILNYFSTRKNSMGIKRPAPQPASGANIPKESEFCSSSN TRNGDYLDVGIGQVSVKYPRLIYKPEIFFAFGSPIGMFLTVRGL KRIDPNYRFPTCKGFFNIYHPFDPVAYRIEPMVVPGVEFEPMLI PHHKGRKRMHLELREGLTRMSMDLKNNLLGSLRMAWKSFTRAPY PALQASETPEETESEPESTEKPSDVNTEETSVAVKEEVLPINV GMLNGGQRIDYVLQEKPIESFNEYLFALQSHLCYWESEDTVLLV LKEIYQTGGIFLDQPLQ 6527 1 922 GWVPLLSRILPSDACKTYKQGINIRLDTTLIDFTDMKCORGDLS	l i	ł		NKYVDYCEGEGOVI ERTYMI AUTO BEWEGGE EGOVI ERTYMI AUTO BEWEGGE
LQIDHLVFVVHGIGPACDLRFRSIVQCVNDFRSVSLNILQTHFK KAQENQQIGRVEFILPVNWHSPLHSTGVDVDLQRITLPSINRLRH FINDTILDVFFYNSPTYCQTIVDTVASEMMRIYTLFLQRNPDFK GGVSIAGHSLGSLILFDILTNQKDSLGDIDSEKGSLNIVMDQGD TPTLEEDLKKLQLSEFFDIFEKEKVDKEALALCTDRDLQEIGIP LGPRKKILNYFSTRKNSMGIKRPAPQPASGANIPKESEFCSSSN TRNGDYLDVGIGQVSVKYPRLIYKPEIFFAFGSPIGMFLTVRGL KRIDPNYRFPTCKGFFNIYHPFDPVAYRIEPMVVPGVEFEPMLI PHHKGRKRMHLELREGLTRMSMDLKNNLLGSLRMAWKSFTRAPY PALQASETPEETEAPPESTSEKPSDVNTEETSVAVKEEVLPINV GMLNGGQRIDYVLQEKPIESFNEYLFALQSHLCYWESEDTVLLV LKEIYQTQGIFLDQPLQ 6527 1 922 GWVPLLSRILPSDACKTYKQGINIRLDTTLIDFTDMKCORGDLS	1			KI.M/HYODVAGGDDUGGTDMEOGDDDTUVDGUGGTDMEIIILHND
KAQENQQIGRVEFLPVNWHSPLHSTGVDVDLQRITLPSINRLRH FTNDTILDVFFYNSPTYCQTIVDTVASEMNRIYTLFLQRNPDFK GGVSLAGHSLGSLILFDILTNQKDSLGDIDSEKGSLNIVMDQGD TPTLEEDLKKLQLSEFFDIFEKEKVDKEALALCTDRDLQEIGIP LGPRKKLLNYFSTRKNSMGIKRPAPQPASGANIPKESEFCSSSN TRNGDYLDVGIGQVSVKYPRLIYKPEIFFAFGSPIGMFLTVRGL KRIDPNYRFPTCKGFFNIYHPFDPVAYRIEPMVVPGVEFEPMLI PHHKGRKRMHLELREGLTRMSMDLKNNLLGSLRMAWKSFTRAPY PALQASETPEETEAEPESTSEKPSDVNTEETSVAVKEEVLPINV GMLNGGQRIDYVLQEKPIESFNEYLFALQSHLCYWESEDTVLLV LKEIYQTQGIPLDQPLQ 6527 1 922 GWVPLLSRILPSDACKIYKQGINIRLDTTLIDFTDMKCORGDLS	l i			
FTNDTILDVFFYNSPTYCQTIVDTVASEMNRIYTLFLQRNPDFK GGVSIAGHSLGSLILFDILTNQKDSLGDIDSEKGSLNIVMDQGD TPTLEEDLKKLQLSEFFDIFEKEKVDKEALALCTDRDLQEIGIP LGPRKKLLNYFSTRKNSMGIKRPAPQPASGANIPKESEFCSSSN TRNGDYLDVGIGQVSVKYPRLIYKPEIFFAFGSPIGMFLTVRGL KRIDPNYRFPTCKGFFNIYHPFDPVAYRIEPMVVPGVEFEPMLI PHHKGRKRMHLELREGLTRMSMDLKNNLLGSLRMAWKSFTRAPY PALQASETPEETEAEPESTSEKPSDVNTEETSVAVKEEVLPINV GMLNGGQRIDYVLQEKPIESFNEYLFALQSHLCYWESEDTVLLV LKEIYQTQGIPLDQPLQ 6527 1 922 GWVPLLSRILPSDACKIYKQGINIRLDTTLIDFTDMKCORGDLS	!			KAOENOOIGRVEFT.PVNWWSPLHSTGVDVDI OP INI DOZWIE DI
GGVSIAGHSLGSLILFDILTNQKDSLGDIDSEKGSLNIVMDQGD TPTLEEDLKKLQLSEFFDIFEKEKVDKEALALCTDRDLQEIGIP LGPRKKILNYFSTRKNSMGIKRPAPQPASGANIPKESEFCSSSN TRNGDPLDVGIGQVSVKYPRLIYKPEIFFAFGSPIGMFLTVRGL KRIDPNYRFPTCKGFFNIYHPFDPVAYRIEPMVVPGVEFEPMLI PHHKGRKRMHLELREGLTRMSMDLKNNLLGSLRMAWKSFTRAPY PALQASETPEETBAEPESTSEKPSDVNTEETSVAVKEEVLPINV GMLNGGQRIDVVLQEKPIESFNEYLFALQSHLCYWESEDTVLLV LKEIYQTQGIFLDQPLQ 6527 1 922 GWVPLLSRILPSDACKIYKQGINIRLDTTLIDFTDMKCORGDLS		}		FINDTILDVFFYNSPTYCOTIVDTVASRMVRIVTI.FLORNDDDV
TPTLEEDLKKLQLSEFFDIFEKEKVDKEALALCTDRDLQEIGIP LGPRKKILNYFSTRKNSMGIKRPAPQPASGANIPKESEFCSSSN TRNGDYLDVGIGQVSVKYPRLIYKPEIFFAFGSPIGMFLTVRGL KRIDPNYRFPTCKGFFNIYHPFDPVAYRIEPMVVPGVEFEPMLI PHHKGRKRMHLELREGLTRMSMDLKNNLLGSLRMAWKSFTRAPY PALQASETPEETBAEPESTSEKPSDVNTEETSVAVKEEVLPINV GMLNGGQRIDYVLQEKPIESFNEYLFALQSHLCYWESEDTVLLV LKEIYQTQGIFLDQPLQ 6527 1 922 GWVPLLSRILPSDACKIYKQGINIRLDTTLIDFTDMKCORGDLS	• 1	1	•	GGVSIAGHSLGSLILFDILTNOKDSLGDIDSEKGSLNTIMDOGD
LGPRKKILNYFSTRKNSMGIKRPAPQPASGANIPKESEFCSSSN TRNGDYLDVGIQQVSVKYPRLIYKPEIFFAFGSPIGMFLTVRGL KRIDPNYRFPTCKGFFNIYHPFDPVAYRIEPMVVPGVEFEPMLI PHHKGRKRMHLELREGLTRMSMDLKNNLLGSLRMAWKSFTRAPY PALQASETPEETEAEPESTSEKPSDVNTEETSVAVKEEVLPINV GMLNGGQRIDYVLQEKPIESFNEYLFALQSHLCYWESEDTVLLV LKEIYQTQGIFLDQPLQ 6527 1 922 GWVPLLSRILPSDACKIYKQGINIRLDTTLIDFTDMKCORGDLS	1		į	TPTLEEDLKKLQLSEFFDIFEKEKVDKEALALCTDPDLOPTCTP
TRNGDYLDVGIGQVSVKYPRLIYKPEIFFAFGSPIGMFLTVRGL KRIDPNYRFPTCKGFFNIYHPFDPVAYRIEPMVVPGVEFEPMLI PHHKGRKRMHLELREGLTRMAWKJETRAPY PALQASETPEETEAEPESTSEKPSDVNTEETSVAVKEEVLPINV GMLNGGQRIDYVLQEKPIESFNEYLFALQSHLCYWESEDTVLLV LKEIYQTGGIFLDQPLQ 6527 1 922 GWVPLLSRILPSDACKIYKQGINIRLDTTLIDFTDMKCORGDLS		}		LGPRKKILNYFSTRKNSMGIKRPAPOPASGANIPKESRFCGGGN
KRIDPNYRFPTCKGFFNIYHPFDPVAYRIEPMVVPGVEFEPMLI PHHKGRKRMHLELREGLTRMSMDLKNNLLGSLRMAWKSFTRAPY PALQASETPEETEAEPESTSEKPSDVNTEETSVAVKEEVLPINV GMLNGGQRIDYVLQEKPIESFNEYLFALQSHLCYWESEDTVLLV LKEIYQTQGIFLDQPLQ 6527 1 922 GWVPLLSRILPSDACKIYKQGINIRLDTTLIDFTDMKCORGDLS		1		TRNGDYLDVGIGQVSVKYPRLIYKPEIFFAFGSPIGMFLTVPGI.
PHHKGRKRMHLELREGLTRMSMDLKNNLLGSLRMAWKSFTRAPY PALQASETPEETEAEPESTSEKPSDVNTEETSVAVKEEVLPINV GMLNGGQRIDYVLQEKPIESFNEYLFALQSHLCYWESEDTVLLV LKEIYQTQGIFLDQPLQ 6527 1 922 GWVPLLSRILPSDACKIYKQGINIRLDTTLIDFTDMKCORGDLS	1	• 1		KRIDPNYRFPTCKGFFNIYHPFDPVAYRIEPMVVPGVEFEPMLT
PALQASETPEETRAEPESTSEKPSDVNTEETSVAVKEEVLPINV GMLNGGQRIDYVLQEKPIESFNEYLFALQSHLCYWESEDTVLLV LKEIYQTQGIFLDQPLQ 6527 1 922 GWVPLLSRILPSDACKIYKQGINIRLDTTLIDFTDMKCORGDLS				PHHKGRKRMHLELREGLTRMSMDLKNNLLGSLRMAWKSFTRAPY
GMLNGGQRIDYVLQEKPIESFNEYLFALQSHLCYWESEDTVLLV LKEIYQTQGIFLDQPLQ 6527 1 922 GWVPLLSRILPSDACKIYKQGINIRLDTTLIDFTDMKCORGDLS	ļ	ļ		PALQASETPEETRAEPESTSEKPSDVNTEETSVAVKEEVLPINV
6527 1 922 GWUPLLSRILPSDACKIYKQGINIRLDTTLIDFTDMKCORGDLS			I	GMLNGGQRIDYVLQEKPIESFNEYLFALQSHLCYWESEDTVLLV
GWVPDLSRIDPSDACKIYKQGINIRLDTTLIDFTDMKCORGDLS	CE38			LKEIYQTQGIFLDQPLQ
FIFNGDAAPSESFVVLDNEOKVYORIHHEESEMETERBUTTIME	034/	1	922	GWVPLLSRILPSDACKIYKQGINIRLDTTLIDFTDMKCQRGDLS
and the second s	-		İ	FIFNGDAAPSESFVVLDNEQKVYQRIHHEESEMETEEEVDILMS
SDIYSATLSTKSISFTRAQTGWLFREDKTERVGNFLADFYLVNG				SDIYSATLSTKSISFTRAQTGWLFREDKTERVGNFLADFYLVNG

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L-Leucine, M-Methionine, N-Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
i	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	_	\=possible nucleotide insertion)
			LVLESRKRREHLSEEDILRNKAIMESLSKGGNIMEQNFEPIRRO
1			SLTPPPQNTITWEEYISAENGKAPHLGRELVCKESKKTFKATIA
ļ			MSQEFPLGIELLLNVLBVVAPFKHFNKLREFVQMKLPPGFPVKL
			DIPVFPTITATVTFQEFRYDEFDGSIFTIPDDYKEDPSRFPDL
6528	1	1073	LTGPAAAEPRCAADAGMKRALGRRKGVWLRLRKILFCVLGLYIA
			IPPLIKLCPGIQAKLIFLNFVRVPYFIDLKKPQDQGLNHTCNYY
1			LQPEEDVTIGVWHTVPAVWWKNAQGKDQMWYEDALASSHPIILY
1			LHGNAGTRGGDHRVELYKVLSSLGYHVVTFDYRGWGDSVGTPSE
1			RGMTYDALHVFDWIKARSGDNPVYIWGHSLGTGVATNLVRRLCE
			RETPPDALILES?FTNIREEAKSHPFSVIYRYFPGFDWFFLDPI
1 1			TSSGIKFANDENVKHISCPLLILHAEDDPVVPFQLGRKLYSIAA
1 1		•	PARSFRDFKVQFVPFHSDLGYRHKYIYKSPELPRILREFLGKSE
<u> </u>			РЕНОН
6529	363	2215	THIRYNKIGVVKTMSCGNEFVETLKKIGYPKADNLNGEDFDWLF
			EGVEDESFLKWFCGNVNEQNVLSERELEAFSILQKSGKPILEGA
ĺ	·		ALDRALKTCKTSDLKTPRLDDKELEKLEDEVQTLLKLKNLKIQR
l			RNKCQLMASVTSHKSLRLNAKEEEATKKLKQSQGILNAMITKIS
			NELQALTDEVTQLMMFFRHSNLGQGTNPLVFLSQFSLEKYLSQE
l i			EQSTAALTLYTKKQFFQGIHEVVESSNESQFFNFLKIQTPSICD
			NQEILEERRLEMARLQLAYICAQHQLIHLKASNSSMKSSIKWAE
]			ESLHSLTSKAVDKENLDAKISSLTSEIMKLEKEVTOIKDRSLPA
1 1			VVRENAQLLNMPVVKGDFDLQIAKQDYYTARQELVLNQLIKOKA
!!			SFELLQLSYEIELRKHRDIYRQLENLVQELSQSNMMLYKOLEML
i I			TDPSVSQQINPRNTIDTKDYSTHRLYQVLEGENKKKELFLTHGN
1 1			LEEVAEKLKONISLVODQLAVSAQEHSFFLSKRNKDVDMLCDTL
1 1			YQGGNQLLLSDQELTEQPHKVESQLNKLNHLLTDILADVKTKRK
			TLANNKLHOMEREFYVYFLKDEDYLKDIVENLETOSKIKAVSLE
6530	- 120		D
8530	128	2986	GAAHHGAIVQVHPLLPGSSTIMIHDLCLVFPAPAKAVVYVSDIQ
-			ELYIRVVDKVBIGKTVKAYVRVLDLHKKPFLAKYFPFMDLKLRA
			ASPIITLVALDEALDNYTITFLIRGVAIGQTSLTASVTNKAGQR
1			INSAPQQIEVFPPFRLMPRKVTLLIGATMQVTSEGGPQPQSNIL
			FSISNESVALVSAAGLVQGLAIGNGTVSGLVQAVDAETGKVVII
			SQDLVQVEVLLLRAVRIRAP_MRMRTGTQMPIYVTGITNHQNPF
			SFGNAVPGLTFHWSVTKRDVLDLRGRHHEASIRLPSQYNFAMNV
		İ	LGRVKGRTGLRAVVKAVDPTSGQLYGLARELSDEIQVQVFEKLQ
			LLNPEIEAEQILMSPNSYIKLQTNRDGAASLSYRVLDGPEKVPV VHVDEKGFLASGSMIGTSTIEVIAQEPFGANQTIIVAVKVSPVS
1	}		VI.DUCMCDULUTONICERI URIDI CUTTUMORTHI URIDI CUTTUMORTI CUTTUMORTI CUTTUMORTHI URIDI CUTTUMORTI CUTTUMORTI CUTTUMORTI CUTTUMORTI CUTTUMORT
			YLRVSMSPVLHTQNKEALVAVPLGMTVTFTVHFHDNSGDVFHAH SSVLNFATNRDDFVQIGKGPTNNTCVVRTVSVGLTLLRVWDAKH
	j	j	PGLSDFMPLPVLQAISPELSGAMVVGDVLCLATVLTSLEGLSGT
1			WSSSANSILHIDPKTGVAVARAVGSVTVYYEVAGHLRTYKEVVV
	İ	ļ	SVPQRIMARHLHPIQTSFQEATASKVIVAVGDRSSNLRGECTPT
		ļ	QREVIQALHPETLISCQSQFKPAVFDFPSQDVFTVEPQFDTALG
		1	QYFCSITMHRLTDKQRKHLSMKKTALVVSASLSSSHFSTEQVGA
		1	EVPFSPGLFADQAEILLSNHYTSSEIRVFGAPEVLENLEVKSGS
l	i	1	PAVLAFAKEKSFGWPSFITYTVGVLDPAAGSQGPLSTTLTFSSP
Į.	(Ì	VTNQAIAIPVTVAFVVDRRGPGPYGASLFQHFLDSYQVMFFTLF
i			ALLACTAUMTTAVUTUCTORDI AURAN MORA ORGANI
1	l	1	ALLAGTAVMI IAYHTVCTPRDLAVPAALTPRASPGHSPHYFAAS
6531	845	1425	SPTSPNALPPARKASPPSGLWSPAYASH
		±443	PSASIPPSASPDPVPDIRTCHFCLVEDPSVGCISGSEKCTISSS
1	ł	1	SLCMVITIYYDVKVRFIVRGCGQYISYRCQEKRNTYFABYWYQA
1	i	•	QCCQYDYCNSWSSPQLQSSLPEPHDRPLALPLSDSQIQWFYQAL
1	I		
			NLSLPLPNFHAGTEPDGLDPMVTLSLNLGLSFAELRRMYLFLNS
6532	2		NLSDPDPNFHAGTEPDGLDPMVTLSINLGLSFAELRRMYLFINS SGLLVLPQAGLLTPHPS AAGPPSEVVNQDSLFPEPEPGPAPQVLLGPQGPGLIKGVAPPTL

SEO	Prodicted	(Bandla Sada	
ID	Predicted beginning	Predicted end	Amino acid segment containing signal peptide
NO:	nucleotide	nucleotide location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1 20.	location	1	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	corresponding	corresponding to first	H=Histidine, I=Isoleucine, K=Lysine,
l.	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
i	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
İ	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
4	sequence	Seduction	Codon, /=possible nucleotide deletion,
	104.00.00		\=possible nucleotide insertion)
f			ITDSTGTHLVLTVTNKNAHSPGLSRGSPQQPSSQPGSPAPAPSA
			QMDLEHPLQPLFGTPTSLLKKEPPGYEEAMSQQPKQQENGSSSQ
I			QMDDLFDILIQSGEISADFKEPPSLPGKEKPSPKTVCWSPLAAQ
İ			PSPSAELPQAAPPPPGSPSLPGRLEDFLESSTGLPLLTSGHDGP EPLSLIDDLHSQMLSSTAILDHPPSPMDTSELHFVPEPSSTMGL
		,	DLADGHLDSMDWLELSSGGPVLSLAPLSTTAPSLPSTDFLDGHD
1)		LOLHWDSCL
6533	1798	373	STISWLARVEPPRRSSGVGAARLRFPGGSRPLRARACVLALAVL
1	1	3.3	ALLERNNADSMSAHSMLCERIAIAKELIKRAESLSRSRKGGIEG
			GAKLCSKLKAELKFLQKVEAGKVAIKESHLQSTNLTHLRAIVES
}	!		AENLEEVVSVLHVFGYTDTLGEKQTLVVDVVANGGHTWVKAIGR
i	1		KAEALHNIWLGRGQYGDKSIIEQAEDFLQASHQQPVQYSNPHII
ł	l		FAFYNSVSSPMAEKLKEMGISVRGDIVAVNALLDHPEELQPSES
İ			ESDDEGPELLQVTRVDRENILASVAFPTEIKVDVCKRVNLDITT
			LITYVSALSYGGCHFIFKEKVLTEQAEQERKEQVLPQLEAFMKD
		· ·	KELFACESAVKDFQSILDTLGGPGERERATVLIKRINVVPDQPS
			ERALRLVASSKINSRSLTIFGTGDTLKAITMTANSGFVRAANNO
			GVKFSVFIHQPRALTESKEALATPLPKDYTTDSEH
6534	47	596	KATRFISAAFVVLNKQGVSPAKLPHTSWSWSLQTLSFLFSGDLA
	1		EKSLQCFPCSAMLLELIPLLGIHFVLRTARAQSVTQPDIHITVS
			EGASLELRCNYSYGATPYLFWMERTVEEAFILLVCLKPWRVASS
.			LEKKEKEDESFQLLLGSRYNVLKAHCLLPLIRWLTSGDSLLSAQ
			PHCPQGL
6535	250	964	LIKTFFRDVAIQRDLLPKEKNLETLLTLAFLEIDKAFSSHARLS
	į.		ADATLLTSGTTATVALLRDGIELVVASVGDSRAILCRKGKPMKL
1			TIDHTPERKDEKERIKKCGGFVAWNSLGQPHVNGRLAMTRSIGD
1	İ		LDLKTSGVIAEPETKRIKLHHADDSPLVLTTDGINFMVNSQEIW
	· ·		DFVNQCHDPNEAAHAVTEQAIQYGTEDNSTAVVVPFGAWGKYKN
6536	242		SEINFSFSRSFASSGRWA
0550	242	1174	SLVKEMTNQYGILFKQEQAHDDAIWSVAWGTNKKENSETVVTGS
J i	1		LDDLVKVWKWRDERLDLQWSLEGHQLGVVSVDISHTLPIAASSS
1	ì	1	LDAHIRLWDLENGKQIKSIDAGPVDAWTLAFSPDSQYLATGTHV
			GKVNIFGVESGKKEYSLDTRGKFILSIAYSPDGKYLASGAIDGI
1 1	ľ		INIFDIATGKLLHTLEGHAMPIRSLTFSPDSQLLVTASDDGYIK
1 1			IYDVQHANLAGTLSGHASWVLNVAFCPDDTHFVSSSSDKSVKVW
1 1			DVGTRTCVHTFFDHQDQVWGVKYNGNGSKIVSVGDDQEIHIYDC PI
6537	1638	921	NRFNPPPTQGPDPSLVYRPDVDPEVAKDKASFRNYTSGPLLDRV
	-		FTTYKLMHTHQTVDFVRSKHAQFGGFSYKKMTVMEAVDLLDGLV
1 1			DESDPDVDFPNSFHAFQTAEGIRKAHPDKDWFHLVGLLHDLGKV
1			LALFGEPQWAVVGDTFPVGCRPQASVVFCDSTFQDNPDLQDPRY
1 1	1		STELGMYQPHCGLDRVLMSWGHDGEARGGQWGGGGRWGTVGGGG
			AEAVPAGDTLSPQSTCTR
6538	3345	2412	PYLYDFLDALITCQTAPEEAFIKLDGLAGMLTEQLRRLTKQVOE
į l	j		ARHNRDDEAIKKAVNEYDETMEKYIPVLMAQAKIYWNLENYPMV
,	ŀ		EKIFRKSVEFCNDHDVWKLNVAHVLFMQENKYKEAIGFYEPIVK
{			KHYDNILNVSAIVLANLCVSYIMTSQNEKAEELMRKIEKEEEQL
	ł	·	SYDDPNRKMYHLCIVNLVIGTLYCAKGNYBFGISRVIKSLEPYN
1 1	1	Ì	KKLGTDTWYYAKRCFLSLLENMSKHMIVIHDSVIQECVQFLGHC
		ļ	ELYGTNIPAVIEQPLEEERMHVGKNTVTDESRQLKALIYEIIGW
			NK
6539	218	339	FLGAASPHPHFSSLAPHPDQPEFTPVQDELEAMELWGPGV
6540	3	391	LERLWLLLLRRPEDAMAECPTLGEAVTDHPDRLWAWEKFVYLDE
	ļ	J	KQHAWLPLTIEIKDRLQLRVLLRREDVVLGRPMTPTQIGPSLLP
			IMWQLYPDGRYRSSDSSFWRLVYHIKIDGVBDMLLELLPDD

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
1D	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ł	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	554455	\=possible nucleotide insertion)
6541	1165	536	RTLVQRRILMLLRKPARGRDLRGRGRGTPRGGRKGLLPTPDEFP
		330	RIDAGERI BURDEN DENGEN BERGER
			RFEGGRKPDSWDGNREPGPGHEHFRDTPRPDHPPHDGHSPASRE
İ			RSSSLQGMDMASLPPRKRPWHDGPGTSEHREMEAPGGPSEDRGG
1	1		KGRGGPGPAQRVPKSGRSSSLDGEHHDGYHRDEPFGGPPGSGTP
6542	3	3775	SRGGRSGSNWGRGSNMNSGPPRRGASRGGGRGR
0342	,	37/5	SWPRGRGETGGHPGALRTRTMQKSVRYNEGHALYLAFLARKEGT
1	1		KRGFLSKKTAEASRWHEKWFALYQNVLFYFEGEQSCRPAGMYLL
1 .			EGCSCERTPAPPRAGAGQGGVRDALDKQYYFTVLFGHEGQKPLE
	[LRCEEEQDGKEWMEAIHQASYADILIEREVLMQKYIHLVQIVET
1			EKIAANQLRHQLEDQDTEIERLKSEIIALNKTKERMRPYQSNQE
ĺ			DEDPDIKKIKKVQSFMRGWLCRRKWKTIVQDYICSPHAESMRKR
1			NQIVFTMVEAESEYVHQLYILVNGFLRPLRMAASSKKPPISHDD
1]		VSSIFLNSETIMFLHEIFHQGLKARIANWPTLILADLFDILLPM
			LNIYQEFVRNHQYSLQVLANCKQNRDFDKLLKQYEANPACEGRM
ł			LETFLTYPMFQIPRYIITLHELLAHTPHEHVERKSLEFAKSKLE
			ELSRVMHDEVSDTENIRKNLAIERMIVEGCDILLDTSQTFIRQG
			SLIQVPSVERGKLSKVRLGSLSLKKEGERQCFLFTKHFLICTRS
	, [SGGKLHLLKTGGVLSLIDCTLIEEPDASDDDSKGSGQVFGHLDF
1			KIVVEPPDRAAFTVVLLAPSRQEKAAWMSDISQCVDNIRCNGLM
į			TIVFEENSKVTVPHMIKSDARLHKDDTDICFSKTLNSCKVPQIR
			YASVERLLERLTDLRFLSIDFLNTFLHTYRIFTTAAVVLGKLSD
			IYKRPFTSIPVRSLELFFATSQNNRGEHLVDGKSPRLCRKFSSP
			PPLAVSRTSSPVRARKLSLTSPLNSKIGALDLTTSSSPTTTTQS
1			PAASPPPHTGQIPLDLSRGLSSPEQSPGTVEENVDNPRVDLCNK
		i	LKRSIQKAVLESAPADRAGVESSPAADTTELSPCRSPSTPRHLR
	•	* *	YROPGGOTADNAHCSVSPASAFAIATAAAGHGSPPGFNNTERTC
			DKEFIIRTATNRVLNVLRHWVSKHAQDFELNNELKMNVLNLLE
			EVLRDPDLLPQERKAAANILMALSQDDQDDIHLKLEDIIQMTDC
			MKAECFESLSAMELAEQITLLDHVIFRSIPYEEFLGQGWMKLDK
1			NERTPYIMKTSQHFNDMSNLVASQIMNYADVSSRANAIEKWVAV
1 1			ADICRCLHNYNGVLEITSALNRSAIYRLKKTWAKVSKQTKALMD
}			KLQKTVSSEGRFKNLRETLKNCNPPAVPYLGMYLTDLAFIEEGT
			PNFTEEGLVNPSKMRMISHIIREIRQFQQTSYRIDHQPKVAQYL
6543	1857	950	LDKDLIIDEDTLYELSLKIEPRLPA
7773	103/	UCE	FVSGCGRAGIGLSWAMAAEARVSRWYFGGLASCGAACCTHPLDL
		•	LKVHLQTQQEVKLRMTGMALRVVRTDGILALYSGLSASLCRQMT
			YSLTRFAIYETVRDRVAKGSQGPLPFHEKVLLGSVSGLAGGFVG
1 1	1		TPADLVNVRMQNDVKLPQGQRRNYAHALDGLYRVAREEGLRRLF
		•	SGATMASSRGALVTVGQLSCYDQAKQLVLSTGYLSDNIFTHFVA
		1	SFIAGGCATFLCQPLDVLKTRLMNSKGEYQGVFHCAVETAKLGP
6544	630	79	LAFYKGLVPAGIRLIPHTVLTFVFLEQLRKNFGIKVPS
"""	0.50	19	PSPCFIRSRLDGQPWMAGLEAWLSQNFSLHQPQSRVRVRRASIS
[1	İ		EPSDTDPEPRTLNPSPAGWFVQQHPBLELMSSFRERFGRNWLQY
j i			RSHLEPSGNPLPATPTTSAPSAPPASSQGPDTAPRPSPPQEEAR
	ſ	ĺ	GPQESPQKMSEEVRAEPQEEEEEKEGKEEKEGEMAPLPEAHLG
L CEAE			EGKQKECP
6545	176	560	PPHSHAALLPAAMTPLLTLILVVLMGLPLAQALDCHVCAYNGDN
, 1	-		CFNPMRCPAMVAYCMTTRTYYTPTRMKVSKSCVPRCFETVYDGY
 			SKHASTTSCCQYDLCNGTGLATPATLALAPILLATLWGLL
6546	1657	364	HLLNGLDEVAAFFVADLGAIVRKHFCFLKCLPRVRPFYAVKCNS
, ,		1	SPGVLKVLAQLGLGFSCANKARMELVQHIGIPASKIICANPCKQ
	j		IAQIKYAAKHGIQLLSFDNEMELAKVVKSHPSAKMVLCIATDDS
			HSLSCLSLKFGVSLKSCRHLLENAKKHHVEVVGVSFHIGSGCPD
	İ		PQAYAQSIADARLVFEMGTELGHKMHVLDLGGGFPGTEGAKVRF
] }	}		EEIASVINSALDLYFPEGCGVDIFAELGRYYVTSAPTVAVSIIA
			KKEVLLDQPGREEENGSTSKTIVYHLDEGVYGIFNSVLFDNICP
			

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ı	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
		<u> </u>	TPILQKKPSTEQPLYSSSLWGPAVDGCDCVAEGLWLPQLHVGDW
ì			LVFDNMGAYTVGMGSPFWGTQACHITYAMSRVAWEALRRQLMAA
ļ			EQEDDVEGVCKPLSCGWEITDTLCVGPVFTPASIM
6547	1	541	LHSKYLAPALCSQPGMMRCCRRRCCCROPPHALRPLILLIPINI
			PPLAAAAAGPNRCDTIYQGFAECLIRLGDSMGRGGELETICRSW
			NDFHACASQVLSGCPEEAAAVWESLQQEARQAPRPNNLHTLCGA
			PVHVRERGTGSETNQETLRATAPALPMAPAPPLLAAALALAYLL
6548	 		RPLA
) 5346	2	219	FVSRLSVRDVRFPTFLGGHGADAMHTDPDYSAAYVPIETDAEDG
6549	73	1490	IKGCGITFTLGKGTEVGELKILSRFQNA
	''	1430	ETGRVCEDARPACGSRSRRRRKEAAPGIPTPSPSSSSPTSSRPA
1			ARAFSKAPARLSRPRAREEPPDPGRRYIQEEIIQARKHKLIKMC
			SSVAAKLWFLTDRRIREDYPQKEILRALKAKCCEEELDFRAVVM DEVVLTIEQGNLGLRINGELITAYPQVVVVRVPTPWVQSDSDIT
Ì			VLRHLEKMGCRLMNRPQAILNCVNKFWTFQELAGHGVPLPDTFS
			YGGHENFAKMIDEAEVLEFPMVVKNTRGHRGKAVFLARDKHHLA
1			DLSHLIRHEAPYLFQKYVKESHGRDVRVIVVGGRVVGTMLRCST
1	ļ		DGRMQSNCSLGGVGMMCSLSEQGKQLAIQVSNILGMDVCGIDLL
1			MKDDGSFCVCEANANVGFIAFDKACNLDVAGIIADYAASLLPSG
ŀ			RLTRRMSLLSVVSTASETSEPELGPPASTAVDNMSASSSSVDSD
L	·		PBSTERELLTKLPGGLFNMNQLLANEIKLLVD
6550	2293	922	FRVSRDGAPDCGIEQMGLAMEHGGSYARAGGSSRGCWYYLRYFF
			LFVSLIQFLIILGLVLFMVYGNVHVSTESNLOATERRAEGLVSO
			LLGLTASQSNLTKELNFTTRAKDAIMQMWLNARRDLDRINASFR
			QCQGDRVIYTNNQRYMAAIILSEKQCRDQFKDMNKSCDALLFML
1 1			NQKVKTLEVEIAKEKTICTKDKESVLLNKRVAEEQLVECVKTRE
1			LQHQERQLAKEQLQKVQALCLPLDKDKFEMDLRNLWRDSIIPRS
١,			LDNLGYNLYHPLGSELASIRRACDHMPSLMSSKVEELARSLRAD
			IERVARENSDLQRQKLEAQQGLRASQEAKQKVEKEAQAREAKLQ AECSRQTQLALEEKAVLRKERDNLAKELEEKKREAEQLRMELAI
1 1			RNSALDTCIKTKSQPMMPVSRPMGPVPNPQPIDPASLEEFKRKI
1 1			LESQRPPAGIPVAPSG
6551	157	748	IQPPDPRNMTLAAYKEKMKELPLVSLFCSCFLADPLNKSSYKYE
1 1		•	ADTVDLNWCVISDMEVIELNKCTSGQSFEVILKPPSFDGVPEFN
]	1		ASLPRRRDPSLEEIQKKLEAAEERRKYQEAELLKHLAEKREHER
	ļ	ļ	EVIQKAIEENNNFIKMAKEKLAQKMESNKENREAHLAAMLERLQ
6552			EKDKHAEEVRKNKELKEBASR
0002	157	748	IQPPDPRNMTLAAYKEKMKELPLVSLFCSCFLADPLNKSSYKYE
			ADTVDLNWCVISDMEVIELNKCTSGOSFEVILKPPSFDGVPEFN
			ASLPRRRDPSLEEIQKKLEAAEERRKYOEAELLKHLAEKREHER
			EVIQKAIEENNNFIKMAKEKLAQKMESNKENREAHLAAMLERLQ
6553	2	1807	EKDKHAEEVRKNKELKEEASR
	- 1	100/	FVWSKMAAHLSYGRVNLNVLREAVRRELREFLDKCAGSKAIVWD
]	Ì	BYLTGPFGLIAQYSLLKEHEVEKMFTLKGNRLPAADVKNIIFFV
	Ì	· '	RPRLELMDIIAENVLSEDRRGPTRDFHILFVPRRSLLCEQRLKD
	ľ	Ì	LGVLGSFIHREEYSLDLIPFDGDLLSMESEGAFKECYLEGDQTS
	1	İ	LYHAAKGLMTLQALYGTIPQIFGKGECARQVANMMIRMKREFTG SQNSIFPVFDNLLLLDRNVDLLTPLATQLTYEGLIDEIYGIQNS
!	1	ŀ	YVKLPPEKFAPKKQGDGGKDLPTEAKKLQLNSAEELYAEIRDKN
	İ		FNAVGSVLSKKAKI ISAAFEERHNAKTVGEIKQFVSQLPHMQAA
			RGSLANHTSIAELIKDVTTSEDFFDKLTVEQEFMSGIDTDKVNN
	1	1	YIEDCIAQKHSLIKVLRLVCLQSVCNSGLKQKVLDYYKREILQT
			YGYEHILTLHNLEKAGLLKPQTGGRNNYPTIRKTLRLWMDDVNE
	}		QNPTDISYVYSGYAPLSVRLAQLLSRPGWRSIEEVLRILPGPHF
		ł.	EERQPLPTGLQKKRQPGENRVTLIFFLGGVTFAEIAALRFLSOL
			EDGGTEYVIATTKLMNGTSWIEALMEKPF

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SEQ	Predicted	Predicted end	Amino acid segment contribution
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
f	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
{	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ſ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
i	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
<u> </u>	sequence	ľ	\=possible nucleotide insertion)
6554	119	1244	FEMGSQVSVESGALHVVIVGGGFGGIAAASQLQALNVPFMLVDM
i			KDSFHHNVAALRASVETGFAKKTFISYSVTFKDNFRQGLVVGID
			LKNOMVLLQGGEALPFSHLILATGSTGPFPGKFNEVSSQQAAIQ
	I		AYEDMVRQVQRSRFIVVVGGGSAGVEMAAEIKTEYPEKEVTLIH
]			SQVALADKELLPSVRQEVKEILLRKGVQLLLSERVSNLEELPLN
Ì			EYREYIKVQTDKGTEVATNLVILCTGIKINSSAYRKAFESRLAS
1	1 .		SGALRVNEHLQVEGHSNVYAIGDCADVRTPKMAYLAGLHANIAV
1	Í		ANIVNSVKQRPLQAYKPGALTFLLSMGRNDGVGQISGFYVGRLM
	<u></u>		VRLTKSRDLFVSTSWKTMRQSPP
6555	1552	498	IHMALLRKINQVLLFLLIVTLCVILYKKVHKGTVPKNDADDESE
1			TPEELEEEIPVVICAAAGRMGATMAAINSIYSNTDANILFYVVG
			LRNTLTRIRKWIEHSKLREINFKIVEFNPMGLKGKIRPDSSRPE
-			LLQPLNFVRFYLPLLIHQHEKVIYLDDDVIVOGDIOELYDTTLA
1			LGHAAAFSDDCDLPSAQDINRLVGLONTYMGYLDYRKKAIKDLG
			ISPSTCSFNPGVIVANMTEWKHORITKOLEKWMOKNVEENLYSS
1			SLGGGVATSPMLIVFHGKYSTINPLWHIRHLGWNPDARYSEHPT.
6556			QEAKLLHWNGRHKPWDFPSVHNDLWESWFVPDPAGIFKLNHHS
6336	241	1449	ASLCKGCFFVTHVLVIILPSLQSPPTFGFLLDIDGVLVRGHRVT
1			PAALKAFRRLVNSQGQLRVPVVFVTNAGNILQHSKAQELSALLG
1			CEVDADQVILSHSPMKLFSEYHEKRMLVSGOGPVMENAOGLGEP
			NVVTVDELRMAFPLLDMVDLERRLKTTPLPRNDFPRIEGVLLLG
1 . 1			EPVRWETSLQLIMDVLLSNGSPGAGLATPPYPHLPVLASNMDLL
1 1	1		WMAEAKMPRFGHGTFLLCLETIYQKVTGKELRYEGLMGKPSILT
1			YQYAEDLIRRQAERRGWAAPIRKLYAVGDNPMSDVYGANLFHQY
			LQKATHDGAPELGAGGTRQQQPSASQSCISILVCTGVYNPRNPQ
1 1	j		STEPVLGGGEPPFHGHRDLCFSPGLMEASHVVNDVNEAVQLVFR KEGWALE
6557	2598	1534	
1]	·		RMCGRTSCHLPRDVLTRACAYQDRRGQQRLPEWRDPDKYCPSYN KSPQSN9PVLLSRLHFEKDADSSERIIAPMRWGLVPSWFKESDP
}		*	SKLQFNTTNCRSDTVMEKRSFKVPLGKGRRCVVLADGFYEWQRC
1 1			QGTNQRQPYFIYFPQIKTEKSGSIGAADSPENWEKVWDNWRLLT
] [MAGIFDCWEPPEGGDVLYSYTIITVDSCKGLSDIHHRMPAILDG
1 1			EEAVSKWLDFGEVSTQEALKLIHPTENITFHAVSSVVNNSRNNT
]]			PECLAPVOLVVKKELRASGSSQRMLQWLATKSPKKEDSKTPQKE
1 1			ESDVPQWSSQFLQKSPLPTKRGTAGLLEQWLKREKEEEPVAKRP
			YSQ
6558	21	1138	FHGRRRGGRKMELGSCLEGGREAAEEEGEPEVKKRRLLCVEFAS
1	•		VASCDAAVAQCFLAENDWEMERALNSYFEPPVEESALERRPETI
] [-		SEPKTYVDLTNEETTDSTTSKISPSEDTQOENGSMFSLITWNID
!		1	GLDLNNLSERARGVCSYLALYSPDVIFLOEVIPPYYSYLKKRSS
1 1)	NYELLTGHEEGYFTAIMLKKSRVKLKSOELLPPPSTKMMPNT.LC
1 1		i	VHVNVSGNELCLMTSHLESTRGHAAERMNOLKMVLKKMOFADES
i i			ATVIFAGDTNLRDREVTRCGGLPNNIVDVWEFLGKPKHCOYTWD
l i			TOMNSNLGITAACKLRFDRIFFRAAAEBGHIIPRSLDLLGLEKL
6559			DCGRFPSDHWGLLCNLDIIL
5555	3	364	GPELSGLPTRPKKLKANQTPIAMDCCASRSCSVPTGPATTICSS
		i i	DKSCRCGVCLPSTCPHTVWLLEPTCCDNCPPPCHTPOPCVDTCP
6560	3		LLNSCQPTPGLETLNLTTFTQPCCEPCLPRGC
	3	1435	TATSGGIWLRRKWRCHWPRPLPQSCVGTEGGLQVRDTSSRIAKG
ł		}	GVDHTKMSLHGASGGHERSRDRRRSSDRSRDSSHERTESOLTEC
[1	1	IRNVTSPTRQHHVEREKDHSSSRPSSPRPOKASPNGSISSAGNS
J			SRNSSQSSSDGSCKTAGEMVFVYENAKEGARNIRTSERVTLIVD
[1	NTRFVVDPSIFTAQPNTMLGRMFGSGREHNFTRPNEKGEYEVAR
		1 '	GIGSTVFRAILDYYKTGIIRCPDGISIPELREACDYLCISFEYS
ł	ĺ	1.	TIKCRDLSALMHELSNDGARRQFEFYLEEMILPLMVASAQSGER
			ECHIVVLTDDDVVDWDEEYPPQMGEEYSQ11YSTKLYRFFKY1E

SEQ	Predicted	Predicted end	Inning agid cognont
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
: CM	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
l l	corresponding	to first	L-Leucine, M-Methionine, N-Asparagine,
i	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	_	\=possible nucleotide insertion)
		T	NRDVAKSVLKERGLKKIRLGIEGYPTYKEKVKKRPGGRPBVIYN
			YVQRPFIRMSWEKEEGKSRHVDFQCVKSKSITNLAAAAADIPQD
			QLVVMHPTPQVDELDILPIHPPSGNSDLDPDAQNPML
6561	3	1086	PGRRFRRKESSSSRWFPADCLLGLRGPASSLLSPEPSPSWPSHS
			PCPMAALTDLSFMYRWFKNCNLVGNLSEKYVFITGCDSGFGNLL
1		!	AKQLVDRGMQVLAACFTEEGSQKLQRDTSYRLQTTLLDVTKSES
	}	İ	IKAAAQWVRDKVGEQGLWALVNNAGVGLPSGPNEWLTKDDFVKV
}	i	į.	INVNLVGLIEVTLHMLPMVKRARGRVVNMSSSGGRVAVIGGGYC
İ	ŀ	Į	VSKFGVEAFSDSIRRELYYFGVKVCIIEPGNYRTAILGKENLES
			RMRKLWERLPQETRDSYGEDYFRIYTDKLKNIMQVAEPRVRDVI
j	1		NSMEHAIVSRSPRIRYNPGLDAKLLYIPLAKLPTPVTDFILSRY
6562	1	1562	LPRPADSV
	_	1562	MSTLYDIRAHKAQLLRFFASSDSNKALEQRRTLHTPKLEHLDRV
1	i		LYEWFLGKRSEGVPVSGPMLIEKAKDFYEQMQLTEPCVFSGGWL
1			WRFKARHGIKKLDASSEKQSADHQAAEQFCAFFRSLAAEHGLSA EQVYNADETGLFWRCLPNPTPEGGAVPGPKQGKDRLTVLMCANA
			TGSHRLKPLAIGKCSGPRAFKGIQHLPVAYKAQGNAWVDKEIFS
ŀ			DWFHHIFVPSVREHFRTIGLPEDSKAVLLLDSSRAHPQEAELVS
1		_	SNVFTIFLPASVASLVQPMEQGIRRDFMRNFINPPVPLQGPHAR
1		•	YNMNDAIFSVACAWNAVPSHVFRRAWRKLWPSVAFAEGSSSEEE
1		·	LEAECFPVKPHNKSFAHILELVKEGSSCPGQLRQRQAASWGVAG
			REAEGGRPPAATSPAEVVWSSEKTPKADODGRGDPGEGEEVAWE
1			QAAVAFDAVLRFAERQPCFSAQEVGQLRALRAVFRSOOOVRRRR
6563	1210		GALGAVVKVEALQEGPGGCGATAOSPLPCSSTAGEN
0303	1319	2694	LARPAQPVLLREPEGAGPPVPAGHLVHHLQGGHLRERAHPDLEA
	i		HEHPLPCDQMFWRQMGGHLRMVEANSRGVVWGIGYDHTAWVYTG
			GYGGGCFQGLASSTSNIYTQSDVKCVHIYENQRWNPVTGYTSRG
1			LPTDRYMWSDASGLQECTKACTKPPSLQWAWVSDWFVDFSVPGG TDQEGWQYASDFPASYHGSKTMKDFVRRRCWARKCKLVTSGPWL
	•		EVPPIALRDVSIIPESPGAEGSGHSIALWAVSDKGDVLCRLGVS
			ELNPAGSSWLHVGTDQPFASISIGACYQVWAVARDGSAFYRGSV
			YPSQPAGDCWYHIPSPPRQRLKQVSAGQTSVYALDENGNLWYRQ
1 1		·	GITPSYPQGSSWEHVSNNVCRVSVGPLDQVWVIANKVQGSHSLS
]]			RGTVCHRTGVQPHEPKGHGWDYGIGGGWDHISVRANATRAPRSS
		-	SQEQEPSAPPEAHGPVCC
6564	1	975	APGSCALWSYCGRGWSRAMRGCQLLGLRSSWPGDLLSARLLSQE
	1	ŀ	KRAAETHFGFETVSEEEKGGKVYQVFESVAKKYDVMNDMMSLGI
			HRVWKDLLLWKMHPLPGTQLLDVAGGTGDIAFRFLNYVOSOHOR
]]			KQKRQLRAQQNLSWEEIAKEYQNEEDSLGGSRVVVCDINKEMI,K
		1	VGKQKALAQGYRAGLAWVLGDAEELPFDDDKFDIYTIAFGIRNV
1			THIDQALQEAHRVLKPGGRFLCLEFSOVNNPLISRLYDLYSFOV
1 1			IPVLGEVIAGDWKSYQYLVESIRRFPSQEEFKDMIEDAGFHKVT
6565	1464	900	YESLTSGIVAIHSGFKL
		999	RSAVANGLTKRRMGLKLNGRYISLILAVQIAYLVQAVRAAGKCD
·	Í		AVFKGFSDCLLKLGDSMANYPQGLDDKTNIKTVCTYWEDFHSCT
1		i	VTALTDCQEGAKDMWDKLRKESKNLNIQGSLFELCGSGNGAAGS LLPAFPVLLVSLSAALATWLSF
6566	3	1385	KYESAODCCTOBERGI CARMATINAAYARATATATATATATATATATATATATATATATATATA
	. 1	-505	KYESAQPGGTQPEPGLGARMATHKALVMCLGLPLFLFPGAWAQG HVPPGCSQGLNPLYYNLCDRSGAWGIVLEAVAGAGIVTTFVLTI
	[İ	ILVASLPFVQDTKKRSLLGTQVFFLLGTLGLFCLVFACVEKPDF
	1	,	STCASRFLFGVLFAICFSCLAAHVFALNFLARKNHGPRGWVIF
			TVALLLTLVEVIINTEWLIITLVRGSGEGGPQGNSSAGWAVASP
		ļ	CAIANMDFVMALIYVMLLLLGAFLGAWPALCGRYKRWRKHGVFV
	İ	ļ	LLTTATSVAIWVVWIVMYTYGNKQHNSPTWDDPTLAIALAANAW
	i		AFVLPYVIPEVSQVTKSSPEQSYQGDMYPTRGVGYETILKEQKG
		. 1	QSMFVENKAFSMDEPVAAKRPVSPYSGYNGQLLTSVYQPTEMAL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S-Coping T-Through R-Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	sequence	Codon, /=possible nucleotide deletion,
<u> </u>	sednerice		\=possible nucleotide insertion)
1			MHKVPSEGAYDIILPRATANSQVMGSANSTLRAEDMYSAQSHQA
			ATPPKDGKNSQVFRNPYVWD
6567	125	863	TKRSNLKAYACSIHHIRTMSYVFVNDSSQTNVPLLQACIDGDFN
1	I	į	YSKRLLESGFDPNIRDSRGRTGLHLAAARGNVDICQLLHKFGAD
Ì	1		LLATDYQGNTALHLCGHVDTIQFLVSNGLKIDICNHQGATPLVL
			AKRRGVNKDVIRLLESLEEQEVKGFNRGTHSKLETMQTAESESA
			MESHSLLNPNLQQGEGVLSSFRTTWQEFVEDLGFWRVLLLIFVI
L			ALLSLGIAYYVSGVLPFVENQPELVH
6568	3	1183	HASDRLLVLPDNYSHFSQASANLQGPSRTTELFHPTLASISSPM
1			LEGAELYFNVDHGYLEGLVRGCKASLLTQQDYINLVQCETLEDL
1			KIHLQTTDYGNFLANHTNPLTVSKIDTEMRKRLCGEFEYFRNHS
1			LEPLSTFLTYMTCSYMIDNVILLMNGALQKKSVKEILGKCHPLG
1			RFTEMEAVNIAETPSDLFNAILIBTPLAPFFQDCMSENALDELN
1			IELLRNKLYKSYLEAFYKFCKNHGDVTAEVMCPILEFEADRRAF
1			IITLNSFGTELSKEDRETLYPTFGKLYPEGLRLLAQAEDFDQMK
			NVADHYGVYKPLFEAVGGSGGKTLEDVFYEREVQMNVLAFNRQF
1		i	HYGVFYAYVKLKEQEIRNIVWIAECISQRHRTKINSYIPIL
6569	205	1532	RRRGPQRLGHGRPTPLLCRWRTAGPSHWEKQARAFQGLRPVDPR
	100	1332	PMCWLEDI TWO 2 COO 2 A CODEGO TO COO CONTROL COO CONTROL COO COO COO COO COO COO COO COO COO C
			RMSWLFPLTKSASSSAAGSPGGLTSLQQQKQRLIESLRNSHSSI
			AEIQKDVEYRLPFTINNLTININILLPPQFPQEKPVISVYPPIR
			HHLMDKQGVYVTSPLVNNFTMHSDLGKIIQSLLDEFWKNPPVLA
			PTSTAFPYLYSNPSGMSPYASQGFPFLPPYPPQEANRSITSLSV
ł			ADTVSSSTTSHTTAKPAAPSFGVLSNLPLPIPTVDASIPTSONG
1 .			FGYKMPDVPDAFPELSELSVSQLTDMNEQEEVLLEQFLTLPQLK
			QIITDKDDLVKSIEELARKNLLLEPSLEAKRQTVLDKYELLTQM
1			KSTFEKKMQRQHELSESCSASALQARLKVAAHEAEEESDNIAED
1			FLEGKMEIDDFLSSFMEKRTICHCRRAKEEKLQQAIAMHSQFHA
6570	330		PL
8570	330	1304	ARLPRLTFLREGFLYVLLSHWVFVGAPRPPASDSWKKGLVPSAP
			PASRKMGSKALPAPIPLHPSLQLTNYSFLQAVNTFPATVDHLQG
			LYGLSAVQTMHMNHWTLGYPNVHEITRSTITEMAAAQGLVDARF
1			PFPALPFTTHLFHPKQGAIAHVLPALHKDRPRFDFANLAVAATQ
i l			EDPPKMGDLSKLSPGLGSPISGLSKLTPDRKPSRGRLPSKTKKE
1			FICKFCGRHFTKSYNLLIHERTHTDERPYTCDICHKAFRRQDHL
) !			RDHRYIHSKEKPFKCQECGKGFCQSRTLAVHKTLHMQTSSPTAA
			SSAAKCSGETVICGGT
6571	169	656	APDMNRKKLQKLTDTLTKNCKHLFRGFDKDNDGCVNVLEWIHGL
			SLFLRGSLEEKMKYCFEVFDLNGDGFISKEEMFHMLKNSLLKQP
	,		SEEDPDEGIKDLVEITLKKMDHDHDGKLSFADYBLAVREETLLL
<u></u>	·		EAFGPCLPDPKSQMEFEAQVFKDPNEFNDM
6572	49	1646	TPERAQPGALLGAAGCCVCGGRWWPRSHERGYFSSAKMGSKRRN
]]	İ		LSCSERHQKLVDENYCKKLHVOALKNVNSOIRNOMVONENDNRV
1			QRKQFLRLLQNEQFELDMBEAIQKAEENKRLKELQLKQEEKLAM
	1		ELAKLKHESLKDEKMRQQVRENSIELRELEKKLKAAYMNKERAA
	i		QIAEKDAIKYEQMKRDAEIAKTMMBEHKRIIKEENAAEDKRNKA
{			KAQYYLDLEKQLBEQEKKKQRAYEQLLKEKLMIDEIVRKIYEED
ļ l			QLEKQQKLEKMNAMRRYIEEFQKEQALWRKKKREEMEEENRKII
1 1	1		EFANMQQQREEDRMAKVQENBEKRLQLQNALTQKLBEMLRQRED
	ŀ		
[•		LEQVRQELYQEEQAEIYKSKLKEEAEKKLRKQKEMKQDFEEQMA
1 1	j	i	LKELVLQAAKEBEBNFRKTMLAKFAEDDRIELMNAQKQRMKQLE
1 1		[HRRAVEKLIEERRQQFLADKQRELEEWQLQQRRQGFINAIIEEE
(l			RLKLLKEHATNLLGYLPKGVFKKEDDIDLLGEEFRKVYQQRSEI
6573	767	776	CEEK
""	,0,	275	GGGGGESQSFRAQDGTRTPATDCLMYLQGPRKLMTQGGYDMVQK
1	.]		LFLDFFRRLSQRFTAEELEQRNILKPRNEQEEQEEKREIKRRL
			TRKLSQRPTVEELRERKILIRFSDYVEVADAQDYDRRADKPWTR

SEO	Predicted	I need to the	
ID	beginning	Predicted end nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
ì	to first	amino acid	L-Leucine, M-Methionine, N-Asparagine,
ł	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
- {	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
}	sequence	quence	Codon, /=possible nucleotide deletion,
			\=possible nucleotide insertion)
6574	204	1159	LTAADKVSRGECWRVGGRTVCWVSLGSPLGSV
J		****	LESSVPVSVGVFWACGVSWTGAAGLQDGALSDTMARNAEKAMTA
[[LARFRQAQLEEGKVKERRPFLASECTBLPKAEKWRRQIIGEISK
1			KVAQIQNAGLGEFRIRDLNDEINKLLREKGHWEVRIKELGGPDY
ł			GKVGPKMLDHEGKEVPGNRGYKYFGAAKDLPGVRELFEKEPLPP
			PRKTRABLMKAIDFEYYGYLDEDDGVIVPLEQEYEKKLRAELVE
ļ			KWKAEREARLARGEKEEEEEEEEEINIYAVTEEESDEEGSQEKG
Ĭ			GDDSQQKFIAHVPVPSQQEIEEALVRRKKMELLQKYASETLQAQ
6575	117	820	SEEARRLLGY
		620	SPALASQSGGITEEKMLEPQENGVIDLPDYEHVEDETFPPFPPP
l l			ASPERQDGEGTEPDEESGNGAPVPVPPKRTVKRNIPKLDAQRLI
1	{		SERGLPALRHVFDKAKFKGKGHEAEDLKMLIRHMEHWAHRLFPK
ŀ			LQFEDFIDRVEYLGSKKEVQTCLKRIRLDLPILHEDFVSNNDEV
1			AENNEHDVTSTELDPFLTNLSESEMFASELSISLTEEQQQRIER
6576	1	1060	NKQLALERRQAKLP
1	-	1080	PEPOALVGOKRGALRLLVARLVLTVSAPAEVRRRVLRPVLSWMD
ļ			RETRALADSHFRGLGVDVPGVGQAPGRVAFVSEPGAFSYADFVR
j	·		GFLLPNLPCVFSSAFTQGWGSRRRWVTPAGRPDFDHLLRTYGDV
			VVPVANCGVQEYNSNPKEHMTLRDYITYWKEYIQAGYSSPRGCL
	,		YLKDWHLCRDFPVEDVFTLPVYFSSDWLNEFWDALDVDDYRFVY
1			AGPAGSWSPFHADIPRSFSWSVNVCGRKKWLLFPPGQEEALRDR
1 .	,		HGNLPYDVTSPALCDTHLHPRNQLAGPPLEITQEAGEMVFVPSG
1			WHHQVHNLVMCCFSCPLSGAFLQEDGSTTSPLSQPELGWNGVAH
6577	2271	987	, =
1 1	 -		SDRMASDDFDIVIEAMLEAPYKKEEDEQQRKEVKKDYPSNTTSS
1 1			TSNSGNETSGSSTIGETSNRSRDRDRYRRRNSRSRSPGRQCRHR
f I	1		SRSWDRRHGSESRSRDHRREDRVHYRSPPLATGYRYGHSKSPHF REKSPVREPVDNLSPBERDARTVFCMQLAARIRPRDLEDFFSAV
1 1			GKVRDVRIISDRNSRRSKGIAYVEFCEIQSVPLAIGLTGQRLLG
1 1	J		VPIIVQASQAEKNRLAAMANNLQKGNGGPMRLYVGSLHFNITED
1 1			MLRGIFEPFGKIDNIVLMKDSDTGRSKGYGFITFSDSECARRAL
1 1			EQLNGFELAGRPMRVGHVTERLDGGTDITFPDGDQELDLGSAGG
1 1			RFQLMAKLAEGAGIQLPSTAAAAAAAAAAAAAQAAALQLNGAVPLGA
	*		LNPAALTALSPALNLASQCLQLSSLFTPQTM
6578	377	1489	PSSSATMNRAPLKRATILHMALTGASDPSAEAEANGEKPFLLRA
1 1			LQIALVVSLYWVTSISMVFLNKYLLDSPSLRLDTPIFVTFYQCL
1]	i	VTTLLCKGLSALAACCPGAVDFPSLRLDLRVARSVLPLSVVFIG
	ļ	ļ	MITFNNLCLKYVGVAFYNVGRSLTTVFNVLLSYLLLKQTTSFYA
1 1	İ		LLTCGIIIGGFWLGVDQEGAEGTLSWLGTVFGVLASLCVSLNAI
1 1	1	j	YTTKVLPAVDGS IWRLTFYNNVNACILFLPLLLLLGELQALRDF
1 .	· 1·		AQLGSAHFWGMMTLGGLFGFAIGYVTGLQIKFTSPLTHNVSGTA
1 1			KACAQTVLAVLYYEETKSFLWWTSNMMVLGGSSAYTWVRGWEMK
L			KTPEEPSPKDSEKSAMGV
6579	2	711	RPPRVWYPELRELSAAAPRWSHRTAPGIMVFYFTSSSVNSSAYT
į į		1	IYMGKDKYENEDLIKHGWPEDIWPHVDKLSSAHVYLRLHKGENI
1 1			EDIPKEVLMDCAHLVKANSIQGCKMNNVNVVYTPWSNLKKTADM
		ı	DVGQIGFHRQKDVKIVTVEKKVNEILNRLEKTKVERFPDLAAEK
į l	1	İ	ECRDREERNEKKAQIQEMKKREKEEMKKKREMDELRSYSSLMKV
]	ENMSSNQDGNDSDEFM
6580	62	1571	LVALKNWKPKGTNI PAPQSPVFGEAVSGVYMMTKVLGMAPVLGF
	Į.		RPPQEQVGPLMVKVEEKEEKGKYLPSLEMFRQRFRQFGYHDTPG
			PREALSQLRVLCCEWLRPEIHTKEQILELLVLEQFLTILPQBLQ
	İ		AWQEHCPESAEEAVTLLEDLERELDEPGHQVSTPPNEQKPVWE
]			KISSSGTAKESPSSMQPQPLETSHKYESWGPLYIQESGEEQEFA
i i	i		QDPRKVRDCRLSTQHEESADEQKGSEAEGLKGDIISVIIANKPE
			ASLERQCVNLENEKGTKPPLQEAGSKKGRESVPTKPTPGERRYI
			TATEL TO LATE DE LA SKAGKES VETKET PGERRYI

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(AmAlanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
l	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
i	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	*	\=possible nucleotide insertion)
			CAECGKAFSNSSNLTKHRRTHTGEKPYVCTKCGKAFSHSSNLTL
1			HYRTHLVDRPYDCKCGKAFGQSSDLLKHQRMHTEEAPYQCKDCG
J	1	Į.	KAFSGKGSLIRHYRIHTGEKPYQCNECGKSFSQHAGLSSHQRLH
ŀ		•	TGEKPYKCKECGKAFNHSSNFNKHIRIHTGEKPYWCHHCGKTFC
1	!		SKSNLSKHORVHTGEGEAP
6581	228	476	RVFLKDLSSTPMASNNTASIAQARKLVEQLKMEANIDRIKVSKA
1			AADLMAYCEAHAKEDPLLTPVPASENPFREKKFFCAIL
6582	1428	718	CFTTKTHCSPVSVPYLSPLVLRKELESLLENEGDQVIHTSSFIN
			QHPIIFWTLVWYFRRLDLPSNLPGLILTSEHCNEGVQLPLSSLS
1			QDSKLVYIQLLWDNINLHQEPREPLYVSWRNFNSEKKSSLLSEE
1			QQETSTLVETIRQSIQHNNVLKPINLLSQQMKPGMKRQRSLYRE
			ILPLSLVSLGRENIDIEAFDNEYGIAYNSLSSEILERLQKIDAP
	,		PSASVEWCRKCFGAPLI
6583	487	41	RIFSMTSGRLRWRCTWRPATALWSASLRLGTSSMHPSPRSISLP
			LSMMLSPLPSNTRGLSPTALFRSPDSEHATSCPRLHLWRCRAPL
			RSPSPLGRLQVLPRSPLHVHTHNSGKEVLGLQVQRSRSGTGPAC
1 1			SQAGSGAVQGGNWCIF
6584	189	1750	PLPMAALGPSSQNVTEYVVRVPKNTTKKYNIMAFNAADKVNFAT
		2.00	WNQARLERDLSNKKIYQEEEMPESGAGSEFNRKLREEARRKKYG
j j			IVLKEFRPEDQPWLLRVNGKSGRKFKGIKKGGVTENTSYYIFTQ
1			CPDGAFEAFPVHNWYNFTPLARHRTLTAEBAEEEWERRNKVLNH
	•		FSIMQQRRLKDQDQDEDEEEKEKRGRRKASELRIHDLEDDLEMS
			SDASDASGEEGGRVPKAKKKAPLAKGGRKKKKKKKGSDDEAFEDS
1			DDGDPEGQEVDYMSDGSSSSQEEPESKAKAPQQEEGPKGVDEQS
			DSSEESEEKPPEEDKEEEEEKKAPTPQBKKRRKDSSEESDSSE
j l			ESDIDSEASSAFFMAKKKTPPKRERKPSGGSSRGNSRPGTPSAE
1			GGSTSSTLRAAASKLEQGKRVSEMPAAKRLRLDTGPQSLSGKST
1 1			POPPSGKTTPNSGDVQVTEDAVRRYLTRKPMTTKDLLKKFQTKK
[[TGLSSEQTVNVLAQILKRLNPERKMINDKMHFSLKE
6585	. 3	1678	GPIRNSRIDDFVGGDPRAEASCSVLHSKPHAMADSRDPASDQMQ
}	,		HWKEQRAAQKADVI.TTGAGNPVGDKLNVITVGPRGPLLVQDVVF
l ,			TDEMAHFDRERIPERVVHAKGAGAFGYFEVTHDITKYSKAKVFE
1	j		HIGKKTPIAVRFSTVAGESGSADTVRDPRGFAVKFYTEDGNWDL
			VGNNTPIFFIRDPILFPSFIHSQKRNPQTHLKDPDMVWDFWSLR
1		i	PESLHQVSFLFSDRGIPDGHRHMNGYGSHTFKLVNANGEAVYCK
			FHYKTDQGIKNLSVEDAARLSQEDPDYGIRDLFNAIATGKYPSW
	1		TFYIQVMTFNQAETFPFNPFDLTKVWPHKDYPLIPVGKLVLNRN
	ľ	ļ	PVNYFAEVEQIAFDPSNMPPGIEASPDKMLQGRLFAYPDTHRHR
			LGPNYLHIPVNCPYRARVANYQRDGPMCMQDNQGGAPNYYPNSF
	!	· 1	GAPEQQPSALEHSIQYSGEVRRFNTANDDNVTQVRAFYVNVLNE
]	ł		EQRKRLCENIAGHLKDAQIFIQKKAVKNFTEVHPDYGSHIQALL
			DKYNAEKPKNAIHTFVQSGSHLAAREKANL
6586	32	804	PLPEQPAZSTSTMPVSGTPAPNKKRKSSKLIMELTGGGQESSGL
Í	ľ	1	NLGKKISVPRDVMLEELSLLTNRGSKMFKLRQMRVEKFIYENHP
1	}	. 1	DVFSDSSMDHFQKFLPTVGGQLGTAGQGFSYSKSNGRGGSQAGG
		1	SGSAGQYGSDQQHHLGSGSGAGGTGGPAGQAGRGGAAGTAGVGE
ł	1		TGSGDQAGGEGKHITVFKTYISPWERAMGVDPQQKMELGIDLLA
	I	i	YGAKAELPKYKSFNRTAMPYGGYBKASKRMTFQMPKV
6587	75	1117	RRVPSLGXMPECUDGEHDIETPYGLLHVVIRGSPKGNRPAILTY
	ļ		HDVGLNHKLCFNTFFNFEDMQEITKHFVVCHVDAPGQQVGASQF
	1	ļ	POGYOFPSMEQLAAMLPSVVQHFGFKYVIGIGVGAGAYVLAKFA
ļ	1		LIFPDLVEGLVLVNIDPNGKGWIDWAATKLSGLTSTLPDTVLSH
	1		LFSQEELVNNTELVQSYRQQIGNVVNQANLQLFWNMYNSRRDLD
	İ		INRPGTVPNAKTLRCPVMLVVGDNAPAEDGVVECNSKLDPTTTT
	1		FLKMADSGGLPQVTQPGKLTEAFKYFLQGMGYMPSASMTRLARS
1]		RTASLTSASSVDGSRPQACTHSESSEGLGQVNHTMEVSC

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i	SEQ	Predicted	Predicted end	Amino agid comment
	ID	beginning	nucleotide	Amino acid segment containing signal peptide (A-Alanine, C-Cysteine, D-Aspartic Acid, E-
	NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
		location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
		corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
		to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
		amino acid	residue of	S=Serine, T=Threonine, V=Valine,
- 1		residue of	amino acid	W=Tryptopnan, Y=Tyrosine, X=Unknown, *=Stop
		amino acid	sequence	Codon, /=possible nucleotide deletion,
ļ		sequence	j	\=possible nucleotide insertion)
٠ ا	6588	137	501	LGLQAQLLELRINNYQLSDELRKNGVELTSLROKVAYLDKRESK
- 1				AQKALSKSKKAQEVEVLLSENEMLQAKLHSQEEDFRLONSTLMA
- }	6589		<u> </u>	EFSKLCSQMEQLEQENQQLKEGAAGAGVAOAGP
-	6583	2	1405	RPWGSAMATFSRQEFFQQLLQGCLLPTAQQGLDQTWLYLATCLA
-				CRLLWRLGLPSYLKHASTVAGGFFSLYHPFOLHMVVVVIJSLIC
- 1				YLVLFLCRHSSHRGVFLSVTILIYLLMGEMHMVDTVTWHKMRGA
- (i			QMIVAMKAVSLGFDLDRGEVGTVPSPVEFMGYLYFVGTTVFGPW
-1				ISFHSYLQAVQGRPLSCRWLQKVARSLALALLCLVLSTCVGPYL
				FPYFIPLNGDRLLRNKKRKARGTMVRWLRAYESAVSFHYSNYFV
- 1				GFLSEATATLAGAGFTEEKDHLEWDLTVSKPLNVBLPRSMVEVV
				TSWNLPMSYWLNNYVFKNALRLGTFSAVLVTYAASALLHGFSPH
-				LAAVLLSLAFITYVEHVLRKRLARILSACVLSKRCPPDCSHQHR
-				LGLGVRALNLLFGALAIFHLAYLGSLFDVDVDDTTEEQGYGMAY TVHKWSELSWASHWVTFGCWIFYRLIG
T	6590	2177	656	VRAYEHVLSLLENVFTPMFCHRDEYFRQLLRGAESPTRNSKLNR
			100	GSLSLDDFRNTQKRGESFGISRIGSKIKGVFKSTTMEGAMLPNY
-	1			GVAEGEDDFIEEGIVVMEDDSPVEAVSTPNTPRNLAAWKISIPY
1	- 1			VDFFEDPSSERKEKKERIPVFCIDVERNDRRAVGHEPEHWSVYR
				RYLEFYVLESKLTEFHGAPPDAQLPSKRIIGPKNYEFLKSKREE
İ	1		•	FQEYLQKLLQHPELSNSQLLADFLSPNGGETQFLDKILPDVNLG
	1			KIIKSVPGKLMKEKGQHLEPFIMNFINSCESPKPKPSRPELTIL
1	i			SPTSENNKKLFNDLFKNNANRAENTERKONONYFMEVMTVEGVV
				DYLMYVGRVVFQVPDWLHHLLMGTRILFKNTLEMYTDVVI.OCKI.
	1			EQLFQEHRLVSLITLLRDAIFCENTEPRSLODKOKGAKOTFFFM
1	.			MNYIPDLLVKCIGEETKYESIRLLFDGLQQPVLNKOLTYVLLDI
┝	6591	2177	656	VIQELFPELNKVQKEVTSVTSWM
1	1000	24//	950	VRAYEHVLSLLENVFTPMFCHRDEYFRQLLRGAESPTRNSKLNR
ı				GSLSLDDFRNTQKRGESFGISRIGSKIKGVFKSTTMEGAMLPNY
	1			GVAEGEDDFIEEGIVVMEDDSPVEAVSTPNTPRNLAAWKISIPY
1	ŀ			VDFFEDPSSERKEKKERIPVFCIDVERNDRRAVGHEPHWSVYR
1				Rylefyvleskltefhgafpdaqlpskriigpknyeflkskree Fqbylqkllqhpblsnsqlladflspnggetqfldkilpdvnlg
1	· .	i		KIIKSVPGKLMKEKGQHLEPFIMNFINSCESPKPKPSRPELTIL
ı	ſ	i	Ì	SPTSENNKKLFNDLFKNNANRABNTERKONONYFMEVMTVEGVY
ı	.			DYLMYVGRVVFQVPDWLHHLLMGTRILFKNTLEMYTDYYLQCKL
Ŀ		Ì		EQLFQEHRLVSLITLLRDAIFCENTEPRSLODKOKGAKOTPERM
L				MNYIPDLLVKCIGEETKYESIRLLFDGLOOPVLNKOLTYVLLDI
-	6592			VIQELFPELNKVQKEVTSVTSWM
	0332	3	1861	APEFLGSTISSGSMIDANLKLLQBAEQRLKAIVAEKFAIATKEG
1	1			DLPQVERFFKIFPLLGLHEEGLRKFSEYLCKOVASKAERNT.LMU
	- 1	1	ļ	LGTDMSDRRAAVIFADTLTLLFEGIARIVETHOPIVETYYGDGD
	1		ľ	LYTLIKYLQVECDRQVEKVVDKFIKQRDYHQQFRHVQNNLMRNS
ı			}-	TTEKIEPRELDPILTEVTLMNARSELYLRFLKKRISSDFEVGDS
				MASEE V KQEHQKCLDKLLNNCLLSCTMOELIGLYVTMERYFMPE
		i	. 1	TVNKAVALDTYEKGQLTSSMVDDVFYIVKKCIGRALSSSIDCL
1	- 1		ĺ	CAMINLATTELESDFRDVLCNKLRMGFPATTFQDIQRGVTSAVN
ĺ	- 1	ł	ļ	IMHSSLQQGKPDTKGIESTDEAKMSFLVTLMNVEVCSENISTLK
l	[İ		KTLESDCTKLFSQGIGGEQAQAKFDSCLSDLAAVSNKFRDLLQE GLTELNSTAIKPQVQPWINSFFSVSHNIEEEEFNDYEANDDWVQ
	1	1		QFILNLEQQMAEFKASLSPVIYDSLTGLMTSLVAVELEKVVLKS
ĺ]	İ	ľ	TFNRLGGLQFDKELRSLIAYLTTVTTWTIRDKFARLSQMATILN
Ī	1	Í		LERVTEILDYWGPNSGPLTWRLTPAEVRQVLALRIDFRSEDIKR
_		<u> </u>		LRL
	6593	3	1837	EAFSAGSRRRGLALQRGVLGGLGGYCPCCCRRRGRLLVLLLLUR
				RGGEGGGGRGRGDKRRRRQARRORRRPEPAEARGGKMADVLSVI.
				RQYNIQKKEIVVKGDEVIFGEFSWPKNVKTNYVVWGTGKEGQPR

	I Book All and the second		
SEQ	Predicted beginning	Predicted end	Amino acid segment containing signal peptide
NO:	nucleotide		(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
"0:	location	location corresponding	Glutamic Acid, F-Phenylalanine, G-Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
ļ	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
1	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
1	sequence	sequence	\=possible nucleotide insertion)
			EYYTLDSILFLLNNVHLSHPVYVRRAATENIPVVRRPDRKDLLG
1			YLNGEASTSASIDRSAPLEIGLQRSTQVKRAADEVLARAKKPRI
1			EDEECVRLDKERLAARLEGHKEGIVQTEQIRSLSEAMSVEKIAA
1			IKAKIMAKKRSTIKTDLDDDITALKQRSFVDAEVDVTRDIVSRE
1			RVWRTRTTILQSTGKNFSKNIFAILQSVKAREEGRAPEQRPAPN
Ì			AAPVDPTLRTKQPIPAAYNRYDQERFKGKEETEGFKIDTMGTYH
}			GMTLKSVTEGASARKTQTPAAQPVPRPVSQARPPPNQKKGSRTP
			IIIIPAATTSLITMLNAKDLLQDLKFVPSDEKKKQGCQRENETL
			IQRRKDQMQ>GGTAISVTVPYRVVDQPLKLMPQDWDRVVAVFVQ
i			GPAWQFKGWPWLLPDGSPVDIFAKIKAFHLKYDEVRLDPNVQKW
L_	1		DVTVLELSYHKRHLDRPVFLRVWETLDRYMVKHKSHLRF
6594	1	1096	EFPGRRFRGSQASPLCATCGPALLRAPTRAAMTRSLFKGNFWSA
1			DILSTIGYDNIIQHLNNGRKNCKEFEDFLKERAAIEERYGKDLL
1	•		NLSRKKPCGQSEINTLKRALEVFKQQVDNVAQCHIQLAQSLREE
İ			ARKMEEFREKQKLQRKKTELIMDAIHKQKSLQFKKTMDAKKNYE
			QKCRDKDEAEQAVSRSANLVNPKQQEKLFVKLATSKTAVEDSDK
	1		AYMLHIGTLDKVREEWQSEHIKACEAFEAQECERINFFRNALWL
İ			HVNQLSQQCVTSDEMYEQVRKSLEMCSIQRDIEYFVNQRKTGQI
1			PPAPIMYENFYSSQKNAVPAGKATGPNLARRGPLPIPKSSPDDP
			NYSLVDDYSLLYQ
6595	57	781	PLGTMSDSDLGEDEGLLSLAGKRKRRGNLPKESVKILRDWLYLH
1			RYNAYPSEQEKLSLSGQTNLSVLQICNWFINARRRLLPDMLRKD
}			GKDPNQFTISRRGGKASDVALPRGSSPSVLAVSVPAPTNVLSLS
1			VCSMPLHSGQGEKPAAPFPRGELESPKPLVTPGSTLTLLTRAEA
1			GSPTGGLFNTPPPTPPEQDKEDFSSFQLLVEVALQRAAEMELQK
6596	2	1026	QQDPSLPLLHTPIPLVSENPQ
"""	1	1026	PRLPVRRYHGRRRLQGRSRGHMAEGDAGSDQRQNEEIEAMAAIY
1			GEEWCVIDDCAKIFCIRISDDIDDPKWTLCLQVMLPNEYPGTAP
ı			PIYQLNAPWLKGQERADLSNSLEEIYIQNIGESILYLWVEKIRD
			VLIQKSQMTEPGPDVKKKTEEEDVECEDDLILACQPESSVKALD FDISETRTEVEVEELPPIDHGIPITDRRSTFQAHLAPVVCPKQV
			KMVLSKLYENKKIASATHNIYAYRIYCEDKQTFLQDCEDDGETA
1			AGGRLLHLMBILNVKNVNVVVSRWYGGILLGPDRFKHINNCARN
1			ILVEKNYTNSPEESSKALGKNKKVRKDKKRNEH
6597	2	1026	PRLPVRRYHGRRRLQGRSRGHMAEGDAGSDQRQNEEIEAMAAIY
1			GEEWCVIDDCAKIFCIRISDDIDDPKWTLCLQVML?NEYPGTAP
			PIYQLNAPWLKGQERADLSNSLEEIYIQNIGESILYLWVEKIRD
			VLIQKSQMTEPGPDVKKKTEEEDVECEDDLILACQPESSVKALD
	Í		FDISETRTEVEVEELPPIDHGIPITDRRSTFQAHLAPVVCPKQV
			KMVLSKLYENKKIASATHNIYAYRIYCEDKQTFLQDCEDDGETA
			AGGRLLHLMEILNVKNVMVVVSRWYGGILLGPDRFKHINNCARN
			ILVEKNYTNSPEESSKALGKNKKVRKDKKRNEH
6598	1099	419	PRVRWATTMAMSFEWPWQYRFPPFFTLQPNVDTRQKQLAAWCSL
	•		VLSFCRLHKQSSMTVMEAQESPLFNNVKLQRKLPVESIQIVLEE
	Į		LRKKGNLEWLDKSKSSFLIMWRRPEEWGKLIYOWVSRSGONNSV
	ł		FTLYELTNGEDTEDEEFHGLDEATLLRALQALQQEHKAEIITVS
! !	i		DGPRRQVLLAGTCLPLLLTSHLSRAFKRRQTQCPPKTGSVTPPD
6599			SKGLQS
עעכס	164	1593	KMAALTTLFKYIDENQDRYIKKLAKWVAIQSVSAWPEKRGEIRR
	ļ		MMEVAAADVKQLGGSVELVDIGKQKLPDGSEIPLPPILLGRLGS
Į			DPQKKTVCIYGHLDVQPAALEDGWDSEPFTLVERDGKLHGRGST
† †)		DDKGPVAGWINALEAYQKTGQEIPVNVRFCLEGMEESGSEGLDE
	1	1	LIFARKDTFFKDVDYVCISDNYWLGKKKPCITYGLRGICYFFIE
1		l	VECSNKDLHSGVYGGSVHEAMTDLILLMGSLVDKRGNILIPGIN
			EAVAAVTEEEHKLYDDIDFDIEEFAKDVGAQILLHSHKKDILMH
L			RWRYPSLSLHGIEGAFSGSGAKTVIPRKVVGKFSIRLVPNMTPE

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, P=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ļ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
[amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ĺ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
	 		VVGEQVTSYLTKKFAELRSPNEFKVYMGHGGKPWVSDFSHPHYL
			AGRRAMKTVFGVEPDLTREGGSIPVTLTFQEATGKNVMLLPVGS
	1		ADDGAHSQNEKLNRYNYIEGTKMLAAYLYBVSQLKD
6600	2	934	PGRLFRVAAMESAGLEQLLRELLLPDTERIRRATEQLQIVLRAP
			AALSALCDLLASAADPQIRQFAAVLTRRRLNTRWRRLAAEQRES
1			LKSLILTALQRETEHCVSLSLAQLSATIFRKEGLEAWPQLLQLL
ì	1		QHSTHSPHSPEREMGLLLLSVVVTSRPEAFQPHHRELLRLLNET
1	1		LGEVGSPGLLFYSLRTLTTMAPYLSTEDVPLARMLVPKLIMAMO
1	<u> </u>		TLIPIDEAKACEALBALDELLESEVPVITPYLSEVLTFCLEVAR
			NVALGNAIRIRILCCLTFLVKVKSKALLKNRLLATLAAHPFPHC
l			GC
6601	529	1420	PRAAARAPPPAVLREDRRAATAPGAGEMTLHGPLAQRYFLNHIE
			KITTWQDPRKAMNQPLNHMNLHPAVSSTPVPORSMAVSOPNLVM
]		NHQHQQQMAPSTLSQQNHPTQNPPAGLMSMPNALTTQQQQQOKL
			RLQRIQMERERIRMRQEELMRQEAALCRQLPMEAETLAPVOAAV
	[NPPTMTPDMRSITNNSSDPFLNGGPYHSREQSTDSGLGLGCYSV
			PTTPEDFLSNVDEMDTGENAGQTPMNINPQQTRFPDFLDCLPGT
			NVDLGTLESEDLIPLFNDVESALNKSEPFLTWL
6602	127	617	LLDFPALPKFVLAQSPKAGKPSTMTSMTQSLREVIKAMTKARNP
			ERVLGKITLVSAAPGKVICEMKVEBEHTNAIGTLHGGLTATLVD
			NISTMALLCTERGAPGVSVDMNITYMSPAKLGEDIVITAHVLKQ
6603			GKTLAFTSVDLTNKATGKLIAQGRHTKHLCN
6603	79	660	PVGPSSLAARTGLGHLPFLHRLASSRGLDMDLLQFLAFLFVLLL
j			SGMGATGTLRTSLDPSLEIYKKMFBVKRREQLLALKNLAQLNDI
			HQQYKILDVMLKGLFKVLEDSRTVLTAADVLPDGPFPQDEKLKD
1 ' :			AFSHVVENTAFFGDVVLRFPRIVHYYFDHNSNWNLLIRWGISFC
6604	3		NCTGVFNQGPHSPILSLM
0004	- 1	688	TSTAQRQGGERMSFRGGGRGGFNRGGGGGFNRGGSSNHFRGGG
1 1			GGGGGNFRGGGRGGFGRGGGRGGFNKGQDQGPPERVVLLGEFL
1			HPCEDDIVCKCTTDENKVPYFNAPVYLENKEQIGKVDE1FGQLR
J d			DFYFSVKLSENMKASSFKKLQKFYIDPYKLLPLQRFLPRPPGEK GPPRGGGRGGGRGGGRGGGRGGGRGGGGGGGFRGGRG
			GGFRGRGH
6605	 7	848	SGSRRGAMRAAGVGLVDCHCHLSAPDFDRDLDDVLEKAKKANVV
[•	U 20	ALVAVAEHSGEFEKIMQLSERYNGFVLPCLGVHPVQGLPPEDQR
i I	[SVTLKDLDVALPIIENYKDRLLAIGEVGLDFSPRFAGTGRQKEE
			QRQVLIRQIQLAKRLNLPVNVHSRSAGRPTINLLQEQGAEKVLL
] . [•	HAPDGRPSVAMEGVRAGYFFSIPPSIIRSGQQKLVKQLPLTSIC
			LETDSPALGPEKQVRNEPWNISISABYIAQVKGISVEEVIBVTT
[·	ſ		QNALKLFPKLRHLLOK
6606	2	1682	FVEIRPRAEVANLSAHSASPIQDAVLKRLSLLEDIVYRQLNGLS
	1		KSLGLIEGYGGRGKGGLPATLSPAEEEKAKGPHEKYGYNSYLSE
			KISLDRSIPDYRPTKCKELKYSKDLPQISIIFIFVNEALSVILR
			SVHSAVNHTPTHLLKEIILVDDNSDEEELKVPLEEYVHKRYPGL
			VXVVRNQKREGLIRARIEGWKVATGQVTGFFDAHVEFTAGWAEP
			VLSRIQENRKRVILPSIDNIKQDNFEVQRYENSAHGYSWELWCM
	ļ		YISPPKDWWDAGDPSLPIRTPAMIGCSFVVNRKFFGEIGLLDPG
	1		MDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIERKKKPYNSNI
	ļ		GFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENPGIDIGDVSER
	ł		RALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGELRNNKAKDVC
].		ļ	LDQGPLENHTAILYPCHGWGPQLARYTKEGFLHLGALGTTTLLP
	1	j	DTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQNGAIMNKGTG
			RCLEVENRGLAGIDLILRSCTGQRWTIKNSIK
6607	137	986	VPACAGLKKEARSLLASPPRLLNTKLQASCRALFSPPIQSRQTT
			GISFQGRGGAGPGVPTRTQVPAAMGAVMGTFSSLQTKORRPSKD
			KIEDELEMTMVCHRPEGLEQLEAQTNFTKRELQVLYRGFKNECP
			- 101 - 101 - 10 - 101 -

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nuclcotide	(A-Alanine, C-Cysteine, D-Aspartic Acid, E-
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
İ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
j	amino acid	sequence	Codon, /-possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
		 -	SGVVNEDTFKQIYAQFFPHGDASTYAHYLFNAFDTTQTGSVKFE
1		1	DFVTALSILLRGTVHEKLRWTFNLYDINKDGYINQEEMMDIVKA
1		İ	IYDMMGKYTYPVLKEDTPRQHVDVPFQKMDKNKDGIVTLDEFLE
İ			SCQEDDNIMRSLQLFQNVM
6608	224	1140	RPCFSSPTGLCPRLSYPMILLQHAVLPPPKQPSPSPPMSVATRS
			TGTLQLPPQKPFGQEASLPLAGEEELSKGGEQDCALEELCKPLY
i			CKLCNVTLNSAQQAQAHYQGKNHGKKLRNYYAANSCPPPARMSN
			VVEPAATPVVPVPPQMGSFKPGGRVILATENDYCKLCDASFSSP
			AVAQAHYQGKNHAKRLRLAEAQSNSFSESSELGQRRARKEGNEF
			KMMPNRRNMYTVQNNSGPYFNPRSRQRIPRDLAMCVTPSGQFYC
1	1		SMCNVGAGEEMEFRQHLESKQHKSKVSEQRYRNEMENLGYV
6609	1	443	FRLRCRRFRVAGGRLAGAGLRESRVPAPEQRLSALTLLSWSAVT
1	1		PAAFPGNEOLS DA EDDGDLA EDVDA A DDA DGDA A EVONT
			PAAEPGNFQLSPAEPRGPLASPVRAAPRAPCPAAEMSELNTKTS
1			PATNQAAGQEEKGKAGNVKKAEEEEEIDIDLTAPETEKAALAIQ GKFRRFQKRKKDPSS
6610	319	881	
		001	GRKSLCNLHIFIRFPLTYPDMYMGMMCTAKKCGIRFQPPAIILI
			YESEIKGKIRQRIMPVRNFSKFSDCTRAAEQLKNNPRHKSYLEQ
1			VSLRQLEKLFSFLRGYLSGQSLAETMEQIQRETTIDPEEDLNKL DDKELAKRKSIMDELFEKNQKKKDDPNFVYDIEVEFPQDDQLQS
			CGWDTESADEP
6611	978	212	PGCSGAGSRVWWLPALRHLAMGSTESSEGRRVSFGVDEBERVRV
		2.12	LOCURE CENTURIDAYERGA DODO DECONDO CONTRA DE SECURIO DE
1 :			LQGVRLSENVVNRMKEPSSPPPAPTSSTFGLQDGNLRAPHKEST
[LPRSGSSGGQQPSGMKEGVKRYEQEHAAIQDKLFQVAKREREAA
	,		TKHSKASLPTGEGSISHBEQKSVRLARELESREAELRRRDTFYK
			EQLERIERKNAEMYKLSSEQFHEAASKMESTIKPRRVEPVCSGL
6612	1724	992	QAQILHCYRDRPHEVLLCSDLVKAYQRCVSAAHKG
''	-/	772	VSTHASALSRTQGQPQRQPRAAASGAGAGTAGGGGSGGAEGSKM
1 1			STEAQRVDDSPSTSGGSSDGDQRESVQQEPEREQVQPKKKEGKI
1 1			SSKTAAKLSTSAKRIQKELAEITLDPPPNCSAGPKGDNIYEWRS
1 1			TILGPPGSVYEGGVFFLDITFSPDYPFKPPKVTFRTRIYHCNIN
1			SQGVICLDILKDNWSPALTISKVLLSICSLLTDCNPADPLVGSI
6613	130	748	ATQYMTNRAEHDRMARQWTKRYAT
1	-30	710	ELELSSNMPEQSNDYRVAVFGAGGVGKSSLVLRFVKGTFRESYI
1			PTVEDTYRQVISCDKSICTLQITDTTGSHQFPAMQRLSISKGHA
]]		FILVYSITSRQSLEELKPIYEQICEIKGDV3SIPIMLVGNKCDE
1 1		,	SPSREVQSSEARALARTWKCAFMETSAKLNHNVKELFQELLNLE
6614	3	1191	KRRTVSLQIDGKKSKQQKRKEKLKGKCVIM
	-	* 7 3 7	SSAABAMRVLVRRCWGPPLAHGARRGRPSPQWRALARLGWBDCR
	!	i	DSRVREKPPWRVLFFGTDQFAREALRALHAARENKEEELIDKLE
] }			VVTMPSPSPKGLPVKQYAVQSQLPVYEWPDVGSGEYDVGVVASF
	·		GRLLNEALILKFPYGILNVHPSCLPRWRGPAPVIHTVLHGDTVT
			GVTIMQIRPKRFDVGPILKQETVPVPPKSTAKELBAVLSRLGAN
i 1			MLISVLKNLPESLSNGRQQPMEGATYAPKISAGTSCIKWEEQTS
			EQIFRLYRAIGNIIPLQTLWMANTIKLLDLVEVNSSVLADPKLT
	ļ		GQALIPGSVIYHKQSQILLVYCKDGWIGVRSVMLKKSLTATDFY
6615	832		NGYLHPWYQKNSQAQPSQCRFQTLRLPTKKKQKKTVAMQQCIE
	0.7.2	35	GRVGAGASAMSELPGDVRAFLREHPSLRLQTDARKVRCILIGHE
		l	LPCRLPELQVYTRGKKYQRLVRASPAFDYAEFEPHIVPSTKNPH
		ļ	QLFCKLTLRHINKCPEHVLRHTQGRRYQRALCKYBECQKQGVEY
l í			VPACLVHRRRREDQMDGDGPRPREAFWEPTSSDEGGAASDDSM
	1		TDLYPPELFTRKDLGSTEDGDGTDDFLTDKEDEKAKPPREKATD
	ŀ		EGRRETTVYRGLVQKRGKKQLGSLKKKFKSHHRKPKSFSSCKQS
6616	343		G
3010	347	1886	LLPPCQGARPLSSPPHASEDNLFLFWNCILCAFPHPSPQPLQYP
			VWPLLLVITQIPAPRHLRNRPFSFSRGGLDSFSGSLSTPSICRS

Desiming mucleotide location corresponding contion corresponding cofirst amino acid amino acid amino acid amino acid sequence se	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Sociation Cortesponding to first Cortesponding to sequence Cor	ID			(A=Alanine, C=Cvsteine, n=Acrastic Acid
corresponding to first amino acid amino acid residue of amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid sequence s	NO:		location	Glutamic Acid, F=Phenylalanine G=Glycine
LaLeucine, M-Methionine, N-Aeparagine, Peroline, quolutamine, Rafyginine, Sasarine, Tentreonine, V-Valine, amino acid amino acid sequence desidue of amino acid sequence desidue of amino acid sequence desidue of amino acid sequence desidue of amino acid sequence desidue of amino acid sequence desidue of amino acid sequence desidue of amino acid sequence desidue of amino acid sequence desidue of the property of t	!	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine
amino acid residue of amino acid sequence of serine, T-Mireonine, V-Valine, M-Tryptophan, Y-Tyrosine, X-Unknown, *-stop code, which sequence of serine, T-Mireonine, V-Valine, M-Tryptophan, Y-Tyrosine, X-Unknown, *-stop code, which sequence of serine, T-Mireonine, V-Valine, M-Tryptophan, Y-Tyrosine, X-Unknown, *-stop code, which sequence of sequence of the sequence	ļ		to first	L=Leucine, M=Methionine, N=Asparagine
sequence Sequen	-			P=Proline, Q=Glutamine, R=Arginine.
### ### ### ### ### ### ### ### ### ##				S=Serine, T=Threonine, V=Valine.
Sequence Codon, /=possible nuclectide deletion, -possible nuclectide insertion PAWNKAPMPPKGUPAVLMGISTFINLEGFYNLOPSPPPGSP -popMpcutroglupsPPMSSERIST PAWNKAPMPPKGUPAVLMGISTFINLEGFYNLOPSPPPGSP POPMPCUTCRUSTYSSPECHALLBISEELVESWHFIKOGOCA POPMPCUTCRUSTYSSPECHALLBISEELVESWHFIKOGOCA POPMPCUTCRUSTYSSPECHALLBISEELVESWHFIKOGOCA POPMPCUTCRUSTYSSPECHALLBISEELVESWHFIKOGOCA POPMPCUTCRUSTYSSPECHALLBISEELVESWHFIKOGOCA OPCUNTESSYECHDCAKACLAGMAGPGRCKKCSSPGCOCA OPCUNTESSYECHDCAKACLAGMAGPGRCKKCSSPGCOCA OPCUNTESSYECHDCAKACLAGMAGPGRCKKCSSPGCOCA OPCUNTESSYECHDCAKACLAGMAGPGRCKKCSSPGCOCA OPCUNTESSYECHDCAKACLAGMAGPGRCKKCSSPGCOCA OPCUNTESSYECHDCAKACLAGMAGPGRCKKCSSPGCOCA OPCUNTESSYECHDCAKACLAGMAGPGRCKKCSSPGCOCA OPCUNTESSYECHDCAKACLAGMAGPGRCKKCSSPGCOCA OPCUNTESSYECHDCAKACLAGMAGPGRCKKCSSPGCOCA OPCUNTESSYECHDCAKACLAGMAGPGRCKKCSSPGCOCA OPCUNTESSYECHDCAKACLAGMAGPGRCKKCSSPGCOCA OPCUNTESSYECHDCAKACLAGMAGPGRCKKCSSPGCOCA OPCUNTESSYECHDCAKACLAGMAGPGRCKKCSSPGCOCA OPCUNTESSYECHDCAKACLAGMAGPGRCKKCSSPGCOCA OPCUNTESSYECHDCAKACLAGMAGPGRCKKCSSPGCOCA OPCUNTESSYECHDCAKACLAGMAGPGRCKKCSSPGCOCA OPCUNTESSYECHDCAKACLAGMAGPGRCKACKCCA OPCUNTESSYECHDCAKACLAGMAGPGRCKACKCCA OPCUNTESSYECHDCAKACLAGMAGPGRCKACKCCA OPCUNTESSYECHDCAKACLAGMAGPGRCKACKCCA OPCUNTESSYECHDCAKACLAGMAGPGRCKACKCCA OPCUNTESSYECHDCAKACLAGACACA OPCUNTESSYECHDCAKACLAGACACACACACACACACACACACACACACACACACA	i			W=Tryptophan, Y=Tyrosine, X=Unknown, *=Ston
Appossible nucleotide insertion			sequence	Codon, /=possible nucleotide deletion
PPOPHPOTTCRGLVDSTNIKGLERTIRDNINGGGNTAWSEENLIST ENSTRLIVEVLEGVCSSUSPIECHLBLISSELVESWHIKOQGEN PDLFQALCSDSLALCCPAGTFGPSCLPCFGGTERPCGGYCOGEN PDLFQALCSDSLALCCPAGTFGPSCLPCFGGTERPCGGYCOGE GPCARCSGFEENCLQCKKGMALHHLKCUDIDECTEGANCSOG GPCARCSGFEENCLQCKKGMALHHLKCUDIDECTEGANCSOG GPCARCSGFEENCLQCKKGMALHHLKCUDIDECTEGANCSOG GPCARCSGFEENCLQCKKGMALHHLKCUDIDECTEGANCSOG GPCARCSGFEENCLQCKKGMALHHLKCUDIDECTEGANCSOG LDVDECTEVCRGENKGCGNTTGGGYRCICAGGYKGMAGGICVYED LDVDECTEVCRGENKGCGNTTGGGYRCICAGGYKGMAGGICVYED LDVDECTEVCRGENKGCGNTTGGGYRCICAGGYKGMAGGICVYED LDVDECTEVCRGENKGCGNTGGGYRCICAGGAGYKGMAGGICVYED LDVBCTEVCRGPKCGANCOGSSLPANGHACHACHACHACHACHACHACHACHACHACHACHACHACH	<u> </u>	sequence		\≃possible nucleotide insertion)
EDSTRIAVEVLEGVCSKSDFECRILLISSELVESWHERKOOPA PDLEONLICSDELKICCPAGTFGSCLPEGGSTGCCEG EDTRIGGSGHCCCQAGTGGEARCGGCGLGYFPASRRASHICASACC GOFARCSGPESSENCLQCKKWARHHLKCVIDICASACC GOFARCSGPESSENCLQCKKWARHHLKCVIDICASACC GOFARCSGPESSENCLQCKKWARHHLKCVIDICASACC GOFARCSGPESSENCLQCKKWARHHLKCVIDICASACC GOFARCSGPESSENCLQCKKWARHHLKCVIDICASACC GOFARCSGPESSENCLQCKKWARHHLKCVIDICASACC GOFARCSGPESSENCLQCKKWARHHLKCVIDICASACC GOFARCSGPESSENCLQCKKWARHHLKCVIDICASACC GOFARCSGPESSENCLQCKCCCC TO THE CANAMYOFAL SERBORUTURGTHEOR TO THE CANAMYOFAL SERBORUTURGTHEOR THE CANAMYOFAL SERBORUTURG THE CANAMYOFAL SERBO	1]	PAWVKMAPWPPKGLVPAVLWGLSLFLNLPGPIWLQPSPPPQSSP
PDLEONLESDSILKLCEPAGTERPEGGGGCEE BETRAGSGRICCOAGYGGEAGGCGLIYFRERNASHIVCSACE GPCARCSGPEESNCLOCKKGMALHILKCVDIDECGTEGANGAD GPCARCSGPEESNCLOCKKGMALHILKCVDIDECGTEGANGAD GPCARCSGPEESNCLOCKKGMALHILKCVDIDECGTEGANGAD GPCARCSGPEESNCLOCKKGMALHILKCVDIDECGTEGANGAD GPCARCSGPEESNCLOCKKGMALHILKCVDIDECGTEGANGAD GPCARCSGPEESNCLOCKGCMAGADGCRKKCSPGYQUGSKC LDVDECETEVCPCENKGCRYCOMAGGCCAMAGGCGCAKKCSPGYQUGSKC LDVDECETEVCPCENKGCKYCOMPFGLITCLATATAAKGOLUPTA IPICAVAAMTOYMLSERSDRVLEGFIKG SPRINGERVALDEGTECGLGGLIGSHGHIPTYTETYCS RMKEBLAALFSERKCECKKVDLIAKLVKNRTRIDGSAPSLCCC LGPATTFIL BYLDTXKRCPNCWQAVDGSSLENVSLAWWIEALRIDGDPEP KVCVHRRPISSERKECKKVDLIAKLVKRTRIDGSAPSLCCC LGPATTFIL GRANGAPSPERKOCKKVDLIAKLVKRTRIDGSAPSLCCC LGPATTFIL GRANGARAPNEPAFONDIYFLVSAFRATTAESPRSKVLONTOCC NVPKMTSSRSRIPCLSAAAAEGTGKKQCGKRAMATLDRKVPSEP AFLICKWSSSWIDAAKLACSINVDLEEARKGGKGKREWALNKEA WKYGT 6619 246 842 PASSEVITAAVMFILLINCITAVSOOMGIGKNOLDERPPLRNER VYCANTTISSVECKONLVINGRATTAESPRSKVLONTOCC NVPKMTSSRSRIPCLSAAAAEGTGKKQCGKRAMATLDRKVPSEP AFLICKWSSTRYTTISSVECKONLVINGRATTAESPRSKVLONTOCC NVPKMTSSRSRIPCLSAAAAEGTGKKQCGCRAMATLDRKVESP YFORMTTISSVECKONLVINGRATTAESPRSKVLONTOCC NVPKMTSSRSRIPCLSAAAAEGTGKKQCGCARMATLDRKVESP AFLICKWSSTRYLKVESP AFLICKWSSTRYLKVESP TYCANTTISSVECKONLVINGRATTAESPRSKVLONTOCC NVPKMTSSRSRIPCLSAAAAEGTGKACGCCGCOLTVILLINGSSV YKRAMHHLGHLKLPVTRIMODPESDTFSEIDLEKVKLLPEYPE DEPARAPALKGRKDEDAFLASSLDALKLTERPELAKVONNINTUSSSV YKRAMHHLGHLKLPVTRIMODPESDTFSEIDLEKVKLLPEYPE DEPARAPALKGRKDEDAFLASSLODATTSERILIDFRSSSSE MGSOOSSILERTKOPSAAAAEGSCROOLGTVACLTACHTYCALTFAT VTVALVMGIYFEDPGITOQGAVVTDAAACTSLIGEVLSKQGSSV DAAVAALCLGLAVAPASSLGGGGGWILVADTIKALLAGLIPBRG VTVALVMGIYFTBPGILGGGGWILVADTIKALLAGLIPBRG VTVALVMGIYFTBPGILGGGWILVADTIKALLAGLIPBRG VTVALVMGIYFTBPGILGGGWILVADTIKALLAGLIPBRG RPGITGSILIRBCALLAGUNATTAENLAGUNATAERQ RPGITGSILIRBCALLAGUNATATAERQ APALREETLORSHTTKPGILLOGGGAWLAUTHAERGEPPETTPLBG RPJLOKASCILKKKREWALAGALAGGCOOLGCCLSVLIML SIPHAAGMG KYUTISSTOTIVLAGAAAGCCCOLOCTIVLATAGAAA LVSKVGCILKKKREWALAGALAGGLIPWGTPALAGGHICVATIANA LVSKVGCILKKEKSPUKALAGGLIGGGCGCTATVISSKN NEGOTISTOTIVLYNIPPEGGLITA	Ì	Ì		PPQPHPCHTCRGLVDSFNKGLERTIRDNPGGGNTAWEEENLSKY
BETHSGSGHCDCQAGYGGEACGGCSLGYFBARRABHLKUCJAGACG GPCARCSGPESENLCJCKKWALHHLKCVIDEGTTEGANCGAD OPCWITGSYECRDCAKACLGCMGAGPGRCKKCSPGYQGGCYGKC LDVDECTETEVCPGENKQCERTEGGTRCICABGYQGGGCVGKC LDVDECTETEVCPGENKQCERTEGGRCICABGYQGGGCVKCGC IPESAGFFSEMTEDBLUVLQQMFFGIIICAATLAAKGDLVFTA IPICAVAAMTOVHLSERSDRVLEGFIKGR 6617 118 673 VWHAWQVSLLELEDBLQCFICLEVFRESIMLQCGHSYCKGCLVS LSYHLDTKVRCPKCWQAVDGSSSLENVSLAWVIEALRLDGDPFP KVCWHRFPBLSHCCKQDELIGCGLGLIGAWHTPTISTVCS RMKEELAALFSELKQCOKKVDELIAKLVKNRTRIDGSAFSLCPC LGPATFTIL 6618 548 136 BGKWARRAPNSDAFONDIYPLVSAGRATTAESPGSKVLQNYDCR NVPRMTSBRSTIPCLSAAABGGTGKKQCGCHANLDRVYDSPB APLGKWGSWIDAAKLHCSDNVDLEEAGKGGGKSREVMRLNKEA APLGKWGSWIDAAKLHCSDNVDLEEAGKGGGKSREVMRLNKEA APLGKWGSWIDAAKLHCSDNVDLEEAGKGGGKSREVMRLNKEA KYGT 6619 246 842 PASSEVLTAAVMFLLLNCTVAVSONMGIGKNGDLPRPPLRNEFR YFGRMTITSSVEGKDLVI IMGKKWFSI FERNRELKDRINVLVS REKKEPPGGAHFLAASLDDALLHCTERELAKWHDMU VGGSSV YKEANMHLGHLKLFYTHIMODFESDTFFSEDLEKYKLLPEYPG ILSDVQEKHIKKYREVCEEDD ANGAAALCLGIVAPHSSGLGGGGVMLVHUTGLFSPSSS MGSOGSPLRETTKDPFSAAABCSCROGGLTVIVTACLTFRTG VTVALVMGIVTEDPOITPOSPLKSRALQENFSSSS MGSOGSPLRETTKDPFSAAABCSCROGGLTVIVTACLTFRTG VTVALVMGIVTEDPOITPOSPLKSRALQENFSSLEIDERVKLLPEYSON DAAVAAALCLGIVAPHSSGLGGGVMLVWIDIRRNESHLIDFRSS APGALREETLGRPGINFALDKVCVVTRGHUTBLEKKGUSSV DAAVAAALCLGIVAPHSSGLGGGVMLVWIDIRRNESHLIDFRSS APGALREETLGRPGINFALVKERVCVVTRGHUTBLEKKGUSV OVLAFAAAVAQOGFRVTHILARALGAGLFOFWORGHERAHGIVELPPS OVLAFAAAVAQOGFRVTHILARALGAGLFOFVDT SAINLEGGRILFSSSSSSSSTEDPRVCVVTRGHUTBLEFTLEVKSLPPS OVLAFAAAVAGDGFRVTHILARALGAGLFOFVDT SAINLEGGRILFSSSSSSSTEDPRVCVVTRGHUTBLEFTLEVKSLPPS OVLAFAAAVAGDGFRVTHILARALGAGLFOFVDT SAINLEGGRILFSSSSSSSTEDPRVCPARTHUTBLEVVALLDPS APATSSLLKSKVAAATJRGHIDSGAAAPTAGGNLTEMVAERQ KENTSSSSSSSSTEDPRVCVARTHUTBLEGGLGCTVTLA LGANGAARGLSGLTQVFTFWLAFFSREPSCGLDCRCLSYLMLV SIPHAAMM CANGARGSCITKRYGARGAGAASSRGSETPERPCPBAGGLGTTTLA LGANGAARGLSGLTQVFTFWLAFFSREPSCGLDCTCLSYLMV IPAMGHPPTEVUKPF AATTSQLDKASGITKRYGKGGGAGRAAASSRGSETPERPCPBAGGLGKK LVSKYGTTKYGKRYGKSCAAAASSRGSETPERPCPBAGGLGKTKYLSKGN ARVOKSCITKKRYCKKPTSVKTAATTGLDYGTKVTKNOMPTFOKAT LVSKYGTTVUCKRUPLOKATH	1	-		KDSETRLVEVLEGVCSKSDFECHRLLELSEELVESWWFHKQQEA
GPCARCSGPEESINCLOCKKGWALHHLIKCVDIDEGGTEGANGGAD OPCCVNTEGSYECDCAKACIGCMGAGGPGKKESSPGYQVGSKC LDVDECTEVCPCENKGCENTEGGYRCTCABGYKOMEGICVKED IPESAGFFSEWTEDELVULQUFFGITICALATLAKGTLVFTA IFIGAVAAMTOVMISERSDRYLEGFIKGR 6617 118 673 VWMAWGYGLLEEBERLQFCTLUEVFKEELLALATLAKGDLVFTA IFIGAVAAMTOVMISERSDRYLEGFIKGR VWMAWGYGLLELEBERLQFCTLUEVFKEELLACHATLAKGCHSYCKGLVVS LSYKLDTTXVRCPMCWQAVDGSSSLENVSLAWVIEAURDGDPEP KVCVHRRPLSIECEKQDELICGLGSLGSHGHFFVTISTVCS RMKEBLAALFSEKKGEKKVDELIAKUVKNRTRDGSAPSLCPC LGPATTFIL 6618 548 135 BGKVARRAPBSPAFQNDIYFLVSAPRATTAESPWSKVLQNTYGCR NVPKMTSSRSRIPCLSAAAAEGTGKKQGGRAMATLDRKVPSEP AFLICKWSSWIPDAAKHLGSULAKUVKNRTRDGSAPSLCPC LGPATTFIL 6619 246 842 PASSEVLTAAVWFLLINCTVAVSONMGIGKNGLPPPPLREFR YFORMTTSSVEGKONLVINGERTWFS IPEKNRPLKONINLVLS RELKEPPOGAHFLASSLDDALLUTERPELJAKVHIVGGGSV YKEANMHLGHLKFVTERMODYESDTFFSEIDLEKYKLLPFYG LISDVGCKMIKKKFEVCEKDD ILSDVGCKMIKKKFEVCEKDD ILSDVGCKMIKKKFEVCEKDD ILSDVGCKMIKKKFEVCEKDD ILSDVGCKMIKKKFEVCEKDD ILSDVGCKMIKKKFEVCEKDD ILSDVGCKMIKKKFEVCEKDD ILSDVGCKMIKKKFEVCEKDD ILSDVGCKMIKKKFEVCEKDD ILSDVGCKMIKKKFEVCEKDD ILSDVGCKMIKKKFEVCEKDD ILSDVGCKMIKKFEVCEKDD ILSDVGCKMIKKKFEVCEKDD ILSDVGCKMIKKKFEVCEKDD ILSDVGCKMIKKKFEVCEKDD ILSDVGCKMIKKKFEVCEKDD ILSDVGCKMIKKKFEVCEKDD ILSDVGCKMIKKKFEVCEKDD ILSDVGCKMIKKKFEVCEKDD ILSDVGCKMIKKKFEVCEKDD ILSDVGCKMIKKFEVCEKDD ILSDVGCKMIKKKFEVCEKDD ILSDVGCKMIKKKFEVCEKDD ILSDVGCKMIKKFEVCEKDD ILSDVGCKMIKKKFEVCEKDD ILSDVGCKMIKKKFEVCEKDD ILSDVGCKMIKKFEVCEKDD ILSDVGCCKMIKKFEVCEKDD ILSDVGCCCCKARA ILSDVGCKMIKKFEVCEKDD ILSDVGCCCCKARA ILSDVGCKMIKKFEVCEKDD ILSDVGCCCCKARA ILSDVGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	ŀ			PDLFQWLCSDSLKLCCPAGTFGPSCLPCPGGTERPCGGYGQCEG
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LDVDECETEVCPGENKQCENTEGGYRCICABGYKQBIGICKEO IPESAGFFSEMTBEDLIVLQQMPFGII ICALATLARAKGDLVFTA IFIGAVAAMTGYMLSERSDRVLBGFTKGR VWRAMQVSLBLEDERIQCFICEFFKESLMLQGHSYCKGCLVS LSYHLDTKVRCPMCWQAVDGSSSLPNVSLAWVIEALRLPGGPSPF KVCVHRRPILSLYCEKDQELICGICGLIGSKQHFVFTISTVCS RMKEBLAALFSEKDGSKVDELIAGUKTGUGSKQHFVFTISTVCS RMKEBLAALFSEKDGSKVDELIAGUKTGUGSKQHFVFTISTVCS RMKEBLAALFSEKDGSKVDELIAGUKTGUGSKQHFVFTISTVCS BOKWARRAPNSPAFQNDTYPLVSAPRATTAESPWSKVLQMTQCR NVPRMTSRRSIPCLSAAAABGGTKKQQGGRAMATLDRKVPSDE APLGKPWSSWIDAAKLHCSDNVDLEEBGKEGGGKSEVMRLNKEA WKYGT 6619 246 842 PASSEVLTAAVMFLLINCTVAVSONMGIGKNGDLPRPPPRNFEFR YFORMTTISSVEKKQNUVIMERKTWSS IPEKNRPLKURINLVLS RELKEPPGGAAFLARSLDDALKLTERPELANKVDMINVCGSSV YKEANHLGHLKLFVTRIMOPDSSDTPSSIDLEKYKLLPEYPG ILSDVQECKHIKKKFEVCEKDD NSRVDDFVARRARMABNEASGESALJAAVSPVDWSITSPFRIDE DEPAPAPARLRGRKDEDAFLGPPTDPDSFLKSARLQRLPSSSSE MGSQOGSUBLRATRKNDPFSAAAAECSCRQDGLTVIVTALLTHATG VTVALVMQIYFGDPQIFQOGAVVTDARCTSIGIEVUSKQGSSV DAAVAAAALCLGIVAPHSSGLGGGGWMLVHDIRRNESHLIDFRSS APGAREETI-GRSWETKSGLUVVPGWMKGRUTLEMAGRAD HAGGUITEBFSMYSALVEKVCGVYRGHLVUSPPPHTOPALI SALNILEGFRILTSUSREGLUVVPGWMKGNITLEMMARAO HAGGUITEBFSMYSALVEKVCGVYRGHLVUSPPPHTOPALI SALNILEGFRILTSUSREGLUVVPGWMKGNITLEMMARAO HAGGUITEBFSMYSALVEKVCGVYRGHLVUSPPPHTOPALI SALNILEGFRITISTUSREGLUVVPGWMKGNITLEMMARAO HAGGUITEBFSMYSALVEKVCGVYRGHLVUSPPPHTOPALI SALNILEGFRITISTUSREGLUVVPGWMKGNITLEMMARAO HAGGUITEBFSMYSALVEKVCGVYRGHLVUSPPPHTOPALI SALNILEGRAPHTSULTSUSREGLUVPGWMKGNITLEMMARAO HAGGUITEBFSMYSALVEKVCGVYRGHLVUSPPPHTOPALI SALNILEGRAPHTSULTSUSREGLUVPGWMKGNITLEMGLIPPM AAQULIMAPDDFTVAMVSSLNGPFSGLITPSGTLIMGMLDFN WPNRTANHSAPSLENSVYDGKRPLSFLLFVVRPAEGLGGTTIAA LGANGAARGISGLTGVYRFTWLAFFSKEPSCGLDCRCLSYLMLV VGITSYQGKLQALRKEKSRBAARSRKENFEFYELAKLILDLE SALNILGLGUTTUSRGFPTVVRPAEGLGGTTIAA LGANGAARGISGLTGVYRFTWLAFFSKEPSCGLDCRCLSYLMLV SKVGIGAGRRSPSALAIEVEGGTLTGSHTDVVFPPALAGLGEN KYLYSETVSTITLTSVYRTAGROPTKOPTKWHVWDREIKVN IPPMGGILSGGTAEDGASSASSSGSETEPVVCPPPASDQFIL ARVGKGCITKRCHTVSKYLTAGTGTGVATKVHVWDREIKVN IPPMGGILSGGTAEDGASSASSSSGSTEPPVCPPPASDQFIL ARVGKGCITKRCHTVSKYLTATGTGVATKVHVWDREIKVN IPPMGGI				GPCARCSGPEESNCLQCKKGWALHHLKCVDIDECGTEGANCGAD
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6617 118 673 WMAMOYSILEIBERGICP CILEPFRESIMIQGSHSYCKGCLVS LSYHLDTKVRCPMCWOADDGSSIPWISLAWVIEALFLEDGDPEP KVCVHRRPDFLSTCER COLLIGSHGHTYCTFISTVCS RMKEELAALFSELKOEOKKVDELIAKLVKNRTHIDDSAPSICCE LGPATFTI. 6618 548 136 DEKVARRAPNSPAFONDTYPLVSAPRATTAESPWSKVLQNTQCR NVPRMTSERSIPCLSAAAABGGTKKOQEGRAWATLDEKVPSEE APLGKPWSSWIDAAKLHCSDNVDLEEAGKEOGKFEVMRINKEA WKYGT 6619 246 842 PASSEVLTAAVMPILLINCTVAVSONNGTGKNGDLPPPPLRNEPP YFQRMTTTSSVEGKONLVIMGRKTWFSIPEKNRPLKUDINLVLIS RELKEPPOGARAFLARSLODALKLTERPELANKVDHINVGGSSV YKRAMHLIGHLKLFVTRIMOPPESDTFFSIDLEKYKLLPEYBG ILSDVGEKHIKKKPVCEKDD 3 1879 NSRVDDFVARRARMABNESAGSBALGAVSPVDYMSITSFPRLPE DEPAPAPAPLRGRKDEDAFLGDPDTDDSFLKSARLORLPSSSSE MGSOOSSILERTRENDFSAAAABCSGOGWULVHDIRRISKHLDFRES APGALREETLQRSWETKSGLLVOVFOMKVGHEAHOLYGGLPSS DAAVAAALCLGIVAPHSSGLGGGWULVHDIRRISKHLDFRES APGALREETLQRSWETKSGLLVOVFOMKVGHEAHOLYGGLPSS VTVALVMOIYFGDPDIFFOOGAVVTUARCTSLGIEVUSKUGSSV DAAVAAAALCLGIVAPHSSGLGGGWULVHDIRRISKHLDFRES APGALREETLGRSWETKSGLLVOVFOMKVGHEAHOLYGGLPSS QVLAPAAAVAAQOOFRVTHDLARALABGLPPNMSERFFETLPSG RPPLOSSILERPDLAEVLUUCTGSGPAPTYAGGNLTLEMVARAQ HAGGUTTEDFSMYSALVERVCGVYRGHLVISPPPPHTOPALI SALNILEGFRATSALTSVRFOGALHAVAEFLKIALALASRLGDPVYD STITESMDDMLSKVERAAYLGGHINDSOAAPAPLLEVYKLDOAPT AAQVIIMGDDFTVAMVSSLTUPTGSGLITPSGLILMSQMLDPS WPNRTANHSAPSLEBSVOPGKRPLSFILLFTVVRPAEGLGSTTLA LGANGAARGLSGLTQVFFTFULAFFSREPSGCLDCRCLSYLMLV SIPHAAMMG AAATTSGLDKASITIRLTSVLKWRDPANGGPPPMLRMEGGPPDNT SVKVIGAQRRRSPSALAIEVPEAHLGSHILJSLODYVKHVUSMEDEINGN LPPGGGLLSGGTAEDGASASSSSSSCSTPEPVVCFPPASDGFLL AATTSGLDKASITILTSVLKWRDPANGGPPPMLRMEGGPPDNT SVKVIGAGRRRSPSALAIEVPEAHLGSHILJSLODYKVHVURDELIKON 1FDMAGGPFTYSVRRPF AAATTSGLDKASVLTATGTGVYKVHVURDELIKON 1FDMAGGPFTYSVRRPF AAVTSGLDKASVLTATGTGVYKVHVURDELIKON 1FDMAGGPFTYSVRRPF AAVERGELIKRYCEKRYSKYLATGTGJVAYKVHVURDELIKON 1FDMAGGPFTYSVRRPF AAFFKUKKRFLHVEEGGILVARTSVLKSVIGNINANSFTOLIKUN 1FDMAGGPFTYSVRRPF ARMENDOLOGUSHLAGGGFOLIKAKULSUKKPDDDINDA AFMLHIDQYDPLYSKRFAVILSEVSENIKKGINIANNENTEDKL LGSKONGTINGELSLHGCVSKIISAALSFYKENLKVUSVKPDDI NREEPPRMGGRRNLEELILVUSSLSHDISRNVTLESIGLDLKKYNT 1FANTAGLONGERISHAGGENIKALEKNIN	ł			IDPOACETEVCPGENKQCENTEGGYRCICAEGYKQMEGICVKEQ
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RVCVHHRNPLSLYCEKDQELICGLIGGLIGSHQHHPYTFISTVCS RMKEBLAALFSELKQEOKKVDELIAKLVKHRTIDGSAPSLCPC LIGPATFTFL DGKVARRAPNSDAPGNDTYPLVSAPRATTAESPWSKVLQNTQCR NVPKMTSERSIPCLSAAAALGTGKKQGEGRAMATLDRKVFSPE APLIGKPWSSWIDAAKLHCSDNYDLEEAGKEGGKGREWARLNKEA NVPKMTSERSIPCLSAAAALGTGKKQGEGRAMATLDRKVFSPE APLIGKPWSSWIDAAKLHCSDNYDLEEAGKEGGKGREWARLNKEA NKYGT 6619 246 842 PASSEVLTAAVMFLLLNCTVAVSONMGIGKNGDLPRPPLRNEFR YFORMTTSVEGKONUJ MIGKKYMFS I PEKNRPLKURINLVLS RELKEPPQGAHFLARSLDDALKLTERPELANKVOMINIVGSSV YKEAMNHLGHLKLFVTRINGDPESDTFFSEIDLERYKLLPEYPG ILSDVGEGKHIKKYREVCKKD NSRVDDFVARARNAENEASGESALGAYSPVDYWSTTSPFRLPE DEPAPAPALGRKNEDEAFLGDPDTDPSFIKSAALGKLPSSSE MGSQCGSPLRETRXDPFSAAAACSCCRODGLTVIVTACLTFATG VTVALVMQIYTGDPQIFQOGAVVTDAARCTSIGLEVISKQGSSV YAVAAAALCLGIVAPHSSGLGGGGWUKUHDIRRKESHLIDFRES APGALREETIQRSWETKEGLLVGVFGWVKGLHEAHOLYGGLPWS CVLAFAAAVAQDCFNTVHLARLARGUHVDIRRRESHLIDFRENS APGALREETIQRSWETKEGLLVGVFGWVKGLHEAHOLYGGLPWS CVLAFAAAVAQDCFNTVHLARLARGUHVDIRRRESHLIDFRENS APGALREETIQRSWETKEGLLVGVFGWVKGLHEAHOLYGGLPWS CVLAFAAAVAQDCFNTVHLARLARGUHVDISPPPHTGPALI SALNILEGFNLTSLVSREQALHWVAETLKIALALASRLGDFVYD AAQVLIMGPDDFTVANVSEKPQGTKPLLSFLLFTVVRPABRGLCGTVLA HAGGVITESDFSNYSALVEKEVCGVVRDWSCGLTESGLINSGMLPS WPNRTANNSAPSLENSVQPGKRPLSFLLFTVVRPABRGLCGTVLA LGANGAARGLGGLTOVTFTPHLAFFSRSCCLDCRCLSYLMLV SIPHAANNG 6621 1 662 VQGTTSYGORLGALRKEKSRDAARSRRGKENFEFYELAKLLELP AAITSQLDXASIIRLTISYLKMRDFANGODPPNNLRMEGPPPNT SVKVIGAQRRRSPSALAIEVERAHLGSHILGLSDGVVRLNOEG KTLYLSETVSIYLGSUGVETTGSSVDVAVHGODEVBMASQLGMK LPPGRGLLSGGTAEDGASSASSSOSETPEPVVCFPPASDQFLI LPPGRGLLSGGTAEDGASSASSSOSETPEPVVCFPPASDQFLI LPPGRGLLSGGTAEDGASSASSSOSETPEPVVCFPPADDQFLI GRASGAGGETAGGGERAAMAEANMEKEGREGRITIKVISMGN APVGKSCTIKTYCEKRFLVEEGGIIYAMYVROTVLKVIKFLITIAYNSA LVSKVQFTVDCNVDIQDDMTGYKHFSCNITMAHLFSKLSFCYLCG VSTYGLTCLTYTLVHLFYNSLRFNSFFYLKRNLKVLSVKFDD MREUPPAMGLENLEELYLUGGLSHDISRNVTLESIRDLKSLKI LPSTNSVSKTPQAVVDVSSKLGMCHTSMINVLESNLKMDL SISHNSVSKLOPAVTONSSKLIGMCTINVILMINLKWTN BELEPPAMGLENLEELYLUGGLSHDISRNVTLESIRDLKSLKIM]	\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \	LSYHLDTKYPCPMCWOAVDGGGGI PMTGI AVILTED BY BCCCUVS
RMKEELRALFSELKQEOKKVDELIAKLVKNRTRIDGSAPSLCPC LGPATFTFL LGPATFTFL BGKVARRADNSPAFQNDIYPJUVSAPRATTAESPWSKVLQNTQCR NVPKMTSERSRIPCLSAAAAEGTGKKQQEGKARAMTLDRKVPSPE AFLGKEWSSWIDAAKLHCSDNVDLEEAGKEGGKSREVMRINKEA WKYGT 6619 246 842 PASSEVLTAAVMFLLLNCIVAVSQNMGIGKNGDLPRPPLRNEFR YFORMTITSSVBGKQNLVIMGRKTWFSIPEKNRPLKDRINLVIS RELKEPPQGAHFLARSLDDALKLTERPELANKUMTWIVGGSSV YKEAMMHLGHLKLPVTRIMGDFESDTFFSEIDLEKYKLJDEYPG ILSDVQEGKHIKYKFEVCEKDD NSRVDDFVARRAMAARENSAGESALGAVSFVDYMSITSFPRIPE DEPAPAAPLRGRKDEDAFLGDPTDPDSFLKSARLQRLPSSSSE MGSQDGSPLRETRKDPFSAAAAECSCROBGITVUTVTACLTFATG VTVALVMGIYFGDPGIFQGAVVTDARKTSLGIEVLSKQGSV DAAVAAALCLGIVAPHSSGLGGGWMLVHDIRRNESHLDFRES APGALRETLQRSWETKFGLILVAVMKGLHEAHGLYGRLPWS QVLAFAAVAQDGFNVTHDLARALABGLPPMMSERFREFTPLDSG RPPLEGSLHRPDLASFUNDULGTSGPAAPYAGGNITLEMVAEAQ HAGGVITEDFSNYSALVEKPVCGVYRGHUVLSPPPPHTGPALI SALNILEGFNITSIVSREQALHWVAETLKIALALASRLDPVYD STITESMDMLSKVEAAYAIRGHINDAAPYAGGNAPPLLPVYPLBLGGPTY AAQVLIMGPDDFIVAWSSLNOPFGSGLITPSGILLNSQMLDPS WPNFRTANISAPSLENSVQDCKRELPLPTVVRPAGGLCGTYLA LGANGAARGLSGLTQVFFTPWLAFFSREPSCGLDCKLSYLMLV SIPHAANMG WONTHANISAPSLENSVQDCKRELPLPTVVRPAGGCTYLA LGANGAARGLSGLTQVFFTPWLAFFSREPSCGLDCKLSYLMLV SIPHAANNG SVENGAGGRRSPSALAIEVPSCHLEDPTVVRFDGHPURMEGGPPDNT SVENGAGGRRSPSALAIEVPSCHLEDPTVVRFDGHPURMEGGPPNT SVENGAGGRRSPSALAIEVPSCHLEDPTVVRFDGHPURMEGGPPNT SVENGAGGRRSPSALAIEVPSCHLEVERGRSCDTREVSIMGN AAVGGRRSPSBALAIEVPSCHLEVRGFGSDGITVSGUM APPGGGLISGGTAEDGASSASSSSSSSETEPPVCFPPASDGFLL GGASGAGGETFAGGEPRARMERMIPKREPGRSGTRIVSIMGN AAVGGCTIKRYCEKFFVSKYATIGIDYGVTKVHVROREIKVN 1FDMAGHPPFYEVERSP AATTGCLDTLWINGFRSPRAAMEANHFRKEPGRSGTRIVSIMGN AAVGGSCITKYCEKFFVSKYATIGIDYGVTKVHVROREIKVN 1FDMAGHPPFYEVERSP AATTGCLDTLWINGFRSPRAAMEANHFRKEPGRSGTRIVSIMGN AAVGGSCITKYCEKFFVSKYATIGIDYGVTKVHVROREIKVN 1FDMAGHPPFYEVERSP AATTGCLTATIVUR SYRSRENSFENKLKQLNIANEWTDKL USIYGLTCITTIVUR SYRSRENSFENKLKQLNIANEWTDKL PRAMMIDQYDPLYSKRPAVELSBUSENKLKQLNIANEWTDKL PRAMMIDQYDPLYSKRPAVELSBUSENKLKQLNIANEWTDKL BRAMMIDQYDPLYSKRPAVELSBUSENKLKQLNIANEWTDKL BRAMMIDQYDPLYSKRPAVELSBUSENKLKGLUNIANEWTDKL BRAMMIDQYDPLYSKRPAVELSBUSENKLKGLUNIANEWTDKL BRAMMI				KVCVHHRNPLSIFCEKDOFI.ICGI.CGI.I.CGUQUUUNDD - CO
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### APPLIES PROMINE HER PELANKUR HER PELANKU	6619	246	842	PASSEVLTAAVMFLLLNCIVAVSONMGIGKNGDI PROPI RNEPR
RELKEPPGGAHFLARSLDDALKLTERPELANKUMIMIVOGSSV YKEAMNILGHLKLFVTRIMQDFESDTFFSEIDLEKYKLLPEYPG ILSDVQEGKHIKKYFFVCEKDD ILSDVQEGKHIKYKFFVCEKDD NSRVDDFVARARMAENEASGESALGAYSPVDYMSITSPPRLPE DEPAPAAPLRGRKDEDAFLEDPDTDPDSFLKSRALQRLPSSSSSE MGSQDGSPLRETRKDPFSARAAECSCRQDGLTVIVTACLTFATG VTVALVMQIYFGDPQIFQQGAVVTDARCTSLGIEVLSKQGSSV DAAVAAALCLGIVAPHSSGLGGGGVMLVHDIRRRESHLIDFRES APGALREETLQRSWETKPGLLVGVPGMVKGLHEAHGLYGFLPWS QVLAFAAAVQDGFNVTHDLARALABQLPPNMSERFRETFLPSG RPPLPGSLLHRPDLAEVLDVLGSPPAPTYAGGNLTLEMVAEAQ HAGGVITEBFSNYSALVEKPVCGVYKGHLWLSPPPPHTGPALI SALNILEGFNLTSLVSREQALHWVAETLKIALALASRLGDPVYD STITESMDDMLSKVERAYLEGHLNDSQAPPPLLPVYELDGAPT AQQVLIMGPDDFIVAMVSSLNQPFGSGLITPSGILLNSQMLDPS WPNRTANHSAPSLENSVQPCKRPLSFLLPVTVVRPAEGLCGTYLA LGANGAARGLSGLTQVRFTPWLAFFSREPSCGLDCRCLSYLWLV SIPHAANMG 6621 1 662 VQGITSYQQRLQALRKEKSRDAARSRRGKENFEFYELAKLLPLP AAITSQLDKASIIRLTISYLMMEDFANQGPPPMILRHEGPPPNT SVKVYIGAQRRASPSALAIEDFANQGPPPNILRHEGPPPNT SVKVYIGAQRRASPSALAIEDFANQGPPPNILRHEGPPPNT SVKVYIGAQRRASPSALAIEDFANGGPPPNILRHEGPPDNT SVKVYIGAGRRASPSALAIEDFANGGPPPNILRHEGPPNT SVKVYIGAGRRASPSALAIEDFANGGPPPNILRHEGPPNT SVKVYIGAGRRASPSALAIEDFANGGPPRNLRHEGPPNLRHEGPPNT SVKVYIGAGRRASPSALAIEDFANGGPPNLRHEGPPNLRHEGPPNT SVKVYIGAGRRASPSALAIEDFANGGPPNRLRHEGPPNT SVKVYIGAGRRASPSALAIEDFANGGPPNLRHEGPPNT SVKVYIGAGRRASPSALAIEDFANGGPPNLRHEGPPNT SVKVYIGAGRRASPSALAIEDFANGGPPNLRHEGPPNT SVKVYIGAGRRASPSALAIEDFANGGPPNLRHEGPPNT SVKVYIGAGRRASPSALAIEDFANGGPPNLRHEGPPNT SVKVYIGAGRRASPSALAIEDFANGGPPNLRHEGPPNT SVKVYIGAGRRASPSALSSYSETPVVCFPPASDOFILL LSSLYSLYCHTVPUCNVDLODMGYNFSCNHTMAHLFSKLSCYYLCF VSIYGLTCLYTLYWLPYRSLSEVSENKLKQLNINNEWTPNKL LVSKVQFTVDCNVDLODMGYNFSCNHTMAHLFSKLSFCYLCF VSIYGLTCLYTLYWLPYRSLSEVSENKLKQLNINNEWTPNKL RQKLQTNAHNRLEDPLINLSGLPDTVPETTELQSIKLEIIKNVM IPATIAGLDINLQELSHQCSVKHSAALSFLKENLKVLSVKPDD MRELPPWMYGLRNLEELYLLVGSLGDISNVYLESLRDLKSLKI LSIKSNYSKIPQAVVDVSSHLQKMCHNDGTHJUVLNINLKMTDN	İ	ł		YFQRMTTTSSVEGKQNLVIMGRKTWFSIPEKNRPLKDRTNLVLS
YKEMMILGHIKLFVTRIMODFESDTFFSEIDLEKYKLLPEYPG ILSDVQEKHKYKFEVCEKDD ILSDVQEKHKYKFEVCEKDD ILSDVQEKHKYKFEVCEKDD SPRPARAPLERGRESGESALGRYSPVDYMSITSFPRIPE DEPARAPLEGRENGEDAFLGDPDTDDDSFLKSARLQRLPSSSSE MGSQDGSPLRETKDPFSARAAECSCRODGUTVIVTACUTFATG VTVALWMQIYFGDPQTFQQGAVVTDARCTSLGIEVLSKQGSSV DAAVAAALCLGIVAPHSSGLGGGGWMLVHDIRRHESHLIDFRES APGALREETLQRSWETKPGLLVGVPGMVKGLHEAHQLYGRLPWS QVLAFAAAVAQDGFNVTHDLARALABGLPPNMSERFETFILPSG RPPLPGSLLHRPDLAEVLDVLGTSGPAAFVAGGNLTLEMVAEAQ HAGGVITEBDFSNYSALVEKPVCGVYRGHLVLSPPPPHTGPALI SALNILEGFNLTSLVSREQALHWVAETLKIALALASRLGPPVYD STITESMDDMLSKVEARYLRGHINDSQAAPAPLLPVYSLDGAPT AAQVLIMGPDDFIVAMVSSLNGPFGSGLITPSGILLNSQMLDPS WPNRTANHSAPSLENSVQPKKRPLSFLLFTVVRPAEGLCGTYLA LGANGAARGLSGLTQVRFTPWLAFFSREDSCGLDCRCLSYLWLV SIPHANNMG VQGITSYQQRLQAIRKEKSRDARSRRGKENFEFYELAKLLPLP AAAITSGLDKASIIRLTISYLKMRDFANQGPPPMNLRMEGGPPPMT SVKVIGAQRRASPSALAIEVFEAHLGSHLQSLDGVVFALNQEG KFLYISETVSIYLGLSQVELTGSSVFDYVHPGDHVEMAEGLGMK LPPGRGLLSQCTAEDGASSASSSOSTPEPVVCFPPASDQFLL LPPGRGLLSQCTAEDGASSASSSOSTPEPVVCFPPASDQFLL AEVGKSCIIKRVCERKFVSKYLATIGLDYGVTKVHVRDREIKVN IFDMAGHPFYEVRRFF SALVSKYGTIKRVCERKFVSKYLATIGLDYGVTKVHVRDREIKVN IFDMAGHPFYFVEVRFF VSIYGLTCLYTLYWLPYRSLRRYSFEYVRQETGFDDIPDVKNDF AFMLMMIDQYDPLYSKRFAVFISCHSKYLATIGLDYGVTKVHVRDREIKVN FORMACHLTURNETPDKL KQKLQTNANNRLEPJLINLSGLPDTVFETELQSKLKEIIKVISNA LVSKVQFTVDCNVDIQDMTGYKNFSCNHTMAHLFSKLSFCYLCF VSIYGLTCLYTLYWLPYRSLRRYSFEYVRQETGFDDIPDVKNDF AFMLMMIDQYDPLYSKRFAVFISCHSKUKKLGLINLNNEWTPDKL RQKLQTNANNRLEPJLINLSGLPDTVFETELQSKLKEIIKVISNK IPATIAGLDNLQEJSHQCSVKHSAALSFLKENLKVLSVKPDD MRELPPWMYGLRNLEELYLVGSLSHDISNVYLESJRDLKSLKI LSIKSNYSKIPQAVDVSSHLGKMCIHNDETHJVKILKKMTN IPATIAGLDNLQEJSHQCSVKHSAALSFLKENLKVLSVKPDD MRELPPWMYGLRNLEELYLVGSLSHDISNVYLESJRDLKSLKI LSIKSNYSKIPQAVDVSSHLGKMCIHNDETHJVKINLKKMTN IPATIAGLDNLGLSHQCKVCHNORCHLONGTHLVVINNIKKMTN	1			RELKEPPQGAHFLARSLDDALKLTERPELANKVDMIWIVGGSSV
1 1879 NSRVDDFVARARMAAENEASQESALGAYSPVDYMSITSFPRLPE DEPAPAAPLRGRKDEDAFIGDPDTDPDSFIKSARLQRLPSSSSE MGSQDGSPLRETRKDPFSAAAAECSCRQDGLTVIVTACLTFATG VTVALVMQIYFGDPQIFQGGGVAVTDARACTSIGIEVLSKQGSSV DAAVAAALCLGIVAPHSGSGGGGGWMLVMDIRRNESHLIDFRES APGALREETLQRSHETKPBFSGLGGGGWMLVMDIRRNESHLIDFRES APGALREETLQRSHETKPGLLVGVPGMVKGLHEAHQLYGRLPMS QVLAFAAAVAQDFNVTHDLARALABQLPPNMSERFRETELPSG RPPLPGSLLHRPDLAEVLDVLGTGGPAAPYAGGNLTLEMVAEAQ HAGGVITEBDFSNYSALVEKPVCGVYRGHLVLSPPPPHTGPALI SALNILEGRNLTSLVSREQALHWAETLKIALALASRLGPPVND STITESMODMLSKVEABAYLGCHINDSGAAPAPLLPVYRLDGAPT AAQVLIMGPDDFIVAMVSSLNQPFGSGLITPSGILINSGMLDPS WNNRTANHSAPSLENSVQPGKRPLSFLLPTVVRPABGLCGTYLA LGGNGAARGISGLTQVRFTPWLAFFSREPSCGLDCRCLSYLWLV SIPHAANMG 6621 1 662 VQGITSYQQRLQALRKEKSRDAARSRRGKENPEFVELAKLLPLP AAITSQLDKASIIRLTISYLKMRDFANQGDPPWNLRMEGFPPNT SVKVIGAQRRRSPSALAIEVPEAHLGSHLQSLDGYVFALNQEG KFLYISETVSIYLGLSQVELTGSSVFDVVHPDGHVEMAEQLGMK LPPGRGLLSQGTAEDGASSASSSSOSETPEPVCFPPASDGFLL SVKVIGAGRRFSFALAIEVPEAHLGSHLQSLDGYVFALNGEG KFLYISETVSIYLGLSQVELTGSSVFDVHPGDHVEMAEQLGMK LPPGRGLLSQGTAEDGASSASSSSSSSTPPVCFPPASDGFLL 6622 2 319 GRASGAQETETAGGPERARMAEMMPKRKEPGRSGIKVISMGN AEVGKSCIIKRYCEKRFVSKYLATIGIDYGVTKVHVRDREIKVN IFDMAGHPFFYEVKRP 6623 1886 189 KALFSKVKKKFLINEEGDILYAMYVRQTVLKVIKFLIIIAYNSA LVSKVQFTVDCNVDLQDMTGYKNFSCNHTMAHLESKLSFCYLCF VSIYGLTCLYTLYWLFYRSLRYSFEYVRQETGFDDIDDVKNDF AFMLHMIDQYDPLYSKRFAVFLSEVSENKKKQLNLNNEWTPDKL RQKLQTNAHNRLELPLMSGLEDTVEFITTLQSLKLEIIKNVM IPATIAQLDNLQELSLHQCSVKHSAALSFLKENLKVLSVKFDD MRELPPWMYGLRNLEELYLVGSSHDISRVVTLESLERLKKJLSVKFDD MRELPPWMYGLRNLEELYLVGSSHDISRVVTLESLERLKKJLSVKFDD MRELPPWMYGLRNLEELYLVGSSHDISRVVTLESLERLKKYLSVKFDD MRELPPWMYGLRNLEELYLVGSSHDISRVVTLESLERLKKYLSVKFND LSIKNSKYPQAVVJOYSSHLQKMCINNDCTKKVMN	1	}		YKEAMNHLGHLKLFVTRIMQDFESDTFFSEIDLEKYKLLPEYPG
DEPAPABPLEGREDEDJEFLESPLEVSKSSE MGSQDGSPLRETRKDPFSAAAAECSCRQDGLTUIVTACLTFATG VTVALWQIYFGDPQIFQQGAVVTDARACTSLGIEVISKQGSSV DAAVAAALCIGIVAPHSSGLGGGGWALVHDIRRNESHLIDFRES APGALREETLQRSWETKPGLLVGVPGMVKGLHEAHOLYGRLPWS QVLAFAAAVAQDGFNVTHOLARALAEQLPPNMSERFRETFLPSG RPPPLPGSLLRPPDLAEVLDVLGTSGPAAPYAGGNLTLEMVAEAQ HAGGVITEBDFSNYSALVEKPVCGVYRGHLVLSPPPFHTGPALI SALNILEGFNLTSLVSREQALHWAEFLLFLLFUNGAPT AQVLIMGPDDFIVAMVSSLNQPFGSGLITPSGILLNSGMLDPS WPNRTANHSAPSLENSVQPGRPLSFLLFTLVTVAPAEGLCGTYLA LGANGAARGLIGGLTQVRFTPWLAFFSREPSCGLDCRCLSYLMLV SIPHAANMG 6621 1 662 VGGITSYQQRLQALRKEKSRDAARSRGKENPEFYELAKLLPLP AAITSQLDKASIIRLTISYLKMRDFANGGDPWNLRMEGEPPNT SVKVIGAQRRRSPSALAIEVFEAHLGSHLQSLDGYVFALNOEG KFLYISETVSIYLGLSQVELTGSSVFDYVHPGDHVEMAEQLGMK LPPGRGLLSQGTAEDGASSASSSSQSETPEPVVCFPPASDQFLL 6622 2 319 GRASGAQETEAGGPERARAMEANMPKREFGRSLRIKVISMGN AEVGKSCIIKRYCEKRFVSKYLATIGIDYGVTKVHVRDREIKVN IFDMAGHPFYFSVRKPF 6623 1886 189 KALFEKVKKKFRLIVEEGDILYAMYVRQTVLKVIKFLIITAYNSA LVSKVQFTVDCNVDLQDMTGYKMFSCHTMAHLESKLSFCYLCF VSIYGLTCLYTLYWLFYRSLRYSFEYVRGETGFDDIDDVKNDF AFMLHMIDQYDPLYSKRFAVFLSEVSENKKKQLNINNEWTPDKL RQKLQTNAHNRLELPLMLSGLPDTVEITTLQGLKLEIIKNVM IPATIAQLDNLQELSLHQCSVKHSALSFLKENLKVLSVKFDD MRELPPWMYGLRNLEELILMSGLPDTVEITTLGSLKKEIIKNVM IPATIAQLDNLQELSLHQCSVKHSALSFLKENLKVLSVKFDD MRELPPRMYGLRNLEELILNGSGLEDTTVEITTLGSLKELKILKNAM LSIKSNVSKIPQAVVDVSSHLQKMCINNDCTKKVINNLKKMTN	- 6600			ILSDVQEGKHIKYKFEVCEKDD
MGSQDGSPLRETRKDPFSAAAAECSCRQDGLTVIVTACLTPATG VTVALVMQIYFGDQGAVVTDAARCTSIGIEVLSKQGSSV DAAVAAALCLGIVAPHSSGIGGGGVMLVHDIRRNESHLIDFRES APGALREETLQRSWETKPGLLVGVPGMVKGLHEAHQLYGRLPWS QVLAFAAAVAQDGFNVTHDLARALAEQLPPMNSERFRETFLPSG RPPLPGSLHRPDLAEVLDVLCTGGPAAPYAGGNLTLEMVAEAQ HAGGVITEBDFSNYSALVEKPVCGVYRCHLVLSPPPPHTGPALI SALNILEGFNLTSLVSREQALHWVAETLKIALALASRLGDPVYD STITESMDDMLSKVEAAYLRGHINDSGAAAPAPLLPVYRLDGAPT AAQVLIMGPDDFIVAMVSSLNQPFGSGLITPSGILINSQMLDPS WPNRTANHSAPSLENSVQPGKRPLSFLLPTVVRPAEGLCGTYLA LGANGAARGLSGLTQVRFTPWLAFFSREPSCGLDCRCLSYLWLV SIPHAAMMG 6621 1 662 VQGITSYQQRLQALRKEKSRDAARSRRGKENFEFYELAKLLPLP AAITSQLDKASIIRLTISYLKMRDFANQGDPPWNLRMEGPPPNT SVKVIGAQRRRSPSALAIEVFEAHLGSHILQSLDGYVFALNQEG KFLYISETVSIYLGLSQVELTGSSVFDYVHPGDHVEMAEQLGMK LPPGRGLLSQGTAEDGASSASSSOSETBEPVVCFPPASDQFILL CHARGAPPFYSEVKLP 6622 2 319 GRASGAQETEAGGPERARMEANMPKRKEPGRSLRIKVISMGN AEVGKSCIIKKYCEKRFVSKYLATIGIDYGVTKVHVRDREIKVN IFDMAGHPFFYEVKRP 6623 1886 189 KALFEKVKKFRLHVEEGDLLYAMYVROTVLKVIKFLIIIAYNSA LVSKVQFTVDCNVDIQDMTGYKNFSCNHTMAHLFSKLSFCYLCF VSIYGLTCLYTLYWLFYRSLRBYSFEYVRQETGFDDJPDVKNDF AFMLHMIDQYDPLYSKRFAVFISEVSENKLKQUNLNEWTPDKL RQKLQTNAHNRLELPLIMLSGLPDTVFEITELQSLKLEIIKNVM IPATIAQLDNLQELSLHQCSVKIHSAALSFLKENLKVLSVKFDD MRELPPWMYGLRNLEELYLVGSLSHDISRNVTLESLRDLKSLKI LSIKSNVSKIPQAVVDVSSHLQKMCIHNDGTKLVMLNNLKKMTN	6620	3	1879	NSRVDDFVARARMAAENEASQESALGAYSPVDYMSITSFPRLPE
VTVALVMQIYFGDPQIFQQGAVVTDAARCTSLGIEVLSKQGSSV DAAVAAALCLGIVAPHSSGLGGGGWMLVHDIRRESHLTDFRES APGALREETLQRSWETKPGLLUGVPGMVKGLHEAHQLYGRLPWS QVLAFAAAVAQDGFNVTHDLARALAEQLPPNMSERFRETFIPBG RPPLPGSLLHRPDLAEVLDVLGTSGPAAFYAGGNLTLEMVAEAQ HAGGVITEBDFSNYSALVEKPVCGVYRGHLVLSPPPHTGPALI SALNILEGFNITSLVSREQALHWVAETLKIALALASRLGDPVYD STITESMDDMLSKVEAAYLRGHINDSQAAPAPLLPVYELDGAPT AAQVLIMGPDDFIVAMVSSLNQPFGSGLITPSGILLNSQMLDPS WPNRTANHSAPSLENSVQPGKRPLSFLLPTVVRPAEGLCGTYLLA LGANGAARGLSGLTQVRFTPWLAFFSREPSCGLDCRCLSYLWLV SIPHAANMG 6621 1 662 VQGITSYQQRLQALRKEKSRDAARSRRGKENFEFYELAKLLPLP AAITSQLDKASIIRLTISYLKMRDFANQGDPPWLIKNEGPPPNT SVKVIGAQRRRSPSSALAIEVFEAHLGSHILQSLDGYVFALNQEG KFLYISETVSIYLGLSQVELTGSSVFDYVHPGDHVEMAEQLGMK LPPGRGLLSQGTAEDGASSASSSSSSFTEPVVCFPPASDQFLL 6622 2 319 GRASGAQEETENGGPERARAMEANMPKKEPGRSLRIKVISMGN AEVGKSCIIKRYCEKFFVSKYLATIGIDYGVTKVHVRDREIKVN IFDMAGHPPFYEVRKPF 6623 1886 189 KALFEKVKKFRLHVEEGDILYAMYVRQTVLKVIKFLIITAYNSA LVSKVQFTVDCNVDIQDMGTKMFSCNHTMAHLFSKLSFCYLCF VSIYGLTCLYTLYWLFYRSLREYSFEYVRQETGFDDIPDVKNDF AFMLHMIDQYDPLYSKRFAVFLSEVSENKLKQLNLNNEWTPDKL RQKLQTNAHNRLELPLIMLSGLPDTVFEITELQSLKLEIIKNVM IPATIAQLDNLQELSLHQCSVKHSAALSFLKENLKVLSVKPDD MRELPPWMYGLRNLBELYLVGSLSHDISRNVTLESLRDLKSLKI LSIKSNVSKIPQAVVDVSSHLQKMCINNDGTKLVMLNNLKKMTN	1			DEPAPAAPLRGRKDEDAFLGDPDTDPDSFLKSARLQRLPSSSSE
DAAVAAALCIGTVAPHSSGIGGGGWALVHDIRRNESHLIDFRES APGALREETLQRSWETKPGLLVGVPGMVKGLHEAHQLYGRLPWS OVLAFAAAVAQDGFNVTHDLARALASQLPPMSERFRETFLPSG RPPLPGSLLHRPDLAEVLDVLGTSGPAAFYAGGNLTLEMVAEAQ HAGGVITEBDFSNYSALVEREVCGYYRGHLVLSPPPPHTGPALI SALNILEGFNLTSLVSREQALHWVAETLKIALALASRLGDPYVD STITESMDDMLSKVEAAYLRGHINDSQAAPAPLLPVYRLDGAPT AAQVLIMGPDDFIVAMVSSLNQPFGSGLITPSGILLNSQMLDPS WPNRTANHSAPSLENSVQPGKRPLSFLLPTVVRPAEGLCGTYLA LGANGAARGLSGLTQVRFTPWLAFFSREPSCGLDCRCLSYLWLV SIPHAANMG 6621 1 662 VQGITSYQQRLQALRKEKSRDAARSRRGKENFEFYELAKLLPLP AALTSGLDKASIIRLTISYLKMRDFANQGDPPMNLRNEGPPPNT SVKVIGAQRRRSPSALAIEVFEAHLGSHIQSLDGYVFALNQEG KFLYISETVSIYLGLSQVELTGSSVFDVVHPGDHVEMAEQLGMK LPPGRGLLSGGTAEDGASSASSSSQSETPEPVVCFPPASDQFLL 6622 2 319 GRASGAQETTEAGGPERARMEANMPKKEPGRSLRIKVISMGN AEVGKSCIIRKYCEKFVSKYLATIGIDYGVTKVHVRDREIKVN IFDMAGHPFFYEVRKPF 6623 1886 189 KALFEKVKKFRLHVEEGDILYAMYVRQTVLKVIKFLIITAYNSA LVSKVQFTVDCNVDIQDMTGYKMFSCHHTMAHLFSKLSFCVLCF VSIYGLTCLYTLYWLFYRSLREYSFEYVRQETGFDDIPDVKNDF AFMLHMIDQYDPLYSKRFAVFLSEVSENKLKQLNLNNEWTPDKL RQKLQTNAHNRLELPLIMLSGLPDTVFEITELQSLKLEIIKNVM IPATIAQLDNLQELSLHQCSVKIHSAALSFLKENLKVLSVKPDD MRELPPWMYGLRNLEELYLVGSLSHDISRNVTLESLRDLKSLKI LSIKSNVSKIPQAVVQVSSHLQKMCINNDGTKLVMLNNLKKMTN	1			MGSQDGSPLRETRKDPFSAAAAECSCRQDGLTVIVTACLTFATG
APGALREETLQRSWETKPGLLVGVPGMVKGLHEAHQLYGRLPWS QVLAFAAAVAQDGFNVTHDLARALABQLPPMMSERFRETFLPGG RPPLPGSLLHRPPDLAEVLDVLGTGGPAAPYAGGNLTLEMVAEAQ HAGGVITEEDFSNYSALVEKPVCGVYRGHLVLSPPPPHTGPALI SALNILEGFNLTSLVSREQALHWVAETLKIALALASRLGDPVYD STITESMDDMLSKVEAAYLRGHINDSOAAPAPLLPVYELDGAPT AAQVLIMGPDDFIVAMVSSLNQPFGSGLITPSGILLNSQMLDPS WPNRTANHSAPSLENSVQPGKRPLSFLLPTVVRPAEGLCGTYLLA LGANGAARGLSGLTQVRFTPWLAFFSREPSCGLDCRCLSYLWLV SIPHAANMG VQGITSYQQRLQALRKEKSRDAARSRRGKENFEFYELAKLLPLP AAITSQLDKASIIRLTISYLKWRDFANQGDPPWNLRMEGPPPNT SVKVIGAQRRRSPSALAIEVPEAHLGSHILQSLDGVVFALNQEG KFLYISETVSIYIGLSQVELTGSSVFDYVHPGDHVEMAEQLGMK LPPGRGLLSQGTAEDGASSASSSSSSETPEPVVCFPPASDQFLL AEVGKSCIIKRYCEKRFVSKYLATIGIDYGVTKVHVRDREIKVN IFDMAGHPPFYEVRKPF 6623 1886 189 KALFEKVKKFRLHVEEGDILYAMYVRQTVLKVIKFLIIIAYNSA LVSKVQFTVDCNVDIQDMTGYKNFSCNHTWAHLFSKLSFCYLCF VSIYGLTCLYTLYWLPYRSLREYSFEYVRGETGFDDIPDVKNDF AFMLHMIDQYDPLYSKRFAVFLSEVSENKLKQLNLINNEWTPDKL RQKLQTNAHNRLELPLIMLSGLPDTVPEITELQSLKLEIIKNVM IPATIAQLDNLQBLSLHQCSVKIHSAALSFLKENLKVLSVKFDD MRELPPWMYGLRNLBELYLVGSLSHDISRNVTLESLRDLKSLKI LSIKSNVSKIPQAVVDVSSHLQKMCIHNDGTKLVMLNNLKKMTN				VTVALVMQIYFGDPQIFQQGAVVTDAARCTSLGIEVLSKQGSSV
QVLAFAAVAQDGFNVTHDLARALAEQLPPMMSERFRETFLPSG RPPLPGSLLHRPDLAEVLDVLGTSGPAAPYAGGNLTLEMVAEAQ HAGGVITEBFSNYSALVEKPVCGVYRGLVLSPPPPTGPALI SALNILEGFNLTSLVSREQALHWVAETLKIALALASRLGDPVYD STITESMDDMLSKVEAAYLRGHINDSQAAPAPLLPVYBLDGAPT AAQVLIMGPDDFIVAMVSSLNQPFGSGLITPSGILLNSQMLDFS WPNRTANHSAPSLENSVQPEGKPLSFLLPTVVRPAEGLCGTYLA LGANGAARGLSGLTQVRFTPWLAFFSREPSCGLDCRCLSYLWLV SIPHAANMG 6621 1 662 VQGITSYQQRLQALRKEKSRDAARSRRGKENFEFYELAKLLPPLP AAAITSQLDKASIIRLTISYLKMRDFANQGDPPWNLRMEGPPPNT SVKVIGAQRRRSPSALAIEVFEAHLGSHILQSLDGYVFALNQEG KFLYISETVSIYLGLSQVELTGSSVFDYVHPGDHVEMAEQLGMK LPPGRGLLSQGTAEDGASSASSSSQSETBEPVVCFPPASDQFLL GRASGAQEETEAGGERARAMEANMPKRKEPGRSLRIKVISMGN AEVGKSCIIKRYCEKRFVSKYLATIGDYGVTKVHVRDREIKVN IFDMAGHPFFYEVRKPF 6623 1886 189 KALFEKVKFRLHVEEGDILYAMYVRQTVLKVIKFLIIIAYNSA LVSKVQFTVDCNNDIQDMTGYXNFSCNHTMAHLFSKLSFCYLCF VSIYGLTCLYTLYWLFYRSLRBYSFEYVRQETGFDDIPDVKNDF AFMLHMIDQYDPLYSKRFAVFLSEVSENKLKQLNINDENTPDKL RQKLQTNAHNRLELPLIMLSGLPDTVFEITELQSLKLEIIKNVM IPATIAQLDNLQELSHHQCSVKIHSAALSFLKENIKKVLSVKFDD MRELPPWMYGLRNLGELSHLQCSVKIHSAALSFLKENIKKVLSVKFDD MRELPPWMYGLRNLGELSHLQCSVKIHSAALSFLKENIKKVLSVKFDD MRELPPWMYGLRNLGELSHLQCSVKIHSAALSFLKENIKKVLSVKFDD MRELPPWMYGLRNLGELSHLQCSVKIHSAALSFLKENIKKVLSVKFDD LSIKSNVSKIPQAVVDVSSHLQKMCINNDGTKLVMLNNIKKMTN	1 .			DAAVAAALCLGIVAPHSSGLGGGGVMLVHDIRRNESHLIDFRES
RPPLPGSLLHRPDLAEVLDULGTSGPAAPYAGGNLTLEMVAEAQ HAGGVITEEDFSNYSALVEKPVCGYYRGHUVLSPPPHTGPALI SALNILEGFNLTSLVSREQALHWVAETLKIALALASRLGDPVYD STITESMDDMLSKVEAAYLRGHINDSQAAPAPLLPVYBLDGAPT AAQVLIMGPDDFIVAMVSSLNQPFGSGLITPSGILLNSQMLDFS WPNRTANHSAPSLENSVQPGKRPLSFILPTVVRPAEGLCGTYLA LGANGAARGLSGLTQVRFTPWLAFFSREPSCGLDCRCLSYLWLV SIPHAANMG SIPHAANMG VQGITSYQQRLQALRKEKSRDAARSRRGKENFEFYELAKLLPLP AAITSQLDKASIIRLTISYLKMRDFANQGDPPWNLRMEGPPPNT SVKVIGAQRRRSPSALAIEVFEAHLGSHIJQSLDGYVFALNQEG KFLYISETVSIYLGLSQVELTGSSVFDYVHPGDHVEMAEQLGMK LPPGRGLLSQGTAEDGASSASSSSQSETPEPVVCFPPASDQFLL CPGRGLLSQGTAEDGASSASSSSSSETPEPVVCFPPASDQFLL GRASGAQEETEAGGPERARMEANMPKRKEPGRSLRIKVISMGN AEVGKSCIIKRYCEKRFVSKYLATIGIDYGVTKVHVRDREIKVN IFDMAGHPFFYEVRKPF KALFEKVKKFRLHVEEGDILYAMYVRQTVLKVIKFLIITAYNSA LVSKVQFTVDCNVDIQDMTGYKNFSCNHTMAHLFSKLSFCYLCF VSIYGLTCLYTLYWLFYRSLRBVSFEYVRQETGFDDIPDVKNDF AFMLHMIDQYDPLYSKRFAVFLSEVSENKLKQLNLNNEWTPDKL RQKLQTNAHNRLELPLIMLSGLPDTVFEITELQSLKLEIIKNVM IPATIAQLDNLQELSHDCSVKIHSAALSFIKKNIKVLSVKFDD MRELPPWMYGLRNLBELYLVGSLSHDISRNVTLESLRDLKSLKI LSIKSNVSKIPQAVVDVSSHLQKMCINNDGTKLVMLNNLKKMTN	1 !			APGALREETLQRSWETKPGLLVGVPGMVKGLHEAHQLYGRLPWS
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SALNILEGRNLTSLVSREQALHWVAETLKIALALSRLGDPVYD STITESMDDMLSKVEAAYLRGHINDSQAPAPLLIPVYBLDGAPT AAQVLIMGPDDFIVAMVSSLNQPFGSGLITPSGILLNSQADPS WPNRTANHSAPSLENSVQPGKRPLSFLLPTVVRPAEGLCGTYLA LGANGAARGLSGLTQVRFTPWLAFFSREPSCGLDCRCLSYLWLV SIPHAANMG OCCUPY VQGITSYQQRLQALRKEKSRDAARSRRGKENFEFYELAKLLPLP AAAITSQLDKASIIRLTISYLKMRDFANQGDPPWNLRMEGPPPNT SVKVIGAQRRRSPSALAIEVFEAHLGSHILQSLDGYVFALNQEG KFLYISETVSIYLGLSQVELTGSSVFDYVHPGDHVEMAEQLGMK LPPGRGLLSQGTAEDGASSASSSSQSETPBPVVCFPPASDQFLL GRASGAQEETEAGGPERARMEANMPKRKEPGRSLRIKVISMGN AEVGKSCIIKRYCEKRFVSKYLATIGIDYGVTKVHVRDREIKVN IFDMAGHPPFYEVRKPF KALFEKVKKFRLHVEEGDILYAMYVRQTVLKVIKFLIIIAYNSA LVSKVQFTVDCNVDIQDMTGYKNFSCNHTMAHLFSKLSFCYLCF VSIYGLTCLYTLYWLFYRSLRBYSFEYVRQETGFDDIPDVKNDF AFMLHNIDQYDPLYSKRFAVFLSEVSENKLKQLNLNNEWTPDKL RQKLQTNAHNRLELPLIMLSGLPDTVFEITELQSLKLEIIKNVM IPATIAQLDNLQELSHQCSVKHSAALSFLKENLKVLSVKFDD MRELPPWMYGLRNLBELYLVGSLSHDISRNVTLESLRDLKSLKI LSIKSNVSKIPQAVVDVSSHLQKMCIHNDGTKLVMLNNLKKMTN	1	ĺ		HAGGUITERDEGNYCATUERDUGGUUDGUUU GDDDDGGGG
STITESMDDMLSKVEAAYLRGHINDSQAAPAPLLPVYBLDGAPT AAQVLIMGPDDFIVAMYSSLNQPFGSGLITPSGILLNSQMLDPS WPNRTANHSAPSLENSVQPGKRPLSFLLPTVVRPAEGLCGTYLA LGANGAARGLSGLTQVRFTPWLAFFSREPSCGLDCRCLSYLWLV SIPHAANMG VQGITSYQQRLQALRKEKSRDAARSRRGKENFEFYELAKLLPLP AAITSQLDKASIIRLTISYLKMRDFANQGDPPWNLRMEGPPPNT SVKVIGAQRRRSPSALAIEVFEAHLGSHILQSLDGYVFALNQEG KFLYISETVSIYLGLSQVELTGSSVFDYVHPGDHVEMAEQLGMK LPPGRGLLSQGTAEDGASSASSSSQSETPEPVVCFPPASDQFLL GRASGAQEETEAGGPERARAMEANMPKRKEPGRSLRIKVISMGN AEVGKSCIIKRYCEKRFVSKYLATIGIDYGVTKVHVRDREIKVN IFDMAGHPFFYEVRRPF KALFEKVKKFRLHVEEGDILYAMYVRQTVLKVIKFLIIIAYNSA LVSKVQFTVDCNVDIQDMTGYKNFSCNHTMAHLFSKLSFCYLCF VSIYGLTCLYTLYWLFYRSLREYSFEYVRQETGFDDIPDVKNDF AFMLHMIDQYDDLYSKRFAVFLSEVSENKLKQLNLNNEWTPDKL RQKLQTNAHNRLELPLIMLSGLPDTVFEITELQSLKLEIIKNVM IPATIAQLDNLQELSLHQCSVKHSAALSFLKENLKVLSVKFDD MRELPPWMYGLRNLBELYLVGSLSHDISRNVTLESLRDLKSLKI LSIKSNVSKIPQAVVDVSSHLQKMCIHNDGTKLVMLNNLKKMTN		Ì		SALNILEGENI TSI VSDEORI HUVAETI VIAI ALAGA GARAGO
AAQVLIMGPDDFIVAMVSSLNQPFGSGLITPSGILLNSQMLDFS WPNRTANHSAPSLENSVQPGKRPLSFILPTVVRPAEGLCGTYLA LGANGAARGLSGLTQVRFTPWLAFFSREPSCGLDCRCLSYLWLV SIPHAANMG OCCUPANT AAITSQLDKASIIRLTISYLKMRDFANQGDPPWNLRMEGPPPNT SVKVIGAQRRRSPSALAIEVPEAHLGSHILQSLDGYVFALNQEG KFLYISETVSIYLGLSQVELTGSSVFDYVHPGDHVEMAEQLGMK LPPGRGLLSQGTAEDGASSASSSSQSETPRPVCFPPASDQFLL GRASGAQEETEAGGPERARAMEANMPKKEPGRSLRIKVISMGN AEVGKSCIIKRYCEKRFVSKYLATIGIDYGVTKVHVRDREIKVN IFDMACHPFFYEVRRPF KALFEKVKKFRLHVEEGDILYAMYVROTVLKVIKFLIIIAYNSA LVSKVQFTVDCNVDIQDMTGYKNFSCNHTMAHLFSKLSFCYLCF VSIYGLTCLYTLYWLFYRSLREYSFEYVRQETGFDDIPDVKNDF AFMLHMIDQYDPLYSKRFAVFLSEVSENKLKQLNLNNEWTPDKL RQKLQTNAHNRLELPLIMLSGLPDTVFEITELQSLKLEIIKNVM IPATIAQLDNLQELSLHQCSVKHSAALSFLKENLKVLSVKFDD MRELPPWMYGLRNLBELYLVGSLSHDISRNVTLESLRDLKSLKI LSIKSNVSKIPQAVVDVSSHLQKMCIHNDGTKLVMLNNLKKMTN	1			STITESMDDMLSKVEAAYLRGHTNDSOAADADLLDIVDLDOND
WPNRTANHSAPSLENSVQPGKRPLSFLLPTVVRPAEGLCGTYLA LGANGAARGLSGLTQVRFTPWLAFFSREPSCGLDCRCLSYLWLV SIPHAANMG VQGITSYQQRLQALRKEKSRDAARSRRGKENFEFYELAKLLPLP AAITSQLDKASIIRLTISYLKMRDFANQGDPPWNLRMEGPPPNT SVKVIGAQRRRSPSALAIEVFEAHLGSHILQSLDGYVFALNQEG KFLYISETVSIYLGLSQVELTGSSVFDYVHPGDHVEMAEQLGMK LPPGRGLLSQGTAEDGASSASSSSSQSETPRPVCFPPASDQFLL GRASGAQEETEAGGPERARAMEANMPKREPGRSLRIKVISMGN AEVGKSCIIKRYCEKRFVSKYLATIGIDYGVTKVHVRDREIKVN IFDMAGHPFFYEVRKPF 6623 1886 189 KALFEKVKKFRLHVEEGDILYAMYVROTVLKVIKFLIIIAYNSA LVSKVQFTVDCNVDIQDMTGYKNFSCNHTMAHLFSKLSFCYLCF VSIYGLTCLYTLYWLPYRSLREYSFEYVRQETGFDDIPDVKNDF AFMLHNIDQYDPLYSKRFAVFLSEVSENKLKQLNLNNEWTPDKL RQKLQTNAHNRLELPLIMLSGLPDTVFEITELQSLKLEIIKNVM IPATIAQLDNLQELSLHQCSVKHSAALSFLKENLKVLSVKFDD MRELPPWMYGLRNLBELYLVGSLSHDISRNVTLESLRDLKSLKI LSIKSNVSKIPQAVVDVSSHLQKMCIHNDGTKLVMLNNLKKMTN		ł		AAQVLIMGPDDFIVAMVSSLNOPFGSGI.TTDSGTT.INGONT.DBG
LGANGAARGLSGLTQVRFTPWLAFFSREPSCGLDCRCLSYLWLV SIPHAANMG OQGITSYQQRLQALRKEKSRDAARSRRGKENFEFYELAKLLPLP AAITSQLDKASIIRLTISYLKMRDFANQGDPPWNLRMEGPPPNT SVKVIGAQRRRSPSALAIEVFEAHLGSHILQSLDGYVFALNQEG KFLYISETVSIYLGLSQVELTGSSVFDYVHPGDHVEMAEQLGMK LPPGRGLLSQGTAEDGASSASSSSSQSETPEPVVCFPPASDQFLL GRASGAQEETEAGGPERARAMEANMPKRKEPGRSLRIKVISMGN AEVGKSCIIKRYCEKRFVSKYLATIGIDYGVTKVHVRDREIKVN IFDMAGHPPFYEVRKPF KALFEKVKKFRLHVEEGDILYAMYVRQTVLKVIKFLIIIAYNSA LVSKVQFTVDCNVDIQDMTGYXNFSCNHTMAHLFSKLSFCYLCF VSIYGLTCLYTLYWLFYRSLREYSFEYVRQETGFDDIPDVKNDF AFMLHNIDQYDPLYSKRFAVFLSEVSENKLKQLNLNNEWTPDKL RQKLQTNAHNRLELPLIMLSGLPDTVFEITELQSLKLEIIKNVM IPATIAQLDNLQELSLHQCSVKHSAALSFLKENLKVLSVKFDD MRELPPWMYGLRNLBELYLVGSLSHDISRNVTLESLRDLKSLKI LSIKSNVSKIPQAVVDVSSHLQKMCIHNDGTKLVMLNNLKKMTN	[]	l		WPNRTANHSAPSLENSVOPGKRPLSFLLPTVVRPAEGI.CGTVI.A
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AAITSQLAKASIIRLTISYLKMRDFANQGDPPWNLRMEGPPPNT SVKVIGAQRRRSPSALAIEVPEAHLGSHILQSLDGYVFALNQEG KFLYISETVSIYLGLSQVELTGSSVFDYVHPGDHVEMAEQLGMK LPPGRGLLSQGTAEDGASSASSSSQSETPEPVVCFPPASDQFLL GRASGAQEETEAGGPERARMEANMPKRKEPGRSLRIKVISMGN AEVGKSCIIKRYCEKRFVSKYLATIGIDYGVTKVHVRDREIKVN IFDMAGHPPFYEVRKPF KALFEKVKKFRLHVEEGDILYAMYVRQTVLKVIKFLIIIAYNSA LVSKVQFTVDCNVDIQDMTGYXNFSCNHTMAHLFSKLSFCYLCF VSIYGLTCLYTLYWLFYRSLREYSFEYVRQETGFDDIPDVKNDF AFMLHNIDQYDPLYSKRFAVFLSEVSENKLKQLNLNNEWTPDKL RQKLQTNAHNRLELPLIMLSGLPDTVFEITELQSLKLEIIKNVM IPATIAQLDNLQELSLHQCSVKHSAALSFLKENLKVLSVKFDD MRELPPWMYGLRNLBELYLVGSLSHDISRNVTLESLRDLKSLKI LSIKSNVSKIPQAVVDVSSHLQKMCIHNDGTKLVMLNNLKKMTN	اا			SIPHAANMG
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SVKVIGAQRRRSPSALAIEVFEAHLGSHILQSLDGYVFALNQEG KFLYISETVSIYLGLSQVELTGSSVFDYVHPGDHVEMAEQLGMK LPPGRGLLSQGTAEDGASSASSSSQSETPEPVVCFPPASDQFLL GRASGAQEETEAGGPERARAMEANMPKRKEPGRSLRIKVISMGN AEVGKSCIIKRYCEKRFVSKYLATIGIDYGVTKVHVRDREIKVN IFDMAGHPFFYEVRKPF KALFEKVKKFRLHVEEGDILYAMYVRQTVLKVIKFLIIIAYNSA LVSKVQFTVDCNVDIQDMTGYKNFSCNHTMAHLFSKLSFCYLCF VSIYGLTCLYTLYWLFYRSLREYSFEYVRQETGFDDIPDVKNDF AFMLHMIDQYDPLYSKRFAVFLSEVSENKLKQLNLNNEWTPDKL RQKLQTNAHNLELPLIMLSGLPDTVFEITELQSLKLEIIKNVM IPATIAQLDNLQELSLHQCSVKHSAALSFLKENLKVLSVKFDD MRELPPWMYGLRNLBELYLVGSLSHDISRNVTLESLRDLKSLKI LSIKSNVSKIPQAVVDVSSHLQKMCIHNDGTKLVMLNNLKKMTN	1 1	1		AAITSOLDKASIIRLTISYLKMRDFANOGDDDWNT.DMFGDDDNT
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GRASGAGETEAGGPERARAMEANMPKRKEPGRSLRIKVISMGN AEVGKSCIIKRYCEKRFVSKYLATIGIDYGVTKVHVRDREIKVN IFDMAGHPPFYEVRKPF KALFEKVKFRLHVBEGDILYAMYVRQTVLKVIKFLIIIAYNSA LVSKVQFTVDCNVDIQDMTGYKNFSCNHTMAHLFSKLSFCYLCF VSIYGLTCLYTLYWLFYRSLRBYSFEYVRQETGFDDIPDVKNDF AFMLHHIDQYDPLYSKRFAVFLSEVSENKLKQLNLNNEWTPDKL RQKLQTNAHNRLELPLHMLSGLPDTVFEITELQSLKLEIIKNVM IPATIAQLDNLQELSLHQCSVKHSAALSFLKENLKVLSVKFDD MRELPPWMYGLRNLBELYLVGSLSHDISRNVTLESLRDLKSLKI LSIKSNVSKIPQAVVDVSSHLQKMCIHNDGTKLVMLNNLKKMTN	6622			LPPGRGLLSQGTAEDGASSASSSSQSETPEPVVCFPPASDOFIJ
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LVSKVQFTVDCNVDIQDMTGYKNFSCNHTMAHLFSKLSFCYLCF VSIYGLTCLYTLYWLFYRSLRBYSFEYVRQETGFDDIPDVKNDF AFMLHMIDQYDPLYSKRFAVFLSEVSENKLKQLNLNNEWTPDKL RQKLOTNAHNRLELPLIMLSGLPDTVFEITELQSLKLEIIKNVM IPATTAQLDNLQELSLHQCSVKIHSAALSFLKENLKVLSVKFDD MRELPPWMYGLRNLBELYLVGSLSHDISRNVTLESLRDLKSLKI LSIKSNVSKIPQAVVDVSSHLQKMCIHNDGTKLVMLNNLKKMTN	6623	1995	105	
LVSKVQFTVDCNVDIQDMTGYKNFSCNHTMAHLFSKLSFCYLCF VSIYGLTCLYTLYWLFYRSLBYSFEYVRQETGFDDIPDVKNDF AFMLHMIDQYDPLYSKRFAVFLSEVSENKLKQLNLINNEWTPDKL RQKLQTNAHNRLELPLIMLSGLPDTVFEITELQSLKLEIIKNVM IPATIAQLDNLQELSLHQCSVKIHSAALSFLKENLKVLSVKFDD MRELPPWMYGLRNLBELYLVGSLSHDISRNVTLESLRDLKSLKI LSIKSNVSKIPQAVVDVSSHLQKMCIHNDGTKLVMLNNLKKMTN	5523	7000	189	KALFEKVKKFRLHVEEGDILYAMYVRQTVLKVIKFLIIIAYNSA
AFMLIMIDQYDPLYSKRFAVFLSEVSENKLKQLNLNNEWTPDKL RQKLQTINAHNRLELPLIMLSGLPDTVFEITELQSLKLEIIKNVM IPATIAQLDNLQELSLHQCSVKIHSAALSFLKENLKVLSVKFDD MRELPPWMYGLRNLBELYLVGSLSHDISRNVTLESLRDLKSLKI LSIKSNVSKIPQAVVDVSSHLQKMCIHNDGTKLVMLNNLKKMTN]			LVSKVQFTVDCNVDIQDMTGYKNFSCNHTMAHLFSKLSFCVLCF
AFMLIMIDQYDPLYSKRFAVFLSEVSENKLKQLNLNNEWTPDKL RQKLQTINAHNRLELPLIMLSGLPDTVFEITELQSLKLEIIKNVM IPATIAQLDNLQELSLHQCSVKIHSAALSFLKENLKVLSVKFDD MRELPPWMYGLRNLBELYLVGSLSHDISRNVTLESLRDLKSLKI LSIKSNVSKIPQAVVDVSSHLQKMCIHNDGTKLVMLNNLKKMTN		İ		VSIYGLTCLYTLYWLFYRSLRBYSFEYVRQETGFDDIPDVKNDF
IPATIAQLDNLQELSLHQCSVKIHSAALSFLKENLKVLSVKFDD MRELPPWMYGLRNLBELYLVGSLSHDISRNVTLESLRDLKSLKI LSIKSNVSKIPQAVVDVSSHLQKMCIHNDGTKLVMLNNLKKMTN		1	ŀ	AFMLHMIDQYDPLYSKRFAVFLSEVSENKLKQLNLNNEWTPDKL
IPATIAQLDNLQELSLHQCSVKIHSAALSFLKENLKVLSVKFDD MRELPPWMYGLRNLBELYLVGSLSHDISRNVTLESLRDLKSLKI LSIKSNVSKIPQAVVDVSSHLQKMCIHNDGTKLVMLNNLKKMTN	1			RQKLQTNAHNRLELPLIMLSGLPDTVFEITELQSLKLEIIKNVM
LSIKSNVSKIPQAVVDVSSHLQKMCIHNDGTKLVMLNNLKKMTN		1	}	IPATIAQLDNLQELSLHQCSVKIHSAALSFLKENLKVLSVKFDD
LSIKSNVSKIPQAVVDVSSHLQKMCIHNDGTKLVMLNNLKKMIN LTELELVHCDLERIPHAVFSLLSLQELDLKENNLKSIEEIVSFQ		į	1	MRELPPWMYGLRNLBELYLVGSLSHDISRNVTLESLRDLKSLKI
LIELELVHCDLERIPHAVFSLLSLQELDLKENNLKSIEEIVSFQ	! !	ſ		LSIKSNVSKIPQAVVDVSSHLQKMCIHNDGTKLVMLNNLKKMTN
	<u> </u>			DIELELVHCDLERIPHAVFSLLSLQELDLKENNLKSIEEIVSFQ

SEQ	Predicted	Predicted end	Amino agid assemble and it
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H-Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ĺ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
]	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence	•	\=possible nucleotide insertion)
		· · · · · · · · · · · · · · · · · · ·	HLRKLTVLKLWHNSITYIPEHIKKLTSLERLSFSHNKIEVLPSH
į			LFLCNKIRYLDLSYNDIRFIPPEIGVLQSLQYFSITCNKVESLP
1			DELYFCKKLKTLKIGKNSLSVLSPKIGNLLFLSYLDGKGNHFEI
L	· ·		LPPELGDCRALKRAGLVVEDALFETLPSDVREQMKTE
6624	218	1786	GSRRGGGSRIPAVSTHVAPGRSVLRPFASGALRLRSLVKALGGC
1	1		RGRPSGLAHLSQETSHWRAKRSGRACLGDFPGEILRSFIMKCTA
	1		REWLRVTTVLFMARAIPAMVVPNATLLEKLLEKYMDEDGEWWIA
ł			KQRGKRAITDNDMQSILDLHNKLRSQVYPTASNMEYMTWDVELE
İ	1		RSAESWAESCLWEHGPASLLPSIGQNLGAHWGRYRPPTFHVQSW
1)		YDEVKDFSYPYEHECNPYCPFRCSGPVCTHYTQVVWATSNRIGC
1	Ì		AINLCHNMNIWGQIWPKAVYLVCNYSPKGNWWGHAPYKHGRPCS
i		•	ACPPSFGGGCRENLCYKEGSDRYYPPREEETNEIERQQSQVHDT
i	[HVRTRSDDSSRNEVISAQQMSQIVSCEVRLRDQCKGTTCNRYEC
1	ļ i		PAGCLDSKAKVIGSVHYEMQSSICRAAIHYGIIDNDGGWVDITR
1			QGRKHYFIKSNRNGIQTIGKYOSANSFTVSKVTVOAVTCETTVE
			QLCPFHKPASHCPRVYCPRKLYASKSTLCSCNWNSSLF
6625	1124	543	PGPRGGGGSLLSTKALGRSRGLGMHPGPSSGGTEGGVPTALRPP
1	· •		GPLVPSTSDDNLLKNIELFDKLALRFHGRLLFLKDVLGDETCCW
	ļ		SFYGQGRKIAEVCCTSIVYATEKKOTKVEFPEARIFEETLATLT
		•	YETPRGPDPALLEATGGAAGAGGAGRGEDBENREHRVRRIHVRR
			HITHDERPHGQQIVFKD
6626	3	1498	SAVEFVYTDRFHLILGISVEFLCSLRSDATMESITACLHALQAL
1			LDVPWPRSKIGSDQDSGIELLNVLHRVILTRESPSIOLASLEVA!
1	i		RQIICAAQEHVKEKRRSAEVDDGAAEKETLPEFGEGKDTGGLUP
			GKSLVFATLELCVCILVRQLPELNPKLTGSPGVKATKPOILLED
1 1	1		GSRLVSAALVILSELPAVCSPEGSISILPTILYLTIGVLRETAV
1			KLPGGQLSSTVAASLQALKGILSSPMARABKSRTAWTDIJLRSAL
	' i		TTILDCWDPVDETHQELDEVSLLTAITVFILSTSPEVTTIPCLO
	•		KRCIDKFKATLEIKDPVVQIKTYOLLHSIFOYPNPAVSYPVIVS
1 1			LASCIMEKLQEIDKRKPENTAELEIFOEGIKVLETLVTVARRHH
1	-		RAQLVACLLPILISFLLDENSLGSATSIMRNLHDFALQNLMQIG
	j		PQYSSVFKSLVASSPALKARLEAAIKGNQRSVKVKIPTSKYTKS
6627			PGKNSSIQLKTSFL
""	-	697	GIPHLSSRDMTGTPGAVATRDGEAPERSPPCSPSYDLTGKVMLL
Ji			GDTGVGKTCFLIQFKDGAFLSGTFIATVGIDFRNKVVTVDGVRV
	•		KLQIWDTAGQERFRSVTHAYYRDAQALLLLYDITNKSSFDNIRA
] [WLTEIHEYAQRDVVIMLLGNKADMSSERVIRSEDGETLAREYGV
			PFLETSAKTGMNVELAFLAIAKELKYRAGHQADEPSFQIRDYVE
6628	1	1861	SQKKRSSCCSFM
	-	1001	OCAEFGGGGGGGGGGGGGGGGGGGEENKENERPSAGSKAN KEEGDSLSLELLINGSGGGGGGGGGGEENKENERPSAGSKAN
	1		KEFGDSLSLEILQIIKESQQQHGLRHGDFQRYRGYCSRRQRRLR
			KTLNFKMGNRHKFTGKKVTEELLTDNRYLLLVLMDAERAWSYAM QLKQEANTEPRKRFHLLSRLRKAVKHAEELERLCESNRVDAKTK
	ļ	İ	LEAQAYTAYLSGMLRFEHQEWKAAIEAFNKCKTIYEKLASAFTE
}	1		EQAVLYNQRVEEISPNIRYCAYNIGDQSAINELMQMRLRSGGTE
			GLLAEKLEALITQTRAKQAATMSEVEWRGRTVPVKIDKVRIFLL
		1	GLADNEAAIVQAESEETKERLFESMLSECRDAIQVVREELKPDO
ļ , l		j	KQRDYILEGEPGKVSNLQYLHSYLTYIKLSTAIKRNENMAKGLQ
]			RALLQQQPEDDSKRSPRPQDLIRLYDIILQNLVELLQLPGLEED
[ŀ		KAFQKEIGLKTLVFKAYRCFFIAQSYVLVKKWSEALVLYDRVLK
			YANEVNSDAGAFKNSLKDLPDVQELITQVRSEKCSLQAAAILDA
ļ j			NDAHQTETSSSQVKDNKPLVERFETFCLDPSLVTKQANLVHFPP
j	}	l	GEOPT PCKDL PEDLAL MUMA PDDI PDAT FORMACO PONTACO
ĺ	į		GFQPIPCKPLFFDLALNHVAFPPLEDKLEQKTKSGLTGYIKGIF GFRS
6629	5653	4549	GATPLGSVGGRTGKMDAATLTYDTLRFAEFEDFPETSEPVWILG
	į		RKYSIFTEKDEILSDVASRLWFTYRKNFPAIGGTGPTSDTGWGC
			THE TENDETH OF THE TE

Deginning No: ulceotide location corresponding coftrat continue corresponding coftrat amino acid amino acid amino acid amino acid amino acid amino acid sequence seque	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
No:	1 ~			(Asalaning CoCuptains Description and
Costion Corresponding Cofirst Samino acid Amino	NO:			Glutamic Acid F-Phonylelanine G-Glycine
L-Leucine, M=Methionine, N=Aeparagine, problem to first amino acid residue of amino acid residue of amino acid sequence S=Serine, T=Threonine, V=Valine, S=Serine, X=Unknown, *=Stop (Codon, /=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide (S=Valine) V=Valine, V=Va	1			H=Histidine T=Tsoleusine K-Tusine
to first amino acid residue of amino acid amino acid amino acid amino acid amino acid amino acid amino acid sequence of seriae. T-Threcnine, V-Valine, M-Tryptophan, Y-Tyrosine, X-duknown, *-Stop Coden, /-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide deletion, V-possible nucleotide sinsertion) M-RGGGMTFAGALVGRIGEMBWINGPRENDESSYSVENAPTDR. KDSYYSIHOIAGMWGGKESIGGWYGDRYNGHOYLKKLAVEDTWS. SLAWHIAMDHTVWERIKIERDBWINGPRENDESSYSVENAPTDR. SLAWHIAMDHTVWERIKIERDBWINGPRENDESSYSVENAPTDR. SLAWHIAMDHTVWERIKIERDBWINGPRENDESSYSVENAPTDR. COLONGRIFAERDBWINGPRENDESSYSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS		corresponding		L-Leucine, M-Methionine, N-Asnaragine
S-Serime, T-Threonine, V-Valine, residue of amino acid sequence sequence maino acid sequence s			1	P=Proline, O=Glutamine, P=Arginine
### ### ##############################		amino acid		S=Serine T=Threonine V=Valine
sequence Sequence		residue of	amino acid	W=Tryptophan, Y=Tyrogine Y=Unknown +-Ston
Nepossible nucleotide insertion	1	amino acid		Codon. /=possible nucleotide deletion
MERGGMIFAGALVERHLIGBDARMTORKROPDSYSTALANE/PITAL KOSYSTSHIOLANGWIGSKASICOGYOPHTAQALVEKLAVEDTUK SLAWHIANDNYVMERIRKICHTSV2CAGATAPPAGDSDRICKEN BLAWHIANDNYVMERIRKICHTSV2CAGATAPPAGDSDRICKEN GAGAVIGKENSAHHFIGYVAGELIVLODHAPTOPAVEPTDACET PRESEPRACHPEPSHEVLULIPLELGILGIUDRAVYBUKHCHENGMP GAGAVIRGSKENSAHHFIGYVAGELIVLODHAPTOPAVEPTDACET TRKTFOFIRAPPSHMAG LVQCGGIRRRSAMGAMPGRHVSRVALDYKRVLQHRVLPPPLKS LGQQTVKDEPRERKTVGSDEAGRYLQSMEVYATALAQANENRA RSTGKACGGTPLDEEKINDPRESGIGQUQELMQEATTERNGOFST SESMEKER LVQCGGIRRRSAMGAMPGRHVSRVALLYKRVLQLHRVLPPPLKS LGQQTVKDEPRERKTVGSDEAGRYLQSMEVYATALAQANENRA RSTGKACGGTPLDEEKINDPRESGIGQUQELMQEATTERNGOFST SESMEKER LGQCTVKDEPRERKTVGSDEAGRYLGSMEVYATALAQANENRA RSTGKACGGTPLDEEKINDPRESGIGQUQELMQEATTERNGOFST SESMEKER ANSRGRTUGGAPLAPAAMKAVVQRVTRASVTVGGSOISNIG RSTGKACGGTFLDEEKINDPRESGIGQUQELMQEATTERNGOFST SESMEKER ANSRGRTUGGAPLAPAAMKAVVQRVTRASVTVGGSOISNIG RKTTRPELLIDGKGAPLAPAAMKAVVQRVTRASVTVGGSOISNIG RKTTRPELLIDGKGAPAMQVALIGNDEPTTLEEBEAGFTATSDP KQLSALERQQQRKEKTAARGGSESSKERNTFRKEDRSASGABB DVSSRRBP ATGRHEGGYPLIGG IQQUINGTTTPATTPSLIGPWQVALHSDRING RKTTRPELLIDGKGAPAMQVALIGNDEPTTLEEBEAGFTATSDP KQLSALERQQCKKENTAARGGSESSKERNTFRKEDRSASGABB DVSSRRBP ATGRHEGGYPLIGG IQQUINGTTTPATTPSLIGPWQVALHSDRING GSGLGCPVCKDDYALGERVRQLPCHNLFHDGCIVPMLECHDEG UCKRSLOQANTAMPDCLTOWSPSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS		sequence	••••••	\=possible nucleotide insertion)
KDSYYSIKOIAOMGVGGGKSIGONYGPHTVAQUIKKLAYFUNG SLAWHAMDINYVMBERRIKLITAYOLGANATPHADSDRICKOS PAGAEVTRRSPWRPLVLLIPLRIGITDIRBAYVSTUKKHCPWRG PAGAEVTRRSPWRPLVLLIPLRIGITDIRBAYVSTUKKHCPWRG GSLGVIGKKNRSAHFYIGVVGGELIVLDPHTOPARSTTDGCFI PDESHTQHPPCHMSIABLD9IAVVRGGHLSTQAPGAECCLGM TRKTPGFLRPFPSMLG LVQCGGIRRSAMGAMPGRHVSRVRALYKRVLQLHRVLPPDLKS LGQVIVKDBYRRHKTVGSDBQGRTLQSWBVYATALLQQANRMG RSTGKACGFTPLBEEKINDPKRDGIQQLGLMGATKPWRQPSI SSBMKDRF SSBMKD				MLRCGOMI PAOALVCRHIGRDWRWTORKRODDSVRCVI NA ETDR
SLAWHANDSTYWEETRELICITSUS_CAGATAFPADSDERICSS PAGAEVTRRESPERIULILIPERICITIONERSYSTIKKSCEMM QSLGVITGSKNISANHYFIGTVGEBLIVLDDHTTOPAVEPTDGCFT PDESFFRQNPPGEMIALDEDPILVVRGGHLESTQAPGAECCLGM TRXTFGFIRFFFRMAG 2 423 LVQCGGIRRESAGMSGRINVSEVRALVYRGGHLSTUAPGAECCLGM NSTRKACGGTPRESEMANDFREQIGQLGLMQEATTERRGFSI ESSMEKKE 6631 2 423 LVQCGGIRRESAGMSGRINVSEVRALVYRGULHSTULPPDLKS LGDQTVKDEFRERKTVGSDEAQRFLQEMMEVYATALLQOANENRQ NSTRKACGGTPLPEEKINDFREGIGQLGLMQEATTERRGFSI ESSMEKKE 6632 LVQCGGIRRESAGMADMFGREVSEVRALLYKEVLQLHRVLPPDLKS LGDQTVKDEFRERKTVGSDEAQRFLQEMMEVYATALLQOANENRQ NSTGKACGGTPLDEEKINDFREGIGQLGLMQEATTERRGFSI ESSMEKKE 6632 LVQCGGIRRESAGMAMAGAVQRFVLGEMEVYATALLQOANENRQ NSTGKACGGTPLDEEKINDFREGIGQLGLMQEATTERRGFSI SESMEKKE 6633 LVQCGGIRRESAGMAMAGAVQRTVTRASVTVGGGGISATGR GICVLLGISLEDTQKELEMMYKLINLEVEEDESGKMEKSKUM KQVELLCVSOPTLQCVLKONKPDPHLAMPTEGAEGFYNSFLGD RKYTRPELITUACKGAAYMQVAILGDGPVTTELESFAGTATSDB KGLSKLEKQQGRKKTTAKGPSESSKENNTTRKEDRSASSGRE DVSSRERB ATGRHEGGYPLKSGTIGGLVNGITTPATTPSLGFWGVLHSENPDG- VCKREATQAGATATPPDCLTGVSPSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS	i			KDSYYSIHOIAOMGVGEGKSIGOWYGPNTVAOVI,KKIAVEDTWG
PAGAEVTRRESPRIPLIVALIPLEALGITDINEATVETTAKICEMMO QSLOVIGGKRSANHY 16VYGGEL YUDHOTAVETTAGCFI PDESFICON PPC CMSTARLOPSIAVORGGHLSTQAPGAECCLGM TRXTFOFTARPFSMLG LGDQYVKDEFRRIKTVGSDEAGRFIQEWEVYATALLQANENRO NSTGKACFGTFILPEEKLINDPROEQIGQLEELWQARTKENROPSI SEMMKRF 6631 2 423 LVQCGGIRRSAMGANFGRHVSRVRALYKRVLQLHRVLEPPLKS LGDQYVKDEFRRIKTVGSDEAGRFIQEWEVYATALLQANENRO NSTGKACFGTFILPEEKLINDPROEQIGQLEELWGARTKENROPSI LGDQYVKDEFRRIKTVGSDEAGRFIQEWEVYATALLQANENRO NSTGKACFGTFILPEEKLINDPROEQIGQLEELWGARTKENROPSI LGQQYVKDEFRRIKTVGSDEAGRFIQEWEVYATALLQANENRO NSTGKACFGTFILPEEKLINDPROEQIGQLEELWGARTKENROPSI LGQQYVKDEFRRIKTVGSDEAGRFIQEWEVYATALLQANENRO NSTGKACFGTFILPEEKLINDPROEQIGQLEELWGARTKENROPSI LGQQYVKDEFRRIKTVGSDEAGRFIQUEWEVYATALLQANENRO NSTGKACFGTFILPEEKLINDPROEQIGGLEELWGARTKENROPSI LGQQYVKDEFRRIKTVGSDEAGRFIQUEWEVYATALLQANENRO NSTGKACFGTFILCEEKLINDFROEQIGGLEELWGARTHNOPLOG NSTGKACFGTFILCEEKLINDFROEQIGGLEELWGARTHNOPLOG NSTGKACFGTFILCEEKLINDFROEQIGGLEELWGARTHNOPLOG NSTGKACFGTFILCEEKLINDFROEQIGGLEELWGATATADE KOLSKLEKQOGRFEKTERAGPSESSKERSPTFRKEDRSASSGEAG GICVLLGISLEEDTQKELEHWVKILINLRYFEEDEAGRFINSFIEGL NSTGKERD ATGRIEGOFTLEOLYGANGATTATATADE NSTGKACFGTTILCEERSTYPTREDEAGRACHINSFIELWGALVCVCV GLCASHILLKINNESIGGRAPSSSSSSSSSSSSINNENATSNS ANGANGLDAI ITQLINGFETTOPPADAKEXTQALPTVPVTEEHW GSCLEEPVCKDDYALGERVRQLPCHHITURSELEWSLIVVCVC GLCASHILLKINNESIGGRAPTRAPAEHPPADAKTVCVCVC GLCASHILLKINNESIGGRAPTRAPAEHPPATARTATURSELEWSLIVVCVC GLCASHILLKINNESIGGRAPTRAPAEHPPATARTATURSELEWSLIVVCVC GLCASHILLKINNESIGGRAPTRAPAEHPPATATURSELSSH WLQODDPOINNILIATICKPERMYKLIVILIPSILSTSH WLQODGATAPTURSELSHIPSINNESIGGRAPTRAPAEHPPATATURSELSH WLQODDPOINNILIATICKPERMYKLIVILIPSILSTSH WLQODGATAPTURSAARTATURSELSH WLQODDPOINNILIATICKPERMYKLIVILIPSILSTSH WLQODGATAPTURSAARTATURSELSH WLQODGATAPTURSAARTATURSELSH WLQODGATAPTURSAARTATURSELSH WLQODGATAPTURSAARTATURSELSH WLQODGATAPTURSAARTATURSELSH WLQODGATAPTURSAARTATURSELSH WLQODGATAPTURSAARTATURSELSH WLQODGATAPTURSAARTATURSELSH WLQODGATAPTURSAARTATURSELSH WLGOGGAEPPLPILSYTHAMCAGSYKACLAGYTGGRCENLIBRGKTCH WLGASGATATURSAARTATURSELTATURSAARTATURSELSH	1]	SLAVHIAMDNTVVMERIRELCRTSVOCAGATA FRADEDRUCMER
GSLGVIGKENSAHFIGYGEELIYLDPHTTQCAVEPTDGCFI PDESFEKQHPCZMISTAELDPSIAVRGGILSTQAGECCUM TRKTFGFRFFFSMIG 6630 2 423 LVQCGGIRRESAMGAMPGRIVSRVRALYKRVLQLHRVLPPDLKS LGDQYVKDEFRRIKTVGSDEAQRFLQKMKVYATALLQQANENRQ NSTGKACRGTFLDEEKLNDPROEQIGQLQELMQEATKENRQFSI SESMKRKF 6631 2 423 LVQCGGIRRESAMGAMPGRIVSRVVRALYKRVLQLHRVLPPDLKS SESMKRKF LGDQYVKDEFRRIKTVGSDEAQRFLQKMKVVATALLQQANENRQ NSTGKACRGTFLDEEKLNDPROEQIGQLQELMQEATKENRQFSI SESMKRKF 6632 1273 588 GNSSGRTOKGAA-LAPAAMKAAVQRVTRASVTVGCGGISAIGR GICVLLGISLEDTQKELEHMVRKLINLRVEDGSGISAIGR GICVLLGISLEDTQKELEHMVRKLINLRVEDGSGISAIGR KOYELLCVSQPTLQCVLKGKKDPFLAMPTEQAEGFYNSFLEQL RKTYRPELIKOKFGAYMQVHIQNDGAVTTALEGPAKGTASDH KQLSKLEKQQGNEKTTAKADPSESSKERNTFKRDRSASSGAER 6633 1145 617 ATGRHEGVPTLGGILQGVLNGTHIPTBCJAGFYNSFLEQL RKTYRPELIKOKFGAYMQVHIQNDGAVTTALEGPAKGTASDH AWGANGLDAITOLLNGFENTGPPAAKKYQALPTVPVTTEHV GSGLECPVCKDDYALGERWQLPCHNHFHGELDFAKGTASDH AWGANGLDAITOLLNGFENTGPPAAKKYQALPTVPVTTEHV GSGLECPVCKDDYALGERWQLPCHNHFHGELDFALGTHEY VVRKSLLGAPRILDKLHGFFSFRYSKYCVCY GLCASIHLLKLINGLGKOPAQTFRPARREHPPACLSDPJLGTHC VVRKSLLGAPRVAAGGRGKFULLLHGFFSFYSKYCVCY GLCASIHLLKLINGLGKOPAQTFRPARREHPPACLSDPJLGTHC VVRKSSLGRYVVALDGLGYCTDAPIHRGNYXLDCLITDIXOILDSLGY SKCVLIGBBGGOMIAMILAICYPELVERLITAVDISPWESTGYS HYATVAMBASHAILALQRPELVERLITAVDISPWESTGYS HYATVAMBASHAILALQRPELVERLITAVDISPWESTGYS HYATVAAMBAINIADELPRSARKLADDCJSCDLLIPGDIADLLDLIDL LGGYGRGCAPPPLEJSYKLLDGEAALPAVVFLHGLFGSKTNFNSIKA ILAQQTGRRUTTVAARHGANIADLEDFSSPSMYSELTBATGTUSAVGVG HYATVAAMBAINIADELPRSARKLADDCJSCDLDLIDLDLD LDFCVVVGHBMGGKTAMLLALQRPELVERLITAVDISPWESTGYS HYATVAAMBAINIADELPRSARKLADDCJSCDLDLDDLD LDGGCCVFF HYATVAAMBAINIADELPRSARKLADDCJSCDLDLDDLD LDGGCCVFF HYATVAAMBAINIADELPRSARKLADDCJSCDLDLDDLDDLD LDGGCCVFF HYATVAAMSAINIADELPRSARKLADDCJSCDLDLDDLDLD LDGGCCCFF HYAGCLGRPPLGGVGCPPSLGPVLSPHSDFGMCRVD DGGCCVF 2 1501 CSSSFCPHODTVLDKAGSYKCACLAGYTGGCCILACREPKISD LVRRRVLYPMOVGSRETELHQUYSAAPSKOKLGGSPTKKPALPFD DLDRMYGHLHTOLOYCLSFF FYRRLGSSRRTCLRTGARGEN CTPLCGXIENITAPRTQGILBPMQAATVRTSCUHDSLIKGM VVSPFCNNSVLYLGBRRTCGQORESKGKOPLIKACARPSIS CTPLCGXIENITAPRTQGILBPMQAATVRTSCUHD	ŀ			PAGAEVTNRPSPWRPIAVILLIPI.RIGI.TDINRAVVETI.VUCEMMP
PDESTRICQHPPCZMSIABLDPSIAVVRGGHLSTQAFGAECCLGM TRKTFGFLRFFSMLG LUVCGGIRRSAWGAMPGRHVSEVRALYKRVLQLHRVLPPDLKS LGDQYVKDEFRRIKTVGSDEAQRFLQEWEVYATALLQANENRQ NSTGKACFGFTLPEKKINDPROEQIGQLEELMQEATKENRGFSI SESMKRKF 6631 2 423 LVVCGGIRRSAWGAMPGRHVSEVRALYKRVLQLHRVLPPDLKS LGDQYVKDEFRRIKTVGSDEAQRFLQEWEVYATALLQANENRQ NSTGKACFGFTLPEKKINDPROEQIGQLQELMQEATKENRGFSI LGDQYVKDEFRRIKTVGSDEAQRFLQEWEVYATALLQANENRQ NSTGKACFGFTLJEEKKINDPROEQIGQLQELMQEATKENRGFSI LGDQYVKDEFRRIKTVGSDEAQRFLQEWEVYATALLQANENRQ NSTGKACFGFTLJEEKKINDPROEQIGGLQELMQEATKENRGPSI LGOQYVKDEFRRIKTVGSDEAQRFLQEMEVYATALLQANENRRQ NSTGKACFGFTLJEEKKINDPROEQIGGLQELMQEATKENPRQFSI GICVLLGISLEDTQUKLEHMVRKILNLRVFEDESGKHNSKSVMD KQYEILCVQSPTLQCVLKGNKDPDFLAMPTEQBSGYNSKSVMD KQYEILCVQSPTLQCVLKGNKDPDFLAMPTEQBSGYNSKSVMD KQYEILCVQSPTLQCVLKGNKDPDFHLAMPTEQBSGYNSKSVMD KQYEILCVQSPTLQCVLKGNKDPDFHLAMPTERDASGFYNSFLQIL RKTTRPELIKOKKFGAMPGVTLQNDSVTTILESPAPGTATSDP KQLSKLEKQQOKEETTRAKGPSESSKSKSSRSKSSSABBD DVSSEREP DVSSEREP ATGRHEGOPTLDSITQLOVNGLITFATIPSLGPWGUHSNPHDY AWGANICDAIITOLLNGFESTGPSPSSSSSSSSSSSSMEMATSNS GGGLEFCVCKDDYALGERVEQUPSSSSSSSSSSSSSMEMATSNS GGGLEFCVCKDDYALGERVEQUPSSSSSSSSSSSSSMEMATSNS GGGLEFCVCKDDYALGERVEQUPSSSSSSSSSSSSMEMATSNS GGGLEFTATANDFLOTEXPSSSSSSSSSSSSMEMATSNS GGGLEFTATANDFLOTEXPSSSSSSSSSSSSMEMATSNS GGGLEFTATANDFLOTEXPSSSSSSSSSSSSMEMATSNS GGGLEFTATANDFLOTEXPSSSSSSSSSSSSSMEMATSNS GGGLEFTATANDFLOTEXPSSSSSSSSSSSSMEMATSNS GGGLEFTATANDFLOTEXPSSSSSSSSSSSMEMATSNS GGGLEFTATANDFLOTEXPSSSSSSSSSSSMEMATSNS KSSTEVVALDLAGGFRETLFMATLFEDCLFFTAGMTVLTSLLEFTATANDFLOTEXPSSSSSSSSSMEMATSNS KSSTEVVALDLAGGFRETLFMATLFEDCLFFTAGMTVLTSLLEFTATANDFLOTEXPSSSSSSSSSSSMEMATSNS GGGLEFTATANDFLOTEXPSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS	1			OSLGVIGGKPNSAHYFIGYVGERI.IVI.DPHTTOPAVERTDGGET
6630 2 423 INVOGGITERSANGAMPGERHVSRVRALYKRVLOLHRVLEPPLKS LIGDQYVKDEFRRIKTVGSDEAGRFIGWHEVYATALLQOANERG NSTGARCGTPLPEKLNDFRDEQIGQLQELMQEATKPNRQFSI SESMKKKF 6631 2 423 LVQCGGIRRESANGAMPGRHVSRVRALYKRVLQLHRVLPPDLKS LIGDQYVKDEFRRIKTVGSDEAGRFIQDEMEVYATALLQOANERG NSTGARCGTPLPEKLNDFRDEQIGQLQELMQEATKPNRQFSI LIGDQYVKDEFRRIKTVGSDEAGRFIQDEMEVYATALLQOANERG NSTGARCGTFLJEEKLNDFRDEQIGQLQELMQEATKPNRQFSI SESMKKF 6632 1273 588 MNSRGRTOKGARJAPARAMKAVVQRVTRASVTGGEGDISAIGR GICVLLGISLEDTQKELEHNVKKILNLRVEBESGKHMSKSVM KOYELLCVSQFTLJCEVLKGHKPDFLAMPTEGAGGFYNSTGE KOYELLCVSQFTLJCEVLKGHKPDFLAMPTEGAGGFYNSTGED KOLSKLEKQOGRKEKTRAKGPSESSKERNTPRKEDRSASSGABG DVSSERED 6633 1145 617 ATGRHEGYPTLEGIIQQLVNGIITPATIPSLGFMGVLHSNFMDY AMGANGLDAIITQLLNGFENTGPPPANKEXQALPTVPVTTEEHV GSGLKCPVCKDDYALGERVQELCHNHLHGIELBSPARGTATSDP VCKKSLTGQNTATNSPOLTGVESSSSSSSSSSSSSPSNENATSNS 6634 1 1134 CGGIFRKSGSPREDPMARIEDCLFRIHLTIKEBLEPARGTATSDP VCKKSLTGQNTATNSPOLTGVESSSSSSSSSSSSSPSNENATSNS 6634 1 1134 CGGIFRKSGSPREDPMARIEDCLFRIHLTIKEBLEPARGTVESTV VCKKSLTGQNTATNSPOLTGVESTSSSSSSSSSSSSPSPENATSNS 6634 1 1134 CGGIFRKSGSPREDPMARIEDCLFRIHLTIKEBLEPARGTVEHV VVXIKDSGLRFNVAAGERGKEVLALHLGFFFFYSKRYQUREF KSSYRVALDLRGYGETDAFIRRONYKLDCLITDIKDLDSLGV VCKKSLTGQNTATNSPOLTGVESTSSLEDFRSTVOLTERLIPSKTVCYC VXXIKDSGLRFNVAAGERGKEVLALLHGFFFYSKRYQUREF KSSYRVALDLRGYGETDAFIRRONYKLDCLITDIKDLLDSLGV SKCVLIGHBKGGNTAMILTSCLIPSKILDGINHYNNITSCLIPLK HMYTTPTLLIMGENDAFMEVMARGVTFYVNYFRITTISSASH MCQDOPDIVNLINTELKEETRKD 6635 1420 470 EMRAGQQLASMENTRAMELTBEGIGFHGPSFARVPVAPSSSSG GRGGAEPPLPLSYKLLDGEAALPAVVTHISLFGSKTNFNSIKA LLQQTGRRUTTVDARHHGSPSHSPBMSVETERDOLLLEDGLIPLDLL LGGNSGYPHSHSHPEIMRLDARGTSHTMATHTAMELDLLDLLLADGE HFATTVAAMSATNIADELPRSARRKLADDCISSTONDLDLLDLDLD LGGNSGYPHSHSHPEIMRLPPRAQQCTVPNAGHHIHARPQDFI LANKQCLGRPLGGVURGVCQCLPPSLGPVLSPHSDFGWCRVD UNGSFCNSVVVUSLUKJGNERTCQQDRESKGQDFILKARRENSI VVSCGGLASHLUKGRVVAARGCVTDLGKEVTMIKTADLKVULKKFYR DDLRMCCLGRFPLGGVASHLORGENGKGPILKGRAPS CTPICGKIENITAPRVQGLERPNQAATRAFREGUERDSLIKGAM PLVCSGALVWBSLIVEGNSRTCQGARMSVLADGSSEPTAMSGLPS CTPICGKIENITAPRVQGLARPNQAATRAFREGUERDSLIKGAM PLVCSGAL		1	ļ	PDESFHCOHPPCRMSIAELDPSIAVVRGGHLSTOAEGAECGICM
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LGDQYYKGEFRRIKTYGSDEAQRELGMMEVYATALLQQANENRQ NSTGKACGTTELPEEKINDFRDEQIGQLQELMQEATKPNRQFSI SESMKKF 1LVQCGGTRRSAWGAMPGRHVSRVRALYKRVLQLHRVLPPDLKS LGQGYVKDEFRRIKTYGSDEAQRELQEMEVYATALLQQANENRQ NSTGKACGGTFLPEEKINDFRDEQIGQLQELMQEATKRNRQFSI SESMKKF 6632 1273 588 WNSGGTGRGAPLAPAAMKAVVQRVTRASVTYGGGDISATGR NSTGKACGGTFLPEEKINDFDEQIGQLQELMQEATKRNRQFSI SESMKKF GCICVLLGISLEDTOKRLEHMVRKILMLRYBDESGKHMSKSVMM KOYELLCVSQFTLQCUKGNKPDFHLAMPTEQAEGFYNSFLEQL RKTYRPELIKDGKFGAYMQVAILGNDGPVTIELBEPAGTATSDP KQLSKLEKQQQRKEKTRAKGSFSSSKENTFIRKEDSASSGABC DVSSREP 6633 1145 617 ATGRHEGGYPTLEGITQQLVNGITFPATTPSLGPWGVLHSNPMDY AWGANGLDAIITQLINQFENTGPPPADKEKTQALPPTYPTEHV GSGLECPUKCNDTALGERYGGLPSHLHFHDCTVPPLEQHDSCD VCKKSLTQONTATNPPGLTGVSFSSSSSSSSSSSSPNENATSNS GGGLECPUKCNDTALGERYGGLPSHLHFHDCTVPPLEQHDSCD VCKKSLTQONTATNPPGLTGVSFSSSSSSSSSSSSSPNENATSNS CGCASTHLUKLINGISKGPAQTFRRAREHPPACLSDPSLGTHC YVRIKDSGLRFHVVAAGBRGKPLMLLLHGFFERWSTRQURFE KSSTRVALDLICRYGGTDAIPHRONYKLDCLITDIKDLIDSLGY SKCVLIGHDWGGMIAMLIAICYPEMWMLIVINPPHPWPTPEYI LGRKGQOLTTEDLEAPIVVESQCRALSGPINHYRNIFSCLPLKH HMVTTPTLLLMGENDAPMEVEMAEVTRFYVKNYFRLITLISEASH MCQDOPDIVNKLINTFILKETTKKD 470 EMRAGQQLASMLEWTRARELPREGUGPHGPSFARVPVAPSSSSG GRGGAEPREPLEYBLINGEALPAVVVEHLSLGSKTHFNSIAK ILAQQTGRRVLTVDARNIGDSPHSSPMSYEIMSQDLODLIPOLG LVPCVVGHSWGGKTAMLLALQPSLUFSHJUTSLGPTHLL LGGNSQFVHPSHHPSIMBLELALPRRQGPHSSTSTGTFTLE LGGNSQFVHPSHHPSIMBLELALPRRQGPHSTGFTLET LGGNSQFVHPSHHPSIMBLALQPSLUFSHJUTSLSPFTGVS HPATYVAAMAAINLADLPRRAQGHTAHLPAGGRACHPADP AAIROPLY 6635 1514 1801 SCNPSHKOSHFQAVPVQEKKRLRRAPWRAPAQOPGLKHPAE OPIVRGCLQRPPLCGVLGPVQQQLPPSLGPVLSPHSGPGKCRVD DGGCAVF DGCGAVF SCNPSHKOSHFQAVPVQCKKRFLRRAPWRAPAQFGRLKHPAE OPIVRGCLQRPPLCGVLGPVQQQLPPSLGPVLSPHSGRACKI LKRXVLYDMQVGRETFLHQLYSAAFSKQKLGSABTKKPALPHPG DLPMYGHLHFULQVECISFFYRGLGSSRKTCLRTGKNSGRAPS CTPICGKIENITAPKTGLEWPMQAATYRPTGCVHDGSLIKGAM FLVCSGALVNERTVVAAHCVTDLGKVTMIKTADLKVULGKFYR DDDRBEKTIGLIQUFSLISFFGRSSIITVAGAMNLADURSPGRNDTI TRVQPICLAASRDLSTSFGSSIITVAGAMNLADURSPGRNDTI TRVQPICLAASRDLSTSFGGSSIITVAGAMNLADURSPGRNDTI TRVQPICLAASRDLSTSFGGSSIITVAGAMNLADURSPGRNDTI	6630	2	423	
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SESMEKE LUQCGGIRRESAMGAMFGRHVSRVRALYKRVLQLHRVLEPPILKS LIGOVYVGEFRRIKKTVGSDEAQRE LOEMEVYATALLQQANENRQ NSTOKACPGTFLJEEKLINDFRDEQIGQLQELMQEAKNROFSI SESMEKEK GICVLLGISLEDTOKELEEMVRKILMLRVEPDESGHMSKSVMM KQYEILCVSQFTLQCVLKGNREPPHLAMPTBCAGEFYNSFLEOL RKYTPRELIKDGKGRAPMVAILONDGPTVREDESGHMSKSVMM KQYEILCVSQFTLQCVLKGNREPPHLAMPTBCAGEFYNSFLEOL RKYTPRELIKDGKGRAPMVAILONDGPTVREDESGHMSKSVMM KQYEILCVSQFTLQCVLKGNREPPHLAMPTBCAGEFYNSFLEOL RKYTPRELIKDGKGRAPMVAILONDGPTVREDESGHMSKSVMM KQYEILCVSQFTLQCVLKGNREPPHLAMPTBCAGEFYNSFLEOL RKYTPRELIKDGKGRAPMVAILONDGPTVSPESSGAGG DVSSEREP 6633 1145 617 ATGRHEGGYPTLEGITQOLVNGITTPATIPSLGPWGVLHSNPMDY AMGANGLDAIITQLLNQFENTGPPPADKEKTQALPFVTYTEHV GSGLECPVCKDDYALGERWRQLDENHLHTDGCIPPHLEOLPFSLVYCVC CLCASIHLLKLLWSLGKGPAQTFRRPAREHPPACLSDPSLJGTHC YVRIKDSGLRRHVVAAGERGKPIMLLLHGFFERWSKRYQUREF KSSYRVALDLRGYGETDAIPHROTYKLDCLITDIKDLLDSLGY SKCVLIGHDWGOMIANLIAICYPEHWMKLUVINPPHPWYTPETI IRRPAQLLKSSYYFFGJPHPFERWSTNUCLUTITIKDLLDSLGY SKCVLIGHDWGOMIANLIAICYPEHWMKLUVINPPHPWFTEYI IRRPAQLLKSSYYFFGJPHPFERWSTNUCHLIKTISHSTG IGRKGGLPRPLUGSGPRAFPAPWFRFSSSG WLQOQDDIVNKLIWTFLKEETRKD 470 EMRAGQQLASMLRWTRARHLPREGIGPHGPSFARVPVAPSSSSG GRGGERPPLEDSTRLLDGBALDPAVVPLWILBLFGSKTHFNSIAK ILAQGTGRRVLTVDARNIGDSPHSPDMSYEIMSGOLDLIPOLG LUPCVVGHBWGGKTAMLLALQRPELVSRLIADDISPETGYS HFATYVAAMRAINIADELPSRARKLADEGLSSVIQDMAVQUL LTMLEVUGGRVWRVNLDALTQHLDKILAFPGCGSVLGPTLQFTLL LGGNSGFVHPSHHPBIRRLPPRAQMQTVPRAGGMHHADRRODPI AAIROPLV 6636 1514 1801 SSCPWSHKOSHPQAVPVQEKKRLRRAPWRAFAQPGRLKHPAE OPIVNGCLQRPPLCGVLGFVQQQLPPSLGPVLSPHSPGMCRVD DGGGCVF USFFCKNSVVLSGMERKTGQNGWSWGKOPLCIKAGRGKSKY KASEDSLSVLEBRNGSDFGGPVNGYQKITGGRCENLLEAGKSKY KASEDSLSVLEBRNGSDFGGPVNGYQKITGGRCENLLEAGKSKY KASEDSLSVLEBRNGSDFGGPVNGYQKITGGRCENLLEAGKSKY KASEDSLSVLEBRNGSDFGGPVNGYQKITGGRCENLLEAGKSKY CKSFCKNSVVLSGMERKTGQNGWSWGKOPLCIKAGRAPS CTPIGGKIENTTAFTGGLEWPMQAATYRTSGOVENGGRAPS CTPIGGKIENTTAFTGGLEWPMQAATYRTSGOVENGGRKNAPS CTPIGGKIENTTAFTGGLEWPMQAATYRTSGOVENGGRKNAPS CTPIGGKIENTTAFTGGLEWPMQAATYRTSGOVENGGRKNAPS CTPIGGKIENTTAFTGGLEWPMQAATYRTGGABPSTAPSDIC BDDDEETTGGLAARBDLSTSFGGSSIITVAGMNVLADURSBFGKNDTL RK				NSTGKACEGTELPEEKINDERDEGIGGI OFLMOFATEUNDORGE
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VCKKSLTGONTATNPPGLTGVSFSSSSSSSSSSSNENATSNS GGASTHLKKLUSGKGPARTERDCLPRIMITIESILFWSLVYYC GLASTHLKKLUSGKGPARTERPAREHPPACLSDPSLGTHC YVRIKDSGLRFHYVAAGERGKPLMLLLHGFPEFWYSWRYQLREF KSSYRVVALDLRGYGETDAPIHRONYKLDCLITDIKDILDSLGY SKCVLIGHDWGMIAHLIALCYPEMWAKLIVINPPHPNYFTEYI IRHPAQLLKSSYYYFFQIPWFPEFMFSINDFKVLKHLFTSHSTG IGRKGCQLTTEDLEAYIVVFSQCGALSGPINHYRNIFSCLPLKH HMVTTPTLLLWGENDAPMEVEMAEVTRFYVKNYFRLTILSEASH WLQDQDPDIVNKLIWTFLKEETRKKD 6635 1420 470 EMRAGQQLASMLRWTRAWRLPREGLGPHGPSFARVPVAPSSSSG GRGABFRRIDLSYRILDGEAALPAVVFLHGLFGSKTNFNSIAK ILAQQTGRRVLTVDARNHGDSPHSPUNSYEIMSGOLDQLLPDLG LVPCVVVGHSMGGKTAMLLALQRPELVERLIAVDISPVESTGVS HFATTVAAMRAINIADELPRSRARKLADEQLSSVIQDMAVRQHL LINLVEVDGRFVWRVNLDALTQHLDKILAFPQRGESYLGPTLFL LGGNSQFVHFSHHPEIMHLFPRAQMQTVPNAGHWIHADRPQDFI AAIRGFLV 6636 1514 1801 SFCMFSHKQDSHFQAVPVQEKKKRLRRAPWRAFAQPQRLKHPAE OPIVRGCLQRPPLCGVLGPVQQLPPSLGPVLSPHSDPGWCRVD DGGDGVF 6637 2 1501 CSSSPCFHDGTCVLDKAGSYKCACLAGYTGQRCENLLEAGKSKI KASEDSLSVLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGT VVSFFCNNSYVLSGNGERTCQQNGEWSGKQPICIKACREPKISD LVRRRVLPMQVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFG DLPMGYQHLHTQLQYECISPFYRLGSSRRTCLRTGKMSGRAPS CIPICGKI ENITAPKTGGLRWPMQAAIYRRTSGVHGSLHKGAW FLVCSGALVNERTVVVAAHCVTDLGKVTMIKTADLKVULGKFYR DDDRBEKTTQSLQISAIILHENYDPILLDADIAILKLLDKARIS TRVQFICLAASRDLSTSFGEHITVAGWNVLADVRSPGFKNDTL RSGVVSVVDSLLCEEGREDHGIPVSVTDNMFCASWEPTAPSDIC				GSGLECPVCKDDYALGERVRQLPCNHLFHDGCIVPWLEOHDSCP
1 1134 CGGIPRGSGPRREDMARLRDCLPRIMLITERSLEPWSLVYCYC GLCASIHLKKLLWSLGKGPAQTFRR PAREHPPACLSDPSLGTHC YVRIKDSGLRPHYVAAGERGKPIMLLHGFPEFWSWRYQLREF KSSYRVALDLRGYGETDAPIHRQNYKLDCLITDIKDILDSLGY SKCVLIGHDWGGMIAMLIAICYPEMYMKLIVINFPHPNVFTEYI LRRPAQLLKSSYYYFFQIPWFPEFMSSINDFKUKLKHETSHSTG IGRKGCQLTTEDLEAYIYVFSQPGALSGPINHYRNIFSCLPLKH HMVTTPILLLWGENDAPMEVEMAEVTRFYYWNYFRLTILSEASH WLQQDQPDIVNKLLWTFIKEETRKKD 6635 1420 470 EMRAGQQLASMLRWTRAWRLPREGLGPHGPSFARVPVAPSSSSG GRGABFPRIPLSYRLLDGEAALPAVVFLHGLFGSKTNFNSIAK ILAQQTGRRVLTVDARNHGDSPHSPDMSYEIMSQDLQDLLPQLG LVPCVVVGHSMGGKTAMLLALQRPELVERLIAVDISPVESTGVS HFATYVAAMRAINIADELPRSRARKLADEQLSSVIQDMAVRQHL LTNLVEVDGRFVWRVNLDALTQHDKILAFPQRQESYLGFTLFL LGGNSGFVWPSHHPEIMRLFPRAQMQTVPNAGHWIHADRPQDFI AAIRGFLV 6636 1514 1801 SFCMFSHKQDSHFQAVPVQEKKKRLRRAPWRAFAQPQRLKHPAE OPIVRGCLQRPPLCGVLGPVQQQLPPSLGPVLSPHSDPGWCRVD DCGCGVF OPIVRGCLQRPPLCGVLGPVQQQLPPSLGPVLSPHSDPGWCRVD DCGCGVF VSSFCMNSYVLSGNERTCQQNGEWSGKQPICIKACREPKISD LVRRRVLPMQVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFG DLPMGYQHLHTQLQYECISFPYRRIGSSRRTCLRTGKWSGRAPS CIPPIGKI ENITAPKTGGLRWPMQAAITRRTSGVHDGSLHKGAW FLVCSGALVNERTVVVAAHCVTDLGKVTMIKTADLKVULGKFFYR DDDRBEKTTQSLQISAIILHENYDPILLDADTAILKLLDKARIS TRVQFICLAASRDLSTSFQEHITVAGWNVLADVRSPGFKNDTL RSGVVSVVDSLLCEEGREDHIGIPVSVTDNMFCASWEPTAPSDIC				VCRKSLTGQNTATNPPGLTGVSFSSSSSSSSSSSSSSSSNENATSNS
GLCASIHLIKLIWSLGKGPAQTFRRPAREHPPACLSDPSLGTHC YVRIKDSGLRPHYVAAGERGKPLMILLHGFPEFWYSARYQUREF KSSYRVVALDURGYGETDAPIHRQNYKLDCLITDIKDILDSLGY SKCVLIGHDWGGMIAWLIAICYPEMVMKLIVINPPHPNVFTEYI IARPAQLLKSSYYYFFQIBWFPEFMFSINDFKVLKHLFTSHSTG IGRKGCQLTTBDLEAYIYVFSQPGALSGPINHYRNIFSCLPLKH HMVTTPTLLLWGENDAFMSVEMAEVTRFYVKNYFRLTILSEASH WLQQDQPDIVNKLIWTFLKEETRKD 470 EMRAGQQLASMLRWTRAWRLPREGLGPHGPSFARVSVAPSSSSG GRGGABFRPLFLSYRLDGGAALPAVVFLHGLFGSKTNFNSIAK ILAQQTGRRVLTVDARNHGDSPHSPDMSYEIMSQDLQDLLPOLG LUPCVVVGHSMGGKTAMLLALQRPELVERIAVDISSVESTGVS HFATYVAAMRAINIADELPRSRARKLADEQLSSVIQDMAVRQHL LINLVEVDGRFVMRVNLDALTQHLDKILAFPGRQESYLGFTLFL LGGNSQFVHPSHHPEIMRLFPRAQMQTVPNAGHWIHADRPQDFI AAIRGFLV 5FCMFSHKQDSHFQAVPVQEKKKRLRRAPWRAFAQPQRLKHPAE OPIVRQCLQRPPLGGVLGPVQQQLPPSLGPVLSPHSDPGWCRVD DGGDGVF 6637 2 1501 CSSSPCFHDGTCVLDKAGSYKCACLAGYTGQRCENLLEAGKSKI KASEDSLSVLEERNCSDPGGPVNGYQKITGGFGLINGRHAKIGT VVSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISD LVRRRVLPMGVQSRETPLHQLVSAAFSKQKLQSAPTKKPALPFG DLPMGYQHLHTQLQYECISSFFYRRLGSSRRTCLRTGKWSGRAPS CIPICGKIENITAPKTQGLRWDWQAAIYRRTSGVHDGSLHKGAW FLVCSGALVNERTVVVAAHCVTDLGKVTMIKTADLKVVLGKFYR DDDRBKTIGSLQISAIILHPNYDPILLDADIAILKLLDKARIS TRVQFICLAASRDLSTSFQSSHITVAGWNVLADVRSPGFKNDTL RSGVVSVVDSLLCEEQHEDHGIPVSVTDNMFCASWEPTAPSDIC	6634	1	1134	CGGIPRKGSGPRRLPMARLRDCLPRLMLTLRSLLPWSLVYCYC
YVRIKDSGLRPHYVAAGERGKPLMLLLHGFPEFWYSWRYQLREF KSEYRVVALDLRGYGETDAPHRQNYKLDCLITDIKDILDSLGY SKCVLIGHDWGGMIAMLIAICYPEMWYKLIVINPPHPNVFTEYI IRHPAQLLKSSYYYFFQIPWFPEFMFSINDFKVLKHLFTSHSTG IGRKGCQLTTBDLEAYIYVFSQPGALSGPINHYRNIFSCLPLKH HMVTTPTLLLWGENDAFMEVEMAEVTRFYVKNYFRLTILSEASH WLQQDQPDIVMKLIWTFLKEETRKD 6635 1420 470 EMRAGQQLASMLRWTRAWRLPREGLGPHGPSFARVPVAPSSSSG GRGABFPRIPLSYRLLDGEAALPAVVFLHGLFGSKTNFNSIAK ILAQQTGRRVLTVDARNHGDSPHSPDMSYEIMSQDLQDLLPQLG LVPCVVVGHSMGKTRAMLLALQRPELVERLIAVDISPVESTGVS HFATYVAAMRAINIADELPRSRARKLADEQLSSVIQDMAVRQHL LTNLVEVDGRFVWRVNLDALTQHLDKILAFPQRGESYLGPTLFL LGGNSQFVHPSHHPEIMRLFPRAQMQTVPNAGHWHADRFQDFI AAIRGFLV 6636 1514 1801 SFCMFSHKQDSHFQAVPVQEKKKRLRRAPWRAFAQPQRLKHPAE OPIVRGCLQRPPLCGVLGPVQQQLPPSLGPVLSPHSDPGWCRVD DGGDGVF 6637 2 1501 CSSSPCPHDGTCVLDKAGSYKCACLAGYTGQRCENLLEAGKSKI KASEDSLSVLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGT VVSFFCNNSVLSGNEKRTCQQNGEWSGKQPICIKACREPKISD LVRRVLPMQVQSRETPLHQLVSAAFSKGKLQSAPTKKPALPFG DLPMGYQHLHTOLQYECISPFYRRLGSSRRTCLRTGKWSGRAPS CIPICGKIENITAPKTGGLRWBWQAIYRRTSGVHDGSLHKGAW FLVCSGALWERTVVVAAHCVTDLGKVTMIKTADLKVVLGKFYR DDDREKTIGSLQISAIILHPNYDPILLDADIAILKLLDKARIS TRVQFICLAASRDLSTSFQESHITVAGMVVLADVRSPGFKNDTL RSGVVSVVDSLLCEEQHEDHGIPVSVTDMFCASWEPTAPSDIC	Ι.			GLCASIHLLKLLWSLGKGPAQTFRRPAREHPPACLSDPSLGTHC
KSSYRVVALDERGYGETDAPIRRQNYKLDCLITDIKDILDSLGY SKCVLIGHDWGGMIAWILIAICYPEMYMKLIVINPPHPNVFTEYI LRHPAQLLKSSYYYFFQIPWFPEFMFSINDFKVLKHLFTSHSTG IGRKGCQLTTBDLEAYIYVFSQPGALSGPINHYRNIFSCLPLKH HMVTTPTLLLWGENDAPMEVEMAEVTRFYVKNYFRLTILSEASH WLQQDQPDIVNKLIWTFLKEETRKKD WLQQDQPDIVNKLIWTFLKEETRKKD 6635 1420 470 EMRAGQQLASMURWTRAWRLPREGLGPHGPSFARVPVAPSSSSG GRGGAEPRPLPLSYRLLDGEAALPAVVFLHGLFGSKTNFNSIAK ILAQQTGRRVLTVDARNHGDSPHSPDMSYEIMSODLQDLLPQLG LVPCVVVGHSMGGKTAMLLALQRPELVERLIAVDISPVESTGVS HRATYVAAMRAINIADELPRSRARKLADEQLSSVIQDMAVRQHL LTNLVEVDGRFVWRVNLDALTQHLDKILAFPQRQESYLGPTLFL LGGNSQFVHPSHHPEIMRLFPRAQMQTVPNAGHWIHADRPQDFI AAIRGPLV 6636 1514 1801 SFCMFSHKQDSHFQAVPVQEKKKRLRRAPWRAFAQPQRLKHPAE OPIVRQCLQRPPLCGVLGPVQQQLPPSLGPVLSPHSDPGWCRVD DCGDGVF 6637 2 1501 CSSSPCFHDGTCVLDKAGSYKCACLAGYTGQRCENLLEAGKSKI KASEDSLSVLEERNCSDPGGPVNGYQKITGGPGLINGRIHAKIGT VVSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISD LVMRRVLPMQVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFG DLPMGYQHLHTQLGYECISPFYRRLGSSRRTCLRTGKWSGRAPS CIPICGKIENITAFRTQGLRWPWQAAIYRRTSGYHDGSLHKGAN FLVCSGALVNERTVVVAAHCVTDLGKVTMIKTADLKVVLGKFYR DDDRDEKTIQSLQISAIILHPNYDPILLDADIAILKLLDKARIS TRVQPICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNDTL RSGVVSVVSDSLLCEEQHEDHGIPVSVTDNMFCASWEPTAPSDIC				YVRIKDSGLRFHYVAAGERGKPLMLLLHGFPEFWYSWRYOLREF
SKCVLIGHDWGGMIAWLIAICYPEMVMKLIVINPPHPNVFTEYI I.RHPAQLLKKSYYYFFQIPWFPEFMFSINDFKVLKHLFTSHSTG IGRKGCQLTTEBDLEAYIYVFSQPGALSGPINHYRNIFSCLPLKH HMVTTPTLLLWGENDAFMEVEMAEVTRFVVKNYFRLTILSEASH WLQQDQPDIVNKLIWTFLKEETRKKD 470 EMRAGQQLASMLEWTRAWRLPREGLGPHGPSFARVPVAPSSSG GRGGAEPRPLPLSYRLJDGEAALPAVVFLHGLFGSKTNFNSIAK ILAQQTGRRVLTVDARNHGDSPHSPDMSYEIMSQDLQDLLPQLG LVPCVVVGHSMGGKTAMLLALQRPELVERLIAVDISPVESTGVS HFATYVAAMRAINIADELPRSRARKLADEQLSSVIQDMAVRQHL LTNLVEVVDGRFVWRVNLDALTQHLDKILAFPQRQESYLGPTLFL LGGNSQFVHPSHHPEIMRLFPRAQMQTVPNAGHWIHADRPQDFI AAIRGPLV 5FCMFSHKQDSHFQAVPVQEKKKRLRRAPWRAFAQPQRLKHPAE QPIVRQCLQRPPLCGVLGPVQQQLPPSLGPVLSPHSDPGWCRVD DGGDGVF 6637 2 1501 CSSSPCFHDGTCVLDKAGSYKCACLAGYTGQRCENLLEAGKSKI KASEDSLSVLEERNCSDPGGPVNGYQKITGGPGLINGHIAKIGT VVSFFCNNSYVLSGNERRTCQQNGEWSGKQPICIKACREPKISD LVRRRVLPMQVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFG DLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKNSGRAPS CIPICGKIENITAPKTQGLRWPWQAAIYRRTSGVHDGSLHKGAN FLVCSGALVNERTVVVAAHCVTDLGKVTMIKTADLKVVLGKFYR DDDRDEKTIQSLQISAILHPNYQPILLDADIAILKLLDKARIS TRVQPICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNDTL RSGVVSVVDSLLCEEQHEDHIIPVSVTDMFCASWBPTAPSDIC	l i			KSEYRVVALDLRGYGETDAPIHRQNYKLDCLITDIKDILDSLGY
IGRKGCQLTTBDLEAYIYVFSQPGALSGPINHYRNIFSCLPLKH HMVTTPTLLLWGENDAFMEVEMAEVTRFYVKNYFRLTILSEASH WLQQDQPDIVNKLIWTFLKEETRKKD 6635 1420 470 EMRAGQQLASMLEWTRAWRLPREGLGPHGPSFARVPVAPSSSSG GRGGAEPRPLPLSYRLLDGEAALPAVVFLHGLFGSKTNFNSIAK ILAQQTGRRVLTVDARNHGDSPHSPDMSYEIMSQDLQDLLPQLG LVPCVVVGHSMGGKTAMLLALQRPELVERLIAVDISPVESTGVS HFATYVAAMRAINIADELPRSRARKLADEQLSSVIQDMAVRQHL LTNLVEVDGRFVWRVNLDALTQHLDKILAFPQRQESYLGPTLFL LGGNSQFVHPSHHPEIMRLFPRAQMQTVPNAGHWIHADRPQDFI AAIRGFLV 6636 1514 1801 SFCMFSHKQDSHFQAVPVQEKKKRLRRAPWRAFAQPQRLKHPAE OPIVRQCLQRPPLCGVLGPVQQQLPPSLGPVLSPHSDPGWCRVD DGGDGVF 6637 2 1501 CSSSPCPHDGTCVLDKAGSYKCACLAGYTGQRCENLLEAGKSKI KASEDSLSVLEERNCSDPGGPVNQVQKITGGPGLINGRHAKIGT VVSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISD LVMRRVLPMQVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFG DLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPS CIPICGKIENITAPKTQGLRWPWQAAIYRRTSGVHDGSLHKGAW FLVCSGALVNERTVVVAAHCVTDLGKVTMIKTADLKVVLGKFFR DDDRDKTIQSLQISAIILHPNYDPILLDAIAILKLLDKARIS TRVQPICLAASRQLSTSFQESHITVAGWWVLADVRSPGFKNDTL RSGVVSVVDSLLCEEQHEDHGIPVSVTDNMFCASWEPTAPSDIC	1 1	1		SKCVLIGHDWGGMIAWLIAICYPEMVMKLIVINFPHPNVFTEYI
IGRKGCQLTTBDLEAYIYVFSQPGALSGPINHYRNIFSCLPLKH HMVTTPTLLLWGENDAFMEVEMAEVTRFYVKNYFRLTILSEASH WLQQDQPDIVNKLIWTFLKEETRKKD 6635 1420 470 EMRAGQQLASMLEWTRAWRLPREGLGPHGPSFARVPVAPSSSSG GRGGAEPRPLPLSYRLLDGEAALPAVVFLHGLFGSKTNFNSIAK ILAQQTGRRVLTVDARNHGDSPHSPDMSYEIMSQDLQDLLPQLG LVPCVVVGHSMGGKTAMLLALQRPELVERLIAVDISPVESTGVS HFATYVAAMRAINIADELPRSRARKLADEQLSSVIQDMAVRQHL LTNLVEVDGRFVWRVNLDALTQHLDKILAFPQRQESYLGPTLFL LGGNSQFVHPSHHPEIMRLFPRAQMQTVPNAGHWIHADRPQDFI AAIRGFLV 6636 1514 1801 SFCMFSHKQDSHFQAVPVQEKKKRLRRAPWRAFAQPQRLKHPAE OPIVRQCLQRPPLCGVLGPVQQQLPPSLGPVLSPHSDPGWCRVD DGGDGVF 6637 2 1501 CSSSPCPHDGTCVLDKAGSYKCACLAGYTGQRCENLLEAGKSKI KASEDSLSVLEERNCSDPGGPVNQVQKITGGPGLINGRHAKIGT VVSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISD LVMRRVLPMQVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFG DLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPS CIPICGKIENITAPKTQGLRWPWQAAIYRRTSGVHDGSLHKGAW FLVCSGALVNERTVVVAAHCVTDLGKVTMIKTADLKVVLGKFFR DDDRDKTIQSLQISAIILHPNYDPILLDAIAILKLLDKARIS TRVQPICLAASRQLSTSFQESHITVAGWWVLADVRSPGFKNDTL RSGVVSVVDSLLCEEQHEDHGIPVSVTDNMFCASWEPTAPSDIC	Ì			LRHPAQLLKSSYYYFFQIPWFPEFMFSINDFKVLKHLFTSHSTG
WLQQDQPDIVNKLIWTFLKEETRKKD 6635 1420 470 EMRAGQQLASMLRWTRAWRLPREGLGPHGPSFARVPVAPSSSSG GRGGAEPRPLPLSYRLLDGEAALPAVVFHGLFGSKTNFNSIAK ILAQQTGRRVLTVDARNHGDSPHSPDMSYEIMSQDLQDLLPQLG LVPCVVVGHSMGGKTAMLLALQRPELVERLIAVDISPVESTGVS HFATYVAAMRAINIADELPRSRARKLADEQLSSVIQDMAVRQHL LTNLVEVDGRFVWRVMLDALTQHLDKILAFPQRQESYLGPTLFL LGGNSQFVHPSHHPEIMRLFPRAQMQTVPNAGHWIHADRPQDFI AAIRGFLV 6636 1514 1801 SFCMFSHKQDSHFQAVPVQEKKKRLRRAPWRAFAQPQRLKHPAE QPIVRQCLQRPPLCGVLGPVQQQLPPSLGPVLSPHSDPGWCRVD DGGDGVF 6637 2 1501 CSSSPCFHDGTCVLDKAGSYKCACLAGYTGQRCBNLLBAGKSKI KASEDSLSVLEBRNCSDPGGPVNGYQKITGGPGLINGRHAKIGT VVSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISD LVRRRVLPMQVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFG DLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPS CIPICCKIENITAPKTQGLRWPWQAAIYRRTSGVHDGSLHKGAW FLVCSGALVNERTVVVAAHCVTDLGKVTMIKTADLKVVLGKFYR DDDRDEKTIQSLQISAIILHPNYDPILLDADIAILKLDKARIS TRVQFICLAASRDLSTSFQBSHITVAGWNVLADVRSPGFKNDTL RSGVVSVVDSLLCEEQHEDHGIPVSVTDNMFCASWEPTAPSDIC				IGRKGCQLTTEDLEAYIYVFSQPGALSGPINHYRNIFSCLPLKH
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GRGGAEPRPLPLSYRLLDGEAALPAVVFLHGLFGSKTNFNSIAK ILAQQTGRRVLTVDARNHGDSPHSPDMSYEIMSQDLQDLLPQLG LVPCVVVGHSMGGKTAMLLALQRPELVERLIAVDISPVESTGVS HFATYVAAMRAINIADELPRSRARKLADEQLSSVIQDMAVRQHL LTNLVEVDGRFVWRVNLDALTQHLDKILAFPQRQESYLGPTLFIL LGGNSQFVHPSHHPEIMRLFPRAQMQTVPNAGHWIHADRPQDFI AAIRGFLV 6636 1514 1801 SFCMFSHKQDSHFQAVPVQEKKKRLRRAPWRAFAQPQRLKHPAE QPIVRQCLQRPPLCGVLGPVQQQLPPSLGPVLSPHSDPGWCRVD DGGDGVF CSSSPCFHDGTCVLDKAGSYKCACLAGYTGQRCENLLEAGKSKI KASEDSLSVLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGT VVSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISD LVRRRVLPMQVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFG DLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPS CIPICCKIENITAPKTQGLWPWQAAIYRRTSGVHDGSLHKGAN FLVCSGALVNERTVVAAHCVTDLGKVTMIKTADLKVVLGKFYR DDDRDEKTIQSLQISAIILHPNYDPILLDADIAILKLLDKARIS TRVQFICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNDTL RSGVVSVVDSLLCEEQHEDHGIPVSVTDNMFCASWEPTAPSDIC				
ILAQQTGRRVLTVDARNHGDSPHSPDMSYEIMSQDLQDLLPQLG LVPCVVVGHSMGGKTAMILIALQRPELVERLIAVDISPVESTGVS HFATYVAAMRAINIADELPRSRARKLADEQLSSVIQDMAVRQNIL LTNLVEVDGRFVWRVNLDALTQHLDKILAFPQRQESYLGPTLFL LGGNSQFVHPSHHPEIMRLFPRAQMQTVPNAGHWIHADRPQDFI AAIRGFLV 6636 1514 1801 SFCMFSHKQDSHFQAVPVQEKKKRLRRAPWRAFAQPQRLKHPAE QPIVRQCLQRPPLCGVLGPVQQQLPPSLGPVLSPHSDPGWCRVD DCGDGVF CSSSPCFHDGTCVLDKAGSYKCACLAGYTGQRCENLLEAGKSKI KASEDSLSVLEERNCSDPGGPVNGYQKITGCPGLINGRHAKIGT VVSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISD LVRRRVLPMQVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFG DLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPS CIPICGKIENITAPKTQGLRWPWQAATYRRTSGYHDGSLHKGAN FLVCSGALVNERTVVVAAHCVTDLGKVTMIKTADLKVVLGKFYR DDDRDEKTIQSLQISAIILHPNYDPILLDADIAILKLLDKARIS TRVQFICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNDTL RSGVVSVVDSLLCEEQHEDHGIPVSVTDNMFCASWEPTAPSDIC	6635	1420	470	
ILAQQTGRRVLTVDARNHGDSPHSPDMSYEIMSQDLQDLLPQLG LVPCVVVGHSMGGKTAMILIALQRPELVERLIAVDISPVESTGVS HFATYVAAMRAINIADELPRSRARKLADEQLSSVIQDMAVRQNIL LTNLVEVDGRFVWRVNLDALTQHLDKILAFPQRQESYLGPTLFL LGGNSQFVHPSHHPEIMRLFPRAQMQTVPNAGHWIHADRPQDFI AAIRGFLV 6636 1514 1801 SFCMFSHKQDSHFQAVPVQEKKKRLRRAPWRAFAQPQRLKHPAE QPIVRQCLQRPPLCGVLGPVQQQLPPSLGPVLSPHSDPGWCRVD DCGDGVF CSSSPCFHDGTCVLDKAGSYKCACLAGYTGQRCENLLEAGKSKI KASEDSLSVLEERNCSDPGGPVNGYQKITGCPGLINGRHAKIGT VVSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISD LVRRRVLPMQVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFG DLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPS CIPICGKIENITAPKTQGLRWPWQAATYRRTSGYHDGSLHKGAN FLVCSGALVNERTVVVAAHCVTDLGKVTMIKTADLKVVLGKFYR DDDRDEKTIQSLQISAIILHPNYDPILLDADIAILKLLDKARIS TRVQFICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNDTL RSGVVSVVDSLLCEEQHEDHGIPVSVTDNMFCASWEPTAPSDIC				GRGGAEPRPLPLSYRLLDGEAALPAVVFLHGLFGSKTNFNSIAK
HFATYVAAMRAINIADELPRSRARKLADEQLSSVIQDMAVRQHL LTNLUEVDGRFVWRVNLDALTQHLDKILAFPQRQESYLGPTLFL LGGNSQFVHPSHHPEIMRLFPRAQMQTVPNAGHWIHADRPQDFI AAIRGFLV 6636 1514 1801 SFCMFSHKQDSHFQAVPVQEKKKRLRRAPWRAFAQPQRLKHPAE QPIVRQCLQRPPLCGVLGPVQQQLPPSLGPVLSPHSDPGWCRVD DGGDGVF CSSSPCFHDGTCVLDKAGSYKCACLAGYTGQRCENLLEAGKSKI KASEDSLSVLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGT VVSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISD LVRRVLPMQVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFG DLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPS CIPICCKIENITAPKTQGLWPWQAAIYRRTSGVHDGSLHKGAW FLVCSGALVNERTVVAAHCVTDLGKVTMIKTADLKVVLGKFYR DDDRDEKTIQSLQISAIILHPNYDPILLDADIAILKLLDKARIS TRVQFICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNDTL RSGVVSVVDSLLCEEQHEDHGIPVSVTDNMFCASWEPTAPSDIC				ILAQQTGRRVLTVDARNHGDSPHSPDMSYEIMSQDLQDLLPQLG
HFATYVAAMRAINIADELPRSRARKLADEQLSSVIQDMAVRQHL LTNLUEVDGRFVWRVNLDALTQHLDKILAFPQRQESYLGPTLFL LGGNSQFVHPSHHPEIMRLFPRAQMQTVPNAGHWIHADRPQDFI AAIRGFLV 6636 1514 1801 SFCMFSHKQDSHFQAVPVQEKKKRLRRAPWRAFAQPQRLKHPAE QPIVRQCLQRPPLCGVLGPVQQQLPPSLGPVLSPHSDPGWCRVD DGGDGVF CSSSPCFHDGTCVLDKAGSYKCACLAGYTGQRCENLLEAGKSKI KASEDSLSVLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGT VVSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISD LVRRVLPMQVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFG DLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPS CIPICCKIENITAPKTQGLWPWQAAIYRRTSGVHDGSLHKGAW FLVCSGALVNERTVVAAHCVTDLGKVTMIKTADLKVVLGKFYR DDDRDEKTIQSLQISAIILHPNYDPILLDADIAILKLLDKARIS TRVQFICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNDTL RSGVVSVVDSLLCEEQHEDHGIPVSVTDNMFCASWEPTAPSDIC		1		LVPCVVVGHSMGGKTAMLLALQRPELVERLIAVDISPVESTGVS
LGGNSQFVHPSHHPEIMRLFPRAQMQTVPNAGHWIHADRPQDFI AAIRGFLV 1801 SFCMFSHKQDSHFQAVPVQEKKKRLRRAPWRAFAQPQRLKHPAE QPIVRQCLQRPPLCGVLGPVQQQLPPSLGPVLSPHSDPGWCRVD DGGDGVF 6637 2 1501 CSSSPCFHDGTCVLDKAGSYKCACLAGYTGQRCENLLEAGKSKI KASEDSLSVLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGT VVSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISD LVRRRVLPMQVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFG DLPMGYQHLHTQLQYECISFFYRRLGSSRRTCLRTGKWSGRAPS CIPICGKIENITAPKTQGLRWPWQAAIYRRTSGYHDGSLHKGAW FLVCSGALVNERTVVAAHCVTDLGKVTMIKTADLKVVLGKFYR DDDRDEKTIQSLQISAIILHPNYDPILLDADIAILKLLDKARIS TRVQFICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNDTL RSGVVSVVDSLLCEEQHEDHGIPVSVTDNMFCASWEPTAPSDIC		1		HFATYVAAMRAINIADELPRSRARKLADEQLSSVIQDMAVRQHL
AAIRGFLV 1514 1801 SFCMFSHKODSHFQAVPVQEKKKRLRRAPWRAFAQPQRLKHPÄE QPIVRQCLQRPPLCGVLGPVQQQLPPSLGPVLSPHSDPGWCRVD DCGCGVF 6637 2 1501 CSSSPCFHDGTCVLDKAGSYKCACLAGYTGQRCENLLEAGKSKI KASEDSLSVLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGT VVSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISD LVRRVLPMQVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFG DLPMGYQHLHTQLQYECISFFYRRLGSSRRTCLRTGKWSGRAPS CIPICGKIENITAPKTQGLRWPWQAATYRRTSGYHDGSLHKGAN FLVCSGALVNERTVVVAAHCVTDLGKVTMIKTADLKVVLGKFYR DDDRDEKTIQSLQISAIILHPNYDPILLDADIAILKLLDKARIS TRVQPICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNDTL RSGVVSVVDSLLCEEQHEDHGIPVSVTDNMFCASWEPTAPSDIC				LTNLVEVDGRFVWRVNLDALTQHLDKILAFPQRQESYLGPTLFL
1514 1801 SFCMFSHKQDSHFQAVPVQEKKKRLRRAPWRAFAQPQRLKHPAE QPIVRQCLQRPPLCGVLGPVQQQLPPSLGPVLSPHSDPGWCRVD DCGDGVF CSSSPCFHDGTCVLDKAGSYKCACLAGYTGQRCENLLEAGKSKI KASEDSLSVLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGT VVSFFCNNSYVLSONEKRTCQQNGEWSGKQPICIKACREPKISD LVRRRVLPMQVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFG DLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPS CIPICCKIENITAPKTQGLWWPWQAAIYRRTSGVHDGSLHKGAW FLVCSGALVNERTVVAAHCVTDLGKVTMIKTADLKVVLGKFYR DDDRDEKTIQSLQISAIILHPNYDPILLDADIAILKLLDKARIS TRVQFICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNDTL RSGVVSVVDSLLCEEQHEDHGIPVSVTDNMFCASWEPTAPSDIC				LGGNSQFVHPSHHPEIMRLFPRAQMQTVPNAGHWIHADRPQDFI
OPIVRQCLQRPPLCGVLGPVQQQLPPSLGPVLSPHSDPGWCRVD DGGDGVF 1501 CSSSPCFHDGTCVLDKAGSYKCACLAGYTGQRCENLLEAGKSKI KASEDSLSVLEERNCSDPGGPVNGYQKITGGPGLINGRIHAKIGT VVSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISD LVRRRVLPMQVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFG DLPMGYQHLHTQLQYECISFFYRLGSSRRTCLRTGKWSGRAPS CIPICGKIENITAFVTQGLRWPWQAAIYRRTSGVHDGSLHKGAW FLVCSGALVNERTVVAAHCVTDLGKVTMIKTADLKVVLGKFYN DDDRDEKTIQSLQISAIILHPNYDPILLDADIAILKLLDKARIS TRVQPICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNDTL RSGVVSVVDGLLCEEQHEDHGIPVSVTDNMFCASWEPTAPSDIC			19.	AAIRGFLV
DGGDGVF CSSSPCFHDGTCVLDKAGSYKCACLAGYTGQRCBNLLBAGKSKI KASEDSLSVLEBRNCSDPGGPVNGYQKITGGPGLINGRIHAKIGT VVSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISD LVRRRVLPMQVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFG DLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPS CIPICCKIENITAPKTQGLRWPWQAAIYRRTSGVHDGSLHKGAW FLVCSGALVNERTVVVAAHCVTDLGKVTMIKTADLKVVLGKFYR DDDRDEKTIQSLQISAIILHPNYDPILLDADIAILKLLDKARIS TRVQPICLAASRDLSTSFQBSHITVAGWNVLADVRSPGFKNDTL RSGVVSVVDSLLCEEQHEDHGIPVSVTDNMFCASWEPTAPSDIC	6636	1514	1801	
CSSSPCFHDGTCVLDKAGSYKCACLAGYTGQRCENLLEAGKSKI KASEDSLSVLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGT VVSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISD LVRRRVLPMQVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFG DLPMGYQHLHTQLYSCLISFFYRLGSSRRTCLKTGKWSGRAPS CIPICGKIENITAPKTQGLRWPWQAAIYRRTSGVHDGSLHKGAW FLVCSGALVNERTVVVAAHCVTDLGKVTMIKTADLKVVLGKFYR DDDRDEKTIQSLQISAIILHPNYDPILLDADIAILKLLDKARIS TRVQPICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNDTL RSGVVSVVDSLLCEEQHEDHGIPVSVTDNMFCASWEPTAPSDIC				
CSSEPTHOSIOVIDAGS I KACLLAGTIGREENLEAGES I KASEDSLSVLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGT VVSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISD LVRRRVLPMQVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFG DLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPS CIPICCKIENITAPKTQGLRWPWQAAIYRRTSGVHDGSLHKGAW FLVCSGALVNERTVVAAHCVTDLGKVTMIKTADLKVVLGKFYR DDDRDEKTIQSLQISAIILHPNYDPILLDADIAILKLLDKARIS TRVQPICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNDTL RSGVVSVVDSLLCEEQHEDHGIPVSVTDNMFCASWEPTAPSDIC				
VVSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISD LVRRRVLPMQVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFG DLPMGYQHLHTQLQYECISFFYRLGSSRRTCLRTGKWSGRAPS CIPICGKIENITAPKTQGLRWPWQAAIYRRTSGVHDGSLHKGAW FLVCSGALVNERTVVVAAHCVTDLGKVTMIKTADLKVVLGKFYR DDDRDEKTIQSLQISAIILHPNYDPILLDADIAILKLLDKARIS TRVQPICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNDTL RSGVVSVVDGLLCEEQHEDHGIPVSVTDNMFCASWEPTAPSDIC	003/	4	1501	CSSSPCFHDGTCVLDKAGSYKCACLAGYTGQRCBNLLEAGKSKI
VVSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISD LVRRRVLPMQVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFG DLPMGYQHLHTQLQYECISFFYRLGSSRRTCLRTGKWSGRAPS CIPICGKIENITAPKTQGLRWPWQAAIYRRTSGVHDGSLHKGAW FLVCSGALVNERTVVVAAHCVTDLGKVTMIKTADLKVVLGKFYR DDDRDEKTIQSLQISAIILHPNYDPILLDADIAILKLLDKARIS TRVQPICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNDTL RSGVVSVVDGLLCEEQHEDHGIPVSVTDNMFCASWEPTAPSDIC				KASEDSLSVLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGT
DLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPS CIPICCKIENITAPKTQGLRWPWQAATYRRTSGVHDGSLHKGAW FLVCSGALVNERTVVAAHCVTDLGKVTMIKTADLKVVLGKFYR DDDRDEKTIQSLQISAIILHPNYDPILLDADIAILKLLDKARIS TRVQPICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNDTL RSGVVSVVDSLLCEEQHEDHGIPVSVTDNMFCASWEPTAPSDIC	İ		1	VVSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISD
DLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPS CIPICCKIENITAPKTQGLRWPWQAATYRRTSGVHDGSLHKGAW FLVCSGALVNERTVVAAHCVTDLGKVTMIKTADLKVVLGKFYR DDDRDEKTIQSLQISAIILHPNYDPILLDADIAILKLLDKARIS TRVQPICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNDTL RSGVVSVVDSLLCEEQHEDHGIPVSVTDNMFCASWEPTAPSDIC		-		
FLVCSGALVNERTVVVAAHCVTDLGKVTMIKTADLKVVLGKFYR DDDRDEKTIQSLQISAIILHPNYDPILLDADIAILKLLDKARIS TRVQPICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNDTL RSGVVSVVDSLLCEEQHEDHGIPVSVTDNMFCASWEPTAPSDIC				DLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPS
DDDRDEKTIQSLQISAIILHPNYDPILLDADIAILKLLDKARIS TRVQPICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNDTL RSGVVSVVDSLLCEEQHEDHGIPVSVTDNMFCASWEPTAPSDIC			ļ	
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RSGVVSVVDSLLCEEQHEDHGIPVSVTDNMFCASWEPTAPSDIC	1			DDDRDEKTIQSLQISAIILHPNYDPILLDADIAILKLLDKARIS
	1			
TAETGGIAAVSFPGRASPEPRWHLMGLVSWSYDKTCSHRLSTAF				
			·	TAETGGIAAVSFPGRASPEPRWHLMGLVSNSYDKTCSHRLSTAF

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			TKVLPFKDWIERNMK
6638	1391	224	GGIPQAGGKMAAPWWRAALCECRRWRGFSTSAVLGRRTPPLGPM
ļ			PNSDIDLSNLERLEKYRSFDRYRRRAEQEAQAPHWWRTYREYFG
	İ		EKTDPKEKIDIGLPPPKVSRTQQLLERKQAIQELRANVEEERAA
		ļ	RLRTASVPLDAVRAEWERTCGPYHKQRLAEYYGLYRDLFHGATF
		ĺ	VPRVPLHVAYAVGEDDLMPVYCGNEVTPTEAAQAPEVTYEAEEG
ļ		ì	SLWTLLLTSLDGHLLEPDAEYLHWLLTNIPGNRVAEGQVTCPYL
ł		ł .	PPFPARGSGIHRLAFLLFKQDQPIDFSEDARPSPCYQLAQRTFR
			TFDFYKKHQETMTPAGLSFFQCRWDDSVTYIFHQLLDMREPVFE
			FVRPPPYHPKQKRFPHRQPLRYLDRYRDSHEPTYGIY
6639	2046	1268	IGCFIMDGGDDGNLIIKKRFVSEAELDERRKRRQEEWEKVRKPE
			DPEECPEEVYDPRSLYERLQEQKDRKQQEYEEQFKFKNMVRGLD
ł	ļ		EDETNFLDEVSRQQELIEKQRREBELKELKEYRNNLKKVGISQE NKKEVEKKLTVKPIETKNKFSQAKLLAGAVKHKSSESGNSVKRL
			1 · · · · · · · · · · · · · · · · · · ·
]	KPDPEPDDKNQEPSSCKSLGNTSLSGPSIHCPSAAVCIGILPGL GAYSGSSDSESSSDSEGTINATGKIVSSIFRTNTFLEAP
6640	117	1043	VLEPPDVSMAESEDRSLRIVLVGKTGSGKSATANTILGEEIFDS
0040		1 1043	RIAAQAVTKNCOKASREWQGRDLLVVDTPGLFDTKESLDTTCKE
			ISRCIISSCPGPHAIVLVLLLGRYTEEEQKTVALIKAVFGKSAM
			KHMVILFTRKEELEGQSFHDFIADADVGLKSIVKECGNRCCAFS
			NSKKTSKAEKESQVQELVELIEKMVQCNEGAYFSDDIYKDTEER
			LKOREEVLRKIYTDOLNEEIKLVBEDKHKSEEKKEKEIKLLKLK
			YDEKIKNIREEAERNIFKDVFNRIWKMLSEIWHRFLSKCKFYSS
6641	1	894	SAAVGRRSEVRGCAPRPRLRRSARRMDPVPGTDSAPLAGLAWSS
			ASAPPPRGFSAISCTVEGAPASFGKSFAQKSGYFLCLSSLGSLE
Į.			NPQENVVADIQIVVDKSPLPLGFSPVCDPMDSKASVSKKKRMCV
Ţ			KLLPLGATDTAVFDVRLSGKTKTVPGYLRIGDMGGFAIWCKKAK
1			APRPVPKPRGLSRDMQGLSLDAASQPSKGGLLERTASRLGSRAS
]	;]	TLRRNDSIYEASSLYGISAMDGVPFTLHPRFEGKSCSPLAFSAF
	I		GDLTIKSLADIEEEYNYGFVVEKTAAARLPPSVS
6642			PLEERMMTKMDPNDOAORDIIFELRRIAFDAESDPSNAPGSGTE
	22	1296	:
	22	1296	KRKAMYTKDYKMLGFTNHINPAMDFTQTPPGMLALDNMLYLAKV
	22	1296	KRKAMYTKDYKMLGFTNHINPAMDFTQTPPGMLALDNMLYLAKV HQDTYIRIVLENSSREDKHECPFGRSAIELTKMLCEILQVGELP
	22	1296	KRKAMYTKDYKMLGFTNHINPAMDFTQTPPGMLALDNMLYLAKV HQDTYIRIVLENSSREDKHECPFGRSAIELTKMLCEILQVGELP NEGRNDYHPMFFTHDRAFEBLFGICIQLLNKTWKEMRATAEDFN
	22	1296	KRKAMYTKDYKMLGFTNHINPAMDFTQTPPGMLALDNMLYLAKV HQDTYIRIVLENSSREDKHECPFGRSAIELTKMLCEILQVGELP NEGRNDYHPMFFTHDRAFEELFGICIQLLNKTWKEMRATAEDFN KVMQVVREQITRALPSKPNSLDQFKSKLRSLSYSEILRLRQSER
	22	1296	KRKAMYTKDYKMLGFTNHINPAMDFTQTPPGMLALDNMLYLAKV HQDTYIRIVLENSSREDKHECPFGRSAIELTKMLCEILQVGELP NEGRNDYHPMFFTHDRAFEELFGICIQLLNKTWKEMRATAEDFN KVMQVVREQITRALPSKPNSLDQFKSKLRSLSYSEILRLRQSER MSQDDFQSPPIVELREKIQPEILELIKQQRLNRLCEGSSFRKIG
	22	1296	KRKAMYTKDYKMLGFTNHINPAMDFTQTPPGMLALDNMLYLAKV HQDTYIRIVLENSSREDKHECPFGRSAIELTKMLCEILQVGELP NEGRNDYHPMFFTHDRAFEELFGICIQLLNKTWKEMRATAEDFN KVMQVVREQITRALPSKPNSLDQFKSKLRSLSYSEILRLRQSER MSQDDFQSPPIVELREKIQPEILELIKQQRLNRLCEGSSFRKIG NRRRQERFWYCRLALNHKVLHYGDLDDNPQGBVTFESLQEKIPV
	22	1296	KRKAMYTKDYKMLGFTNHINPAMDFTQTPPGMLALDNMLYLAKV HQDTYIRIVLENSSREDKHECPFGRSAIELTKMLCEILQVGELP NEGRNDYHPMFFTHDRAFEELFGICIQLLNKTWKEMRATAEDFN KVMQVVREQITRALPSKPNSLDQFKSKLRSLSYSEILRLRQSER MSQDDFQSPPIVELREKIQPEILELIKQQRLNRLCEGSSFRKIG
	22	1296	KRKAMYTKDYKMLGFTNHINPAMDFTQTPPGMLALDNMLYLAKV HQDTYIRIVLENSSREDKHECPFGRSAIELTKMLCEILQVGELP NEGRNDYHPMFFTHDRAFEELFGICIQLLNKTWKEMRATAEDFN KVMQVVREQITRALPSKPNSLDQFKSKLRSLSYSEILRLRQSER MSQDDFQSPPIVELREKIQPEILELIKQQRLNRLCEGSSFRKIG NRRRQERFWYCRLALNHKVLHYGDLDDNPQGBVTFESLQEKIPV ADIKAIVTGKDCPHMKEKSALKQNKEVLELAPSILYDPDETLNF
6643	3049	1296	KRKAMYTKDYKMLGFTNHINPAMDFTQTPPGMLALDNMLYLAKV HQDTYIRIVLENSSREDKHECPFGRSAIELTKMLCEILQVGELP NEGRNDYHPMFFTHDRAFEELFGICTQLLNKTWKEMRATAEDFN KVMQVVREQITRALPSKPNSLDGFKSKLRSLSYSEILRLRQSER MSQDDFQSPPIVELREKIQPEILELIKQQRLNRLCEGSSFRKIG NRRRQERFWYCRLALNHKVLHYGDLDDNPQGBVTFBSLQEKIPV ADIKAIVTGKDCPHMKEKSALKQNKEVLELAFSILYDPDETLNF IAPNKYEYCIWIDGLSALLGKDMSSELTKSDLDTLLSMEMKLRL
6643			KRKAMYTKDYKMLGFTNHINPAMDFTQTPPGMLALDNMLYLAKV HQDTYIRIVLENSSREDKHECPFGRSAIELTKMLCEILQVGELP NEGRNDYHEMFFTHDRAFEELFGICIQLLNKTWKEMRATAEDFN KVMQVVREQITRALPSKPNSLDQFKSKLRSLSYSEILRLRQSER MSQDDFQSPPIVELREKIQPEILELIKQQELNRLCEGSSFRKIG NRRQERFWYCRLALNHKVLHYGDLDDNPQGEVTFESLQEKIPV ADIKAIVTGKDCPHMKEKSALKQNKEVLELAFSILYDPDETLNF IAPNKYEYCIWIDGLSALLGKDMSSELTKSDLDTLLSMEMKLRL LDLENIQIPEAPPPIPKEPSSYDFVYHYG
6643			KRKAMYTKDYKMLGFTNHINPAMDFTQTPPGMLALDNMLYLAKV HQDTYIRIVLENSSREDKHECPFGRSAIELTKMLCEILQVGELP NEGRNDYHPMFFTHDRAFEELFGICIQLLNKTWKEMRATAEDFN KVMQVVREQITRALPSKPNSLDQFKSKLRSLSYSEILRIRQSER MSQDDFQSPPIVELREKIQPEILELIKQQRLNRLCEGSSFRKIG NRRRQERFWYCRLALNHKVLHYGDLDDNPQGEVTFESLQEKIPV ADIKAIVTGKDCPHMKEKSALKQNKEVLELAPSILYDPDETLNF IAPNKYEYCIWIDGLSALLGKDMSSELTKSDLDTLLSMEMKLRL LDLENIQIPEAPPPIPKEPSSYDFVYHYG SLHAPAEGRTRGRLAEKPKMLTRKIKLWDINAHITCRLCSGYLI
6643			KRKAMYTKDYKMLGFTNHINPAMDFTQTPPGMLALDNMLYLAKV HQDTYIRIVLENSSREDKHECPFGRSAIELTKMLCEILQVGELP NEGRNDYHPMFFTHDRAFEELFGICIQLLNKTWKEMRATAEDFN KVMQVVREQITRALPSKPNSLDQFKSKLRSLSYSEILRILRQSER MSQDDFQSPPIVELREKIQPEILELIKQQRLNRLCEGSSFRKIG NRRRQERFWYCRLALNHKVLHYGDLDDDPQGEVTFESLQEKIPV ADIKAIVTGKDCPHMKEKSALKQNKEVLELAPSILYDPDETLNF IAPNKYEYCIWIDGLSALLGKDMSSELTKSDLDTILLSMEMKLRL LDLENIQIPEAPPPIPKEPSSYDFVYHYG SLHAPAEGRTRGRLAEKPKMLTRKIKLWDINAHITCRLCSGYLI DATTVTECLHTFCRSCLVKYLEENNTCPTCRIVIHQSHPLQYIG
6643			KRKAMYTKDYKMLGFTNHINPAMDFTQTPPGMLALDNMLYLAKV HQDTYIRIVLENSSREDKHECPFGRSAIELTKMLCEILQVGELP NEGRNDYHPMFFTHDRAFEELFGICIQLLNKTWKEMRATAEDFN KVMQVVREQITRALPSKPNSLDQFKSKLRSLSYSEILRLRQSER MSQDDFQSPPIVELREKIQPEILELIKQQRLNRLCEGSSFRKIG NRRQERFWYCRLALNHKVLHYGDLDDNPQGEVTFESLQEKIPV ADIKAIVTGKDCPHMKEKSALKQNKEVLELAPSILYDPDETLNF IAPNKYEYCIWIDGLSALLGKDMSSELTKSDLDTILLSMEMKLRL LDLENIQIPEAPPPIPKEPSSYDFVYHYG SLHAPAEGRTRGRLAEKPKMLTRKIKLWDINAHTTCRLCSGYLI DATTVTECLHTFCRSCLVKYLEENNTCPTCRIVIHQSHPLQYIG HDRTMQDIVYKLVPGLQBAEMRKQREFYHKLGMEVPGDIKGETC
			KRKAMYTKDYKMLGFTNHINPAMDFTQTPPGMLALDNMLYLAKV HQDTYIRIVLENSSREDKHECPFGRSAIELTKMLCEILQVGELP NEGRNDYHPMFFTHDRAFEELFGICTQLLNKTWKEMRATAEDFN KVMQVVREQITRALPSKPNSLDGFKSKLRSLSYSEILRLRQSER MSQDDFQSPPIVELREKIQPEILELIKQQRLNRLCEGSSFRKIG NRRRQERFWYCRLALNHKVLHYGDLDDNPQGBVTFSSLQEKIPV ADIKAIVTGKDCPHMKEKSALKQNKEVLELAFSILYDPDETLNF IAPNKYEYCIWIDGLSALLGKDMSSELTKSDLDTLLSMEMKLRL LDLENIQIPEAPPPIPKEPSSYDFVYHYG SLHAPAEGRTRGRLAEKPKMLTRKIKLWDINAHTTCRLCSGYLI DATTVTECLHTFCRSCLVKYLEENNTCPTCRIVIHQSHPLQYIG HDRTMQDIVYKLVPGLQBAEMRKQREFYHKLGMEVPGDIKGETC SAKQHLDSHRNGETKADDSSNKEAAEEKPEEDNDYHRSDEQVSI CLECNSSKLRGLKRKWIRCSAQATVLHLKKFIAKKLNLSSFNEL DILCNEEILGKDHTLKFVVVTRWRFKKAPLLLHYRPKMDLL
6643			KRKAMYTKDYKMLGFTNHINPAMDFTQTPPGMLALDNMLYLAKV HQDTYIRIVLENSSREDKHECPFGRSAIELTKMLCEILQVGELP NEGRNDYHPMFFTHDRAFEELFGICTQLLNKTWKEMRATAEDFN KVMQVVREQITRALPSKPNSLDQFKSKLRSLSYSEILRLRQSER MSQDDFQSPPIVELREKIQPEILELIKQQRLNRLCEGSSFRKIG NRRQERFWYCRLALNHKVLHYGDLDDNPQGBVTFSSLQEKIPV ADIKAIVTGKDCPHMKEKSALKQNKEVLELAFSILYDPDETLNF IAPNKYEYCIWIDGLSALLGKDMSSELTKSDLDTLLSMEMKLRL LDLENIQIPEAPPPIPKEPSSYDFVYHYG SLHAPAEGRTRGRLAEKPKMLTRKIKLWDINAHTTCRLCSGYLI DATTVTECLHTFCRSCLVKYLEENNTCPTCRIVHQSHPLQYIG HDRTMQDIVYKLVPGLQBAEMRKQREFYHKLGMEVPGDIKGETC SAKQHLDSHRNGETKADDSSNKEAAEEKPEEDNDYHRSDEQVSI CLECNSSKLRGLKRKWIRCSAQATVLHLKKFIAKKLNLSSFNEL DILCNEEILGKDHTLKFVVVTRWRFKKAPLLLHYRPKMDLL
	3049	2265	KRKAMYTKDYKMLGFTNHINPAMDFTQTPPGMLALDNMLYLAKV HQDTYIRIVLENSSREDKHECPFGRSAIELTKMLCEILQVGELP NEGRNDYHPMFFTHDRAFEELFGICTQLLNKTWKEMRATAEDFN KVMQVVREQITRALPSKPNSLDQFKSKLRSLSYSEILRLRQSER MSQDDFQSPPIVELREKIQPEILELIKQQRLNRLCEGSSFRKIG NRRQERFWYCRLALNHKVLHYGDLDDNPQGEVTFESLQEKIPV ADIKAIVTGKDCPHMKEKSALKQNKEVLELAPSILYDPDETLNF IAPNKYEYCIWIDGLSALLGKDMSSELTKSDLDTLLSMEMKLRL LDLENIQIPEAPPPIPKEPSSYDFVYHYG SLHAPAEGRTRGRLAEKPKMLTRKIKLWDINAHTTCRLCSGYLI DATTVTECLHTFCRSCLVKYLEENNTCPTCRIVIHQSHPLQYIG HDRTMQDIVYKLVPGLQBAEMRKQREFYHKLGMEVPGDIKGETC SAKQHLDSHRNGETKADDSSNKEAAESKPEEDNDYHRSDEQVSI CLECNSSKLRGLKRKWIRCSAQATVLHLKKFIAKKLNLSSFNEL DILCNEEILGKDHTLKFVVVTRWRFKKAPLLLHYRPKMDLL FRPLATEPRGSSPVQLVSSTMSVRTLPLLFLNLGGEMLYILDQR LRAQNIPGDKARKVLNDIISTMFNRKFMEELFKPQELYSKKALR
	3049	2265	KRKAMYTKDYKMLGFTNHINPAMDFTQTPPGMLALDNMLYLAKV HQDTYIRIVLENSSREDKHECPFGRSAIELTKMLCEILQVGELP NEGRNDYHMFFTHDRAFEELFGICIQLLNKTWKEMRATAEDFN KVMQVVREQITRALPSKPNSLDQFKSKLRSLSYSEILRLRQSER MSQDDFQSPPIVELREKIQPEILELIKQQRLNRLCEGSSFRKIG NRRQERFWYCRLALNHKVLHYGDLDDNPQGEVTFESLQEKIPV ADIKAIVTGKDCPHMKEKSALKQNKEVLELAFSILYDPDETLNF IAPNKYEYCIWIDGLSALLGKDMSSELTKSDLDTILLSMEMKLRL LDLENIQIPEAPPPIPKEPSSYDFVYHYG SLHAPAEGRTRGRLAEKPKMLTRKIKLWDINAHITCRLCSGYLI DATTVTECLHTFCRSCLVKYLEENNTCPTCRIVINQSHPLQYIG HDRTMQDIVYKLVPGLQBAEMRKQREFYHKLGMEVPGDIKGETC SAKQHLDSHRNGETKADDSSNKEAAEEKPEEDNDYHRSDEQVSI CLECNSSKLRGLKRKWIRCSAQATVLHLKKFIAKKLNLSSFNEL DILCNEEILGKDHTLKFVVVTRWRFKKAPLLHYRPKMDLL FRPLATEPRGSSPVQLVSSTMSVRTLPLLFLNLGGEMLYILDQR LRAQNIPGDKARKVLNDIISTMFNRKFMEELFKPQELYSKKALR TVYERLAHASIMKLNQASMDKLYDLMTMAFKYQVLLCPRPKDVL
	3049	2265	KRKAMYTKDYKMLGFTNHINPAMDFTQTPPGMLALDNMLYLAKV HQDTYIRIVLENSSREDKHECPFGRSAIELTKMLCEILQVGELP NEGRNDYHPMFFTHDRAFEELFGICTQLLNKTWKEMRATAEDFN KVMQVVREQITRALPSKPNSLDQFKSKLRSLSYSEILRLRQSER MSQDDFQSPPIVELREKIQPEILELIKQQRLNRLCEGSSFRKIG NRRQERFWYCRLALNHKVLHYGDLDDNPQGEVTFESLQEKIPV ADIKAIVTGKDCPHMKEKSALKQNKEVLELAPSILYDPDETLNF IAPNKYEYCIWIDGLSALLGKDMSSELTKSDLDTLLSMEMKLRL LDLENIQIPEAPPPIPKEPSSYDFVYHYG SLHAPAEGRTRGRLAEKPKMLTRKIKLWDINAHITCRLCSGYLI DATTVTECLHTFCRSCLVKYLEENNTCPTCRIVIHQSHPLQYIG HDRTMQDIVYKLVPGLQBAEMRKQREFYHKLGMEVPGDIKGETC SAKQHLDSHRNGETKADDSSNKEAAEEKPEEDNDYHRSDEQVSI CLECNSSKLRGLKRKWIRCSAQATVLHLKKFIAKKLNLSSFNEL DILCNEEILGKDHTLKFVVVTRWRPKKAPLLHYRPKMDLL FRPLATEPRGSSPVQLVSSTMSVRTLPFLFLNLGGEMLYILDQR LRAQNIPGDKARKVLNDIISTMFNKFMEELFKPQELYSKKALR TVYERLAHASIMKLNQASMDKLYDLMTMAFKYQVLLCPRPKDVL LVTFNHLDTIKGFIRDSPTILQQVDETLRQLTEIYGGLSAGEFQ
	3049	2265	KRKAMYTKDYKMLGFTNHINPAMDFTQTPPGMLALDNMLYLAKV HQDTYIRIVLENSSREDKHECPFGRSAIELTKMLCEILQVGELP NEGRNDYHPMFFTHDRAFEELFGICTQLLNKTWKEMRATAEDFN KVMQVVREQITRALPSKPNSLDQFKSKLRSLSYSEILRLRQSER MSQDDFQSPPIVELREKIQPEILELIKQQRLNRLCEGSSFRKIG NRRRQERFWYCRLALNHKVLHYGDLDDNPQGBVTFESLQEKIPV ADIKAIVTGKDCPHMKEKSALKQNKEVLELAPSILYDPDETLNF IAPNKYEYCIWIDGLSALLGKDMSSELTKSDLDTLLSMEMKLRL LDLENIQIPEAPPPIPKBPSSYDFVYHYG SLHAPAEGRTRGRLAEKPKMLTRKIKLWDINAHTTCRLCSGYLI DATTVTECLHTFCRSCLVKYLEENNTCPTCRIVIHQSHPLQYIG HDRTMQDIVYKLVPGLQBAEMRKQREFYHKLGMEVPGDIKGETC SAKQHLDSHRNGETKADDSSNKEAAEEKPEDNDYHRSDEQVSI CLECNSSKLRGLKRKWIRCSAQATVLHLKKFIAKKLNLSSFNEL DILCNEEILGKDHTLKFVVVTRWRFKKAPLLLHYRPKMDLL FRPLATEPRGSSPVQLVSSTMSVRTLPLLFLNLGGEMLYILDQR LRAQNIPGDKARKVLNDISTMFNRKFMEELFKPQELYSKKALR TVYERLAHASIMKLNQASMDKLYDLMTMAFKYQVULCPRPKDVL LVTFNHLDTIKGFIRDSPTILQQVDETLRQLTEIYGGLSAGEFQ LIRQTLLIFFQDLHIRVSMPLKDKVQNNNGRFVLPVSGPVPWGT
	3049	2265	KRKAMYTKDYKMLGFTNHINPAMDFTQTPPGMLALDNMLYLAKV HQDTYIRIVLENSSREDKHECPFGRSAIELTKMLCEILQVGELP NEGRNDYHPMFFTHDRAFEELFGICTQLLNKTWKEMRATAEDFN KVMQVVREQITRALPSKPNSLDQFKSKLRSLSYSEILRLRQSER MSQDDFQSPPIVELREKIQPEILELIKQQRLNRLCEGSSFRKIG NRRRQERFWYCRLALNHKVLHYGDLDDNPQGBVTFSSLQEKIPV ADIKAIVTGKDCPHMKEKSALKQNKEVLELAFSILYDPDETLNF IAPNKYEYCIWIDGLSALLGKDMSSELTKSDLDTLLSMEMKLRL LDLENIQIPEAPPPIPKEPSSYDFVYHYG SLHAPAEGRTRGRLAEKPKMLTRKIKLWDINAHTTCRLCSGYLI DATTVTECLHTFCRSCLVKYLEENNTCPTCRIVIHQSHPLQYIG HDRTMQDIVYKLVPGLQBAEMRKQREFYHKLGMEVPGDIKGETC SAKQHLDSHRNGETKADDSSNKEAAEEKPEEDNDYHRSDEQVSI CLECNSSKLRGLKRKWIRCSAQATVLHLKKFIAKKLNLSSFNEL DILCNEEILGKDHTLKFVVVTRWFFKKAPLLHYRPKMDLL FRPLATEPRGSSPVQLVSSTMSVRTLPLLFLNLGGEMLYILDQR LRAQNIPGDKARKVLNDIISTMFNRKFMEELFKPQELYSKKALR TVYERLAHASIMKLNQASMDKLYDLMTMAFKYQVLLCPRPKDVL LVTFNHLDTIKGFIRDSPTILQQVDETLRQLTEIYGGLSAGEFQ LIRQTLLTFFQDLHIRVSMFLKDKVQNNNGRFVLPVSGPVPWGT EVPGLIRMFNNKGEEVKRIEFKHGGNYVPAPKEGSFEFYGDRVL
	3049	2265	KRKAMYTKDYKMLGFTNHINPAMDFTQTPPGMLALDNMLYLAKV HQDTYIRIVLENSSREDKHECPFGRSAIELTKMLCEILQVGELP NEGRNDYHPMFFTHDRAFEELFGICTQLLNKTWKEMRATAEDFN KVMQVVREQITRALPSKPNSLDGYKSKLRSLSYSEILRLRQSER MSQDDFQSPPIVELREKIQPEILELIKQQRLNRLCEGSSFRKIG NRRQGERFWYCRLALNHKVLHYGDLDDNPQGBVTFSSLQEKIPV ADIKAIVTGKDCPHMKEKSALKQNKEVLELAFSILYDPDETLNF IAPNKYEYCIWIDGLSALLGKDMSSELTKSDLDTLLSMEMKLRL LDLENIQIPEAPPPIPKEPSSYDFVYHYG SLHAPAEGRTRGRLAEKPKMLTRKIKLWDINAHTTCRLCSGYLI DATTVTECLHTFCRSCLVKYLEENNTCPTCRIVHQSHPLQYIG HDRTMQDIVYKLVPGLQBAEMRKQREFYHKLGMEVPGDIKGETC SAKQHLDSHRNGETKADDSSNKEAAEEKPEEDNDYHRSDEQVSI CLECNSSKLRGLKRKWIRCSAQATVLHLKKFIAKKLNLSSFNEL DILCNEEILGKDHTLKFVVVTRWRFKKAPLLLHYRPKMDLL FRPLATEPRGSSPVQLVSSTMSVRTLPLLFLNLGGEMLYILDQR LRAQNIPGDKARKVLNDIISTMFNRKFMEELFKPQELYSKKALR TVYERLAHASIMKLNQASMDKLYDLMTMAFKYQVLLCPRPKDVL LVTFNHLDTIKGFIRDSPTILQQVDETLRQLTEIYGGLSAGEFQ LIRQTLLIFFQDLHIRVSMPLKDKVQNNNGRFVLPVSGPVPWGT EVPGLIRMFNNKGEEVKRIEFKHGGNYVPAPKEGSFEFYGDRVL KLGTNMYSVNQPVETHVSGSSKNLASWTQESIAPNPLAKEELNF
	3049	2265	KRKAMYTKDYKMLGFTNHINPAMDFTQTPPGMLALDNMLYLAKV HQDTYIRIVLENSSREDKHECPFGRSAIELTKMLCEILQVGELP NEGRNDYHPMFFTHDRAFEELFGICIQLLNKTWKEMRATAEDFN KVMQVVREQITRALPSKPNSLDQFKSKLRSLSYSEILRLRQSER MSQDDFQSPPIVELREKIQPEILELIKQQRLNRLCEGSSFRKIG NRRQERFWYCRLALNHKVLHYGDLDDNPQGEVTFESLQEKIPV ADIKAIVTGKDCPHMKEKSALKQNKEVLELAFSILYDPDETLNF IAPNKYEYCIWIDGLSALLGKDMSSELTKSDLDTILLSMEMKLRL LDLENIQIPEAPPPIPKEPSSYDFVYHYG SLHAPAEGRTRGRLAEKPKMLTRKIKLWDINAHITCRLCSGYLI DATTVTECLHTFCRSCLVKYLEENNTCPTCRIVIHQSHPLQYIG HDRTMQDIVYKLVPGLQBAEMRKQREFYHKLGMEVPGDIKGETC SAKQHLDSHRNGETKADDSSNKEAAEEKPEEDNDYHRSDEQVSI CLECNSSKLRGLKRKWIRCSAQATVLHLKKFIAKKLNLSSFNEL DILCNEEILGKDHTLKFVVTRWRFKKAPLLHYRPKMDLL FRPLATEPRGSSPVQLVSSTMSVRTLPLLFTNLGGEMLYILDQR LRAQNIPGDKARKVLNDIISTMFNRKFMEELFKPQELYSKKALR TVYERLAHASIMKLNQASMDKLYDLMTMAFKYQVLLCPRPKDVL LVTFNHLDTIKGFIRDSPTILQQVDETLRQLTEIYGGLSAGEFQ LIRQTLLIFFQDLHIRVSMFLKDKVQNNNGRFVLPVSGPVPWGT EVPGLIRMFNNKGEEVKRIEFKHGGNYVPAPKEGSFEFYGDRVL KLGTNMYSVNQPVETHVSGSSKNLASWTQESIAPNPLAKEELNF LARLMGGMEIKKPSGPEPGFRLNLFTTDEEEEQAALTRPEELSY
	3049	2265	KRKAMYTKDYKMLGFTNHINPAMDFTQTPPGMLALDNMLYLAKV HQDTYIRIVLENSSREDKHECPFGRSAIELTKMLCEILQVGELP NEGRNDYHPMFFTHDRAFEELFGICTQLLNKTWKEMRATAEDFN KVMQVVREQITRALPSKPNSLDGYKSKLRSLSYSEILRLRQSER MSQDDFQSPPIVELREKIQPEILELIKQQRLNRLCEGSSFRKIG NRRQGERFWYCRLALNHKVLHYGDLDDNPQGBVTFSSLQEKIPV ADIKAIVTGKDCPHMKEKSALKQNKEVLELAFSILYDPDETLNF IAPNKYEYCIWIDGLSALLGKDMSSELTKSDLDTLLSMEMKLRL LDLENIQIPEAPPPIPKEPSSYDFVYHYG SLHAPAEGRTRGRLAEKPKMLTRKIKLWDINAHTTCRLCSGYLI DATTVTECLHTFCRSCLVKYLEENNTCPTCRIVHQSHPLQYIG HDRTMQDIVYKLVPGLQBAEMRKQREFYHKLGMEVPGDIKGETC SAKQHLDSHRNGETKADDSSNKEAAEEKPEEDNDYHRSDEQVSI CLECNSSKLRGLKRKWIRCSAQATVLHLKKFIAKKLNLSSFNEL DILCNEEILGKDHTLKFVVVTRWRFKKAPLLLHYRPKMDLL FRPLATEPRGSSPVQLVSSTMSVRTLPLLFLNLGGEMLYILDQR LRAQNIPGDKARKVLNDIISTMFNRKFMEELFKPQELYSKKALR TVYERLAHASIMKLNQASMDKLYDLMTMAFKYQVLLCPRPKDVL LVTFNHLDTIKGFIRDSPTILQQVDETLRQLTEIYGGLSAGEFQ LIRQTLLIFFQDLHIRVSMPLKDKVQNNNGRFVLPVSGPVPWGT EVPGLIRMFNNKGEEVKRIEFKHGGNYVPAPKEGSFEFYGDRVL KLGTNMYSVNQPVETHVSGSSKNLASWTQESIAPNPLAKEELNF

WO 01/53312

PCT/US00/34263

650	Dwadi an-d	T-3-4	
SEQ	Predicted beginning	Predicted end	Amino acid segment containing signal peptide
NO:	nucleotide	nucleotide location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
10:	location		Glutamic Acid, P-Phenylalanine, G-Glycine,
1	corresponding	corresponding to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
ł	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
ł	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
l l	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	seduence	Codon, /=possible nucleotide deletion,
6645	6530	4646	\=possible nucleotide insertion)
	0550	1040	FVEGLAGYVYKAASEGKVLTLAALLLNRSESDIRYLLGYVSQQG
	i		GORSTPLIIAARNGHAKVVRLLLEHYRVQTQQTGTVRFDGYVID
1			GATALWCAAGAGHFEVVKLLVSHGANVNHTTVTNSTPLRAACFD
1	}		GRLDIVKYLVENNANISIANKYDNTCLMIAAYKGHTDVVRYLLE
1			QRADPNAKAHCGATALHFAAEAGHIDIVKELIKWRAAIVVNGHG
ĺ			MTPLKVAAESCKADVVELLLSHADCDRRSRIEALELLGASFAND
1			RENYDIIKTYHYLYLAMLERFQDGDNILEKEVLPPIHAYGNRTE
ı			CRNPQELESIRQDRDALHMEGLIVRERILGADNIDVSHPIIYRG
			AVYADNMEFEQCIKLWLHALHLRQKGNRNTHKDLLRFAQVFSQM
			IHLNETVKAPDIECVLRCSVLEIEQSMNRVKNISDADVHNAMDN
			YECNLYTFLYLVCISTKTQCSEEDQCKINKQIYNLIHLDPRTRE
	!		GFTLLHLAVNSNTPVDDFHTNDVCSFPNALVTKLLLDCGAEVNA VDNEGNSALHIIVQYNRPISDFLTLHSIIISLVEAGAHTDMTNK
l l			QNKTPLDKSTTGVSEILLKTQMKMSLKCLAARAVRANDINYQDQ
			IPRTLEEFVGFH
6646	176	890	PSSRMNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESY
1			EGREKKGISDVRRTFCLFVTFDLLFVTLLWIIELNVNGGIENTL
			EKEVMQYDYYSSYFDIFLLAVFRFKVLILAYAVCRLRHWWAIAL
			TTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFLD
			PKVLPQEAEEENRLLIVQDASERAALIPGGLSDGQFYSPPESEA
			GSEEAEEKQDSEKPLLEL
6647	176	890	PSSRMNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESY
ł			EGREKKGISDVRRTFCLFVTFDLLFVTLLWIIELNVNGGIENTL
			EKEVMQYDYYSSYFDIFLLAVFRFKVLILAYAVCRLRHWWAIAI.
			TTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFLD
			FKVLPQEAEEENRLLIVQDASERAALIPGGLSDGQFYSPPESEA
			GSEEAEEKQDSEKPLLEL
6648	413	897	RNCWNCFTKYFNSPPEDIDHKDSYLITRSIMAEPDYIEDDNPEL
1 1	i i		IRPQKLINPVKTSRNHQDLHRELLMNQKRGLAPONKPBLOKVME
1 1			KRKRDQVIKQKEEEAQKKKSDLEIELLKRQOKLEOLELEKOKLO
6640			BEQENAPEFVKVKGNLRRTGQEVAQAQES
6649	1357	832	WIPRAAGIRHEVKWDVKEIMSQHNIYVDALLKEFEQFNRRLNEV
} .			SKRVRIPLPVSNILWEHCIRLANRTIVEGYANVKKCSNEGRALM
1 1			QLDFQQFLMKLEKLTDIRPIPDKEFVETYIKAYYLTENDMERWI
6650	32		KEHREYSTKQLTNLVNVCLGSHINKKARQKLLAAIDDIDRPKR
0030	32	765	LVPLVFSLLVQSCKQVYRSIAMKFVPCLLLVTLSCLGTLGQAPR
1 1			QKQGSTGEEFHFQTGGRDSCTMRPSSLGQGAGEVWLRVDCRNTD
			QTYWCEYRGQPSMCQAFAADPKSYWNQALQELRRLHHACQGAPV
			LRPSVCREAGPQAHMQQVTSSLKGSPEPNQQPEAGTPSLRPKAT
			VKLTEATQLGKDSMEELGKAKPTTRPTAKPTQPGPRPGGNEEAK
6651	3425	1353	KKAWEHCWKPFQALCAFLISFFRG
		1333	AKELLKVGDFSLCAGPYQNTADTMENLSKEPLASFVSESFDISA
[CGIATEHVKIDNSGEGLTAEAGSETLSRDGEVGVNSDMHYELSG
	1		DSDLDLLGDCRNPRLDLEDSYTLRGSYTRKKDVPTDGYESSLNF
			HNNNQEDWGCSSWVPGMETSLPPGHWTAAVKKEEKCVPPYVQIR DLHGILRTYANFSITKBLKDTMRTSHGLRRHPSFSANCGLPSSW
	. 1		TSTWQVADDLTQNTLDLEYLRFAHKLKQTIKNGDSQHSASSANV
	1		FPKESPTQISIGAFPSTKISEAPFLHPAPRSRSPLLVTVVESDP
			RPQGQPRRGYTASSLDSSSSWRERCSHNRDLRNSQRNHTVSFHL
[ŀ		NKLKYNSTVKESRNDISLILNEYAEFNKVMKNSNQFIFQDKELN
			DVSGEATAQEMYLPFPGRSASYEDIIIDVCTNLHVKLRSVVKEA
	ļ		CKSTFLFYLVETEDKSFFVRTKNLLRKGGHTEIEPQHFCQAFHR
		1	ENDTLIIIIRNEDISSHLHQIPSLLKLKHPPSVIFAGVDSPGDV
		ł	LDHTYQELFRAGGFVISDDKILEAVTLVQLKEIIKILEKLNGNG
		Ì	RWKWLLHYRENKKLKEDERVDSTAHKKNIMLKSFQSANIIELLH
			YHQCDSRSSTKAEILKCLLNLQIQHIDARFAVLLTDKPTIPREV
			THE VIEW TO THE VEHICLE OF THE VEHIC

SEQ	Predicted	Predicted end	Amino acid cognosti contribution
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ļ	amino acid	sequence	Codon, /=possible nucleotide deletion,
L.	sequence	"	\=possible nucleotide insertion)
			FENNGILVTDVNNFIENIEKIAAPFRSSYW
6652	2	1343	IPGSTISCSCHSRRLRGGSPAPRLSLGAASPRPRPPSLPLPLPL
ł			PFPLFLPTRPAERAWIRSRRASEWVGKMEVPRLDHALNSPTSPC
			EEVIKNLSLEAIQLCDRDGNKSQDSGIAEMEELPVPHNIKISNI
1	1		TCDSFKISWEMDSKSKDRITHYFIDLNKKENKNSNKFKHKDVPT
			KLVAKAVPLPMTVRGHWFLSPRTEYTVAVQTASKQVDGDYVVSE
			WSEIIEFCTADYSKVHLTQLLEKAEVIAGRMLKFSVFYRNQHKE
			YFDYVREHHGNAMQPSVKDNSGSHGSPISGKLEGIFFSCSTEFN
			TGKPPODSPYGRYRFEIAAEKLFNPNTNLYFGDFYCMYTAYHYV
l l	Í		ILVIAPVGSPGDEFCKQRLPQLNSKDNKFLTCTEEDGVLVYHHA
1			QDVILEVIYTDPVDLSLGTVAEITGHQLMSLSTANAKKDPSCKT
			CNISVGR
6653	170	1910	FFLEPRLRPFPASRARFVPARTRPSPLHPCCFCFEGGGSMLSPQ
T .			RVAAAASRGADDAMESSKPGPVQVVLVQKDQHSFELDEKALASI
			LLQDHIRDLDVVVVSVAGAFRKGKSFILDFMLRYLYSOKESGHS
			NWLGDPERPLTGFSWRGGSDPETTGIQIWSEVFTVEKPGGKKVA
ŀ	·		VVLMDTQGAFDSQSTVKDCATIFALSTMTSSVQIYNLSQNIQED
1			DLQQLQLFTEYGRLAMDEIFQXPFQTLMPLVRDWSFPYEYSYGL
,			QGGMAFLDKRLQVKEHQHEEIQNVRNHIHSCFSDVTCFLLPHPG
1 1		•	LQVATSPDFDGKLKDIAGEFKEQLQALIPYVLNPSKLMEKEING
			SKVTCRGLLEYFKAYIKIYQGEDLPHPKSMLQATAEAYNLAAAA
			SAKDIYYNNMEEVCGGEKPYLSPDILEEKHCEFKQLALDHFKKT
1 1		•	KKMGGKDFSFRYQQELEEEIKELYENFCKHNGSKNVFSTFRTPA
			VLFTGIVALYIASGLTGFIGLEVVAQLFNCMVGLLLIALLTWGY
1			IRYSGQYRELGGAIDFGAAYVLEQASSHIGNSTQATVRDAVVGR PSMDKKAO
6654	<u> </u>	705	RTSLSPSQCSSFNLAMASAGMQILGVVLTLLGWVNGLVSCALPM
	1		WKVTAFIGNSIVVAQVVWEGLWMSCVVQSTGQMQCKVYDSLLAL
			PQDLQAARALCVIALLVALFGLLVYLAGAKCTTCVEEKDSKARL
1	}		VLTSGIVFVISGVLTLIPVCWTAHAVIRDFYNPLVAEAQKRELG
			ASLYLGWAASGLLLLGGGLLCCTCPSGGSQGPSHYMARYSTSAP
L	j		AISRGPSEYPTKNYV
6655	341	16	KDAYMPKKGLLALALVFSLPVFAAEHWIDVRVPEQYQQEHVQGA
1	i		INIPLKEVKERIATAVPDKNDTVKVYCNAGRQSGQAKEILSEMG
L			YTHVENAGGLKDIAMPKVKG
6656	2	1212	TELPPRPANLAIQPPLSPLRALAPLPEKPGAVPPPQKRMAKVAK
1			DLNPGVKKMSLGQLQSARGVACLGCKGTCSGFEPHSWRKICKSC
<u> </u>	,		KCSQEDHCLTSDLEDDRKIGRLLMDSKYSTLTARVKGGDGIRIY
[]			KRNRMIMTNPIATGKDPTFDTITYEWAPPGVTOKLGLOYMELIP
[[KBKQPVTGTEGAFYRRRQLMHQLPIYDQDPSRCRGLLENELKLM
1	1		EEFVKQYKSEALGVGEVALPGOGGLPKEEGKOORKPEGARTTAA
	1	.]	TTNGSLSDPSKEVEYVCELCKGAAPPDSPVVYSDRAGYNKOWHP
			TCFVCAKCSEPLVDLIYFWKDGAPWCGRHYCESLRPRCSGCDET
	1		IFAEDYQRVEDLAWHRKHFVCEGCEQLLSGRAYIVTKGQLLCPT
6657	830		CSKSKRS
""	030	2120	LLTCQERAGDCLLSASTMKEVVYWSPKKVADWLLENAMPEYCEP
1			LEHFTGQDLINLTQEDFKKPPLCRVSSDNGQRLLDMIETLKMEH
	!		HLEAHKNGHANGHLNIGVDIPTPDGSFSIKIKPNGMPNGYRKEM
	·		IKIPMPELERSQYPMEWGKTFLAFLYALSCFVLTTVMISVVHER
	1	ł	VPPKEVQPPLPDTFFDHFNRVQWAFSICEINGMILVGLWLIQWL
	•	j	LLKYKSIISRRFFCIVGTLYLYRCITMYVTTLPVPGMHFNCSPK
į.		1	LFGDWEAQLRRIMKLIAGGGLSITGSHNMCGDYLYSGHTVMLTL
		1	TYLFIKEYSPRRLWWYHWICWLLSVVGIFCILLAHDHYTVDVVV
		Į.	AYYITTRLFWWYHTMANQQVLKEASQMNLLARVWWYRPFQYPEK
6658	35	855	NVQGIVPRSYHWPFPWPVVHLSRQVKYSRLVNDT
		000	HCCALGAPGSPYRGLYFSSAAPCTAPRKAKHQSTLEGLTKRMLM

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F-Phenylalanine, G-Glycine,
ľ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
-	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
i	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
- }	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	_	\=possible nucleotide insertion)
			FDPVPVKQEAMDPVSVSYPSNYMESMKPNKYGVIYSTPLPEKFF
]	ļ	QTPEGLSHGIQMEPVDLTVNKRSSPPSAGNSPSSLKFPSSHRRA
			SPGLSMPSSSPPIKKYSPPSPGVQPFGVPLSMPPVMAAALSRHG
f			IRSPGILPVIQPVVVQPVPFMYTSHLQQPLMVSLSEEMENSSSS
	Ì		MQVPVIESYEKPISQKKIKIEPGIEPQRTDYYPEEMSPPLMNSV
			SPPQALLQE
6659	18	523	EPQRGDCETWFQNCSLPKFVCFFCWGFWLWRAHSMSNLHSLPGL
			RGLTSISRNQLQCTNAMRVINNYQRRWKNQNTFLLATFANVVNV
			CGNPTITCPHNRTLNNCHHSGVQVPLMYCNLTTPSPQNISNCRY
			AQTPANMFYIVACDNRDQRRDPPQYPVVPVHLHTII
6660	514	1707	CAASLDCRHHLCEPDMKLVWPSAKLLQAAAGASARACDSVTSNV
1	ļ		LPLLLEQFHKHSQSSQRRTILEMLLGFLKLOOKWSYEDKDORPI.
			NGFKDQLCSLVFMALTDPSTQLQLVGIRTLTVLGAOPDLLSVED
			LELAVGHLYRLSFLKEDSQSCRVAALEASGTLAAT, YPVAFSSHI.
			VPKLAEELRVGESNLTNGDEPTQCSRHLCCLOALSAVSTHPSIV
			KETLPLLLQHLWQVNRGNMVAQSSDVIAVCOSLROMARKCOODP
1 1			ESCWYFHQTAIPCLLALAVQASMPEKEPSVLRKVLLEDEVLAAM
1 1			VSVIGTATTHLSPELAAQSVTHIVPLFLDGNVSFLPENSFPSRF
1 1			QPFQDGSSGQRRLIALLMAFVCSLPRNVSEHIWEVLLFNLDKVT
6661			PG
6007	179	430	GVHAASGTLSATWLAEAKMFDSLAKAGKYLGQAAKLMIGMPDYD
6662	3.05		NYVEHMRVNHPDQTPMTYEEFFRERQDARYGGKGGARCC
5002	185	423	RSLPKPAPAQPASIHCARFSGVTPPTAKTAMSDGNTAFNALMYC
6663	3		GPKADDGNIFSACAPASSAVKASVSVAQPGQAVIP
0003	3	1005	RPVLSSRVDDFVPPLPETSGRRKKLERMYSVDRVSDDIPIRTWF
1 1			PKENLFSFQTASTTMQAISNFRKHLRMVGSRRVKAQTFAERRER
1			SFSRSWSDPTPMKADTSHDSRDSSDLQSSHCTLDEAFEDLDWDT
1 1]		EKGLEAVACDTEGFVPPKVMLISSKVPKAEYIPTIIRRDDPSII
1 1	i		PILYDHEHATFEDILEEIERKLNVYHKGAKIWKMLIFCQGGPGH
1 1			LYLLKNKVATFAKVEKBEDMIHFWKRLSRLMSKVNPEPNVIHIM
}			GCYILGNPNGEKLFQNLRTLMTPYRVTFBSPLELSAQGKQMIET
6664	58	968	YFDFRLYRLWKSRQHSKLLDFDDVL
] [200	PRLLRLPRSVVVMDSPWDELALAFSRTSMPPFFDIAHYLVSVMA
	1		VKRQPGAAALAWKNPISSWFTAMLHCFGGGILSCLLLAEPPLKF
1	Ī		LANHTNILLASSIWYITFFCPHDLVSQGYSYLPVQLLASGMKEV
1			TRTWKIVGGVTHANSYYKNGWIVMIAIGWARGAGGTIITNFERL
1			VKGDWKPEGDEWLKMSYPAKVTLLGSVIFTFQHTQHLAISKHNL MFLYTIFIVATKITMMTTQTSTNTFAPFEDTLSWMLFGWQQPFS
[]		İ	SCEKKSEAKSPSNGVGSLASKPVDVASDNVKKKHTKKNE
6665	171	1278	DERRLACRQVVTQQRSELYPGFQKRQRFLPKAGEEAAAQGGRHL
1	ļ	• •	PGRWLGPGCTQNPCSVHTATGPEPRKLPLLPPDSPNSGYPKEPA
1 1	[ALCPGIPSPCRMTHQDLSITAKLINGGVAGLVGVTCVFPIDLAK
	1		TRLQNQHGKAMYKGMIDCLMKTARAEGFFGMYRGAAVNLTLVTP
1	ļ	}	EKAIKLAANDFFRRLLMEDGMQRNLKMEMLAGCGAGMCQVVVTC
1			PMEMLKIQLQDAGRLAVHHQGSASAPSTSRSYTTGSASTHRRPS
1 1]	j	ATLIAWELLRTQGLAGLYRGLGATLLRDIPFSIIYFPLFANLNN
] [ļ		LGFNELAGKASFAHSFVSGCVAGSIAAVAVTPLDVLKTRIQTLK
			KGLGEDMYSGITDCAR
6666	498	2868	MTTFLPVPQMMAGFSFGTFGNPPMESPSAWQTIHQPFIVSCLTL
1 1			WSPGCWPQPIQKEGVGLWDIRKPQSSLLRYGGNLSLQSAMSVRF
			NSNGTQLLALRRRLPPVLYDIHSRLPVFQFDNQVYFNSCTMKSC
1		ì	CFAGDRDQYILSGSDDFNLYMWRIPADPBAGGIGRVVNGAFMVL
1 1	1	1	KGHRSIVNQVRFNPHTYMICSSGVEKIIKIWSPYKQPGCTGDLD
l J			GRIEDDSRCLYTHEEYISLVLNSGSGLSHDYANQSVQEDPRMMA
	!	l	FFDSLVRREIEGWSSDSDSDLSESTILQLHAGVSERSGYTDSES
<u></u> .		ļ	SASLPRSPPPTVDESADNAFHLGPLRVTTINTVASTPPTPTCED

SEQ Predicted Predicted end Amino acid segment containing ID beginning nucleotide (A=Alanine, C=Cysteine D=Ass	
	a graugi bebelue
ID beginning nucleotide (A=Alanine, C=Cysteine, D=As) NO: nucleotide location Glutamic Acid, F=Phenylalania	partic Acid, Es
location corresponding H-Histidine, I-Isoleucine, K	ne, G=Glycine,
corresponding to first L=Leucine, M=Methionine, N=A	=bysine,
to first amino acid P=Proline, Q=Glutamine, R=Arg	sparagine,
amino acid residue of S=Serine, T=Threonine, V=Val	ginine,
residue of amino acid W=Tryptophan, Y=Tyrosine, X=1	ine,
amino acid sequence Codon, /=possible nucleotide	Unknown, *=Stop
sequence _=possible nucleotide insert:	deletion,
AASRQQRLSALRRYQDKRLLALSNESDSI	ion;
PRSPSPEDESSSSSSSSSEDBEELNERI	EENVCEVELDTDLPPR
TREDKPSAPIKPTNTYIGEDNYDYPQIK	KASTWORNAMRRROKT
STLEIQPSRASPTSDIESVERKIYKAYK	VDDLSSSPTSSPERST
TSLVTGEADEGRAGTSHKDNPAPSSSKE	WLKYSYISYSNNKDGE
EGCSKDTFKEBTPRTPSNGPGHEHSSHAV	ACLINIAMAQRIQOLPP
SVEHPFETKKLNGKALSSRAEEPPSPPVE	MAEVPEGISUDIGNSG
RTQSDDSEERSLETICANHNNGRLHPRPE	PRASOSTLINSGSGNCP
AYSSPGHSDTDRDNSSLTGTLLHKDCCGS	FREADURGELEVV
TDTPATDSSRAVHGHSGLKRQRIELEDTI	Dermererant am
6667 171 1310 ABEVERLAAMRSDSLVPGTHTPPIRRRSH	VENNI COTEVOLUCIONE
KKSEKFKHTSAALERKISMRQSREELIKE	SCAL KELADADADA V.
SNEEDSLENGQSLSSSQLSLPALSEMEPV	ADMEDDE DE CARITA CASA
DIMDGPDPGAPVKLPPLPPKK	MMICMBUCCEDS OF U
SYTAQKSGQQGVAQHHHTVLPSQIQHQLQ	VACCHARDO THORYSOV
PMHPSGCRMIDELNKTLAMTMORLESSEC	DEVECTORATE TO SE
GDGVTKAGPMGLPEIRQVPTVVIECDDNK	(ENVEREDA EUG COL
YTREEEEEBDEDDDSSLYTSSLAMKVCR	KUSI'Y I KBENDBEKD
ELEEKNI LPROTDEERLE LROOTGTKI.	
6668 714 358 TLAVATGPALTLRCHVCTSSSNCKHSVVC	PASSPECKTTNTOPP
LRGNLVKKDCAESCTPSYTLQGQVSSGTS	STOCCOEDI CNEKLU
NAAPTRTALAHSALSLGLALSLLAVILAP	SL
6669 459 1207 KDEETRKDYDYMLDHPEBYYSHYYHYYSR	RLAPKVDVRVVTLVS
VCAISVFQFFSWWNSYNKAISYLATVPKY	RIOATEIAKOOGIIK
KAKEKGKNKKSKEEIRDBEENIIKNIIKS	KIDIKGGYOKPOICO
LLLFQIILAPFHLCSYIVWYCRWIYNFNI	KGKEYGEEERLYIIR
KSMKMSKSQFDSLEDHQKETFLKRELWIK	ENYEVYKQEQEEELK
KKLANDPRWKRYRRWMKNEGPGRLTFVDD	1
6670 184 594 VARI*GEAAKMSSEPPPPYPGGPTAPLLE	EKSGAPPTPGRSSPA
VMQPPPGMPLPPADIGPPPYEPPGHPMPO	PGFIPPHMSADGTVM
· PPGFYPPPGPHPPMGYYPPGPYTPGPYPG	PGGHTATVLVPSGAA
6671 1 763 LDBEVERGERBANG GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	
DPAERPRSAPMAGGRCGPQLTALLAAWI	AAVAATAGPEEAALP
PEQSRVQPMTASNWTLVMEGEWMLKFYAPI	WCPSCQQTDSEWEAF
AKNGEILQISVGKVDVIQEPGLSGRFFVT	TLPAFFHAKDGIFRR
YRGPGIFEDLQNYILEKKWQSVEPLTGWK	SPASLTMSGMAGLFS
ISGKIWHLHNYFTVTLGIPAWCSYVFFVI	ATLVFGLSMDLVL*V
ISQCNWDPPYRHVS±/RPSTNLGVHTAHTS	SEHLRL
AFGSRF VQFMDFEGRISFGMSVFNLSNAI	MGSGILGLAYAMAHT
GVIFFLALLCTALLSSYSIHLLLTCAGIA	AGIRAYEQLGQRAFG
PAGKVVVATVICLHNVGAMSSYLFIIKSEI	LPLVIGTFLYMDPEG
DWFLKGNLLIIVSVLIILPLALMKHLGYI	LGYTSGLSLTCMLFF
LVSVIYKKFQLGLCYRATMKQQWESEALVC	3TPQPRDSTAAVKAQ
MFHS*LTGVLTQWPIMAFAFVCHPGGAGPS 6673 1116 1963 LOIOTHHTHHGARVTHIGSHOLLANAGTWI	SITELCRAFQAQD
DOINTH THE GROUND ANAGTMI	LCRQQSSSMAPAFSQ
SVTCGPSPCVRKQESATKCLHIGACGSDLW	WARGWEQG*G*GLNV
WLCPCVAFHRGARPQAEEGGARWNSLVSSF	PWIPPNP*HSSIGAE
NAVPRP+QG+KVNPSGQERQS\WVLPLPVP	GEPLKLPGLPG*NK
SFSRV/SGSKGKWILPRQLM*AS*R\TPRF	VPGTQWVPITW/PL
ITWH*SAPTPPLKACPAPRESDPCSSCLSC	PCVTQHPRFSDTGW
FGAGHCHSSCDFTRKGAAGGPG 6674 1 440 LEEDYMONDYUGUDUGDUGDUGDUGDUGDUGDUGDUGDUGDUGDUGDUGD	
LEFDIMCQYDYVEVRDGDNRDGQIIKRVCG	NERPAPIQSIGSSL
HVLFHSDGSKNFDGFHAIYEEITACSSSPC	FHDGTCVLDKAGSY
KCACLAGYTGQRCENLLEERNCSDPG/WPS	QWVPENNRGPWAYQ
PTPC*IGTRVAFFLT	

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
i	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
ŀ	sequence	•	\=possible nucleotide insertion)
6675	277	1678	GNWPTERMAFLDNPTIILAHIRQSHVTSDDTGMCEMVLIDHDVD
			LEKIHPPSMPGDSGSEIQGSNGETQGYVYAQSVDITSSWDFGIR
ļ	ļ	}	RRSNTAQRLERLRKERQNQIKCKNIQWKERNSKQSAQELKSLFE
1			KKSLKEKPPISGKQSILSVRLEQCPLQLNNPFNEYSKFDGKGHV
			GTTATKKIDVYLPLHSSQDRLLPMTVVTMASARVQDLIGLICWQ
			YTSEGREPKLNDNVSAYCLHIAEDDGEVDTDFPPLDSNEPIHKF
i			GFSTLALVEKYSSPGLTSKESLFVRINAAHGFSLIQVDNTKVIM
1			KEILLKAVKRRKGSQKVSGSRADGVFEEDSQIDIATVQDMLSSH
ŀ			HYKSFKVSMIHRLRFTTDVQL/GCALFPGVLRKRAAPVDCLRPS
			ADTWRQEQIGCCGAACAALRS*DSHKC*EGISGDKVEIDPVTNQ
			KASTKFWIKQKPISIDSDLLCAC\DLAEE
6676	277	1678	GNWPTERMAFLDNPTIILAHIRQSHVTSDDTGMCEMVLIDHDVD
1			LEKIHPPSMPGDSGSEIQGSNGETQGYVYAQSVDITSSWDFGIR
1			RRSNTAQRLERLRKERQNQIKCKNIQWKERNSKQSAQELKSLFE
			KKSLKEKPPISGKQSILSVRLEQCPLQLMNPFNEYSKFDGKGHV
1			GTTATKKIDVYLPLHSSQDRLLPMTVVTMASARVQDLIGLICWQ
1			YTSEGREPKLNDNVSAYCLHIAEDDGEVDTDFPPLDSNEPIHKF
1			GFSTLALVEKYSSPGLTSKESLFVRINAAHGFSLIQVDNTKVTM
Ì			KEILLKAVKRRKGSQKVSGSRADGVFEEDSQIDIATVQDMLSSH
			HYKSFKVSMIHRLRFTTDVQL/GCALFPGVLRKRAAPVDCLRPS
			ADTWRQEQIGCCGAACAALRS*DSHKC*EGISGDKVEIDPVTNQ
L			KASTKFWIKQKPISIDSDLLCAC\DLAEE
6677	277	1678	GNWPTERMAFLDNPTIILAHIRQSHVTSDDTGMCEMVLIDHDVD
1			LEKIHPPSMPGDSGSEIQGSNGETQGYVYAQSVDITSSWDFGIR
			RRSNTAQRLERLRKERQNQIKCKNIQWKERNSKQSAQELKSLFE
			KKSLKEKPPISGKQSILSVRLEQCPLQLNNPFNEYSKFDGKGHV
1			GTTATKKIDVYLPLHSSQDRLLPMTVVTMASARVQDLIGLICWQ
1			YTSEGREPKLNDNVSAYCLHIAEDDGEVDTDFPPLDSNEPIHKF
		•	GFSTLALVEKYSSPGLTSKESLFVRINAAHGFSLIQVDNTKVTM
1 1			KEILLKAVKRRKGSQKVSGSRADGVFEEDSQIDIATVQDMLSSH
			HYKSFKVSMIHRLRFTTDVQL/GCALFPGVLRKRAAPVDCLRPS
			ADTWRQEQIGCCGAACAALRS*DSHKC*EGISGDKVEIDPVTNQ
			KASTKFWIKQKPISIUSDLLCAC\DLAEE
6678	221	865	GPSNQSSGSLSLIVTGCSSYWS*INDTCTILRVLSSNFGRQ*LR
	1		PFPCSQLPMSQGCLWHLDCCCPWVPYIPGQQWRKGRQRMRN*QS
]			LLGSDQESVGLEDLCVFVNFLLHVLLGLFP*PHELFLLPVVDLG
			FLFPLLLQGGCHCLVLPANLVSQAPQIGKLSCRLQTHDLEGSRN
		<u> </u>	HHPLFLVVGRWDAVKHLETVQSGLASLGFVGQHTSHGPP
6679	2	786	LEFARGAMPFLGQDWRSPGQNWVKTVDGWKRFLDEKSGSFVSDL
]	į.		SSYCNKEVYNKENLFNSLNYD/SCSQEEKEGHAE*QNQNS\DFH
]	ĺ		QEKWIYVHKGSTKERHGYCTLGEAFNRLDFSTAILDSRRFNYVV
	ļ		RLLELIAKSQLTSLSGIAQKNFMNILEKVVLKVLEDQQNITLIR
į J	j		ELLQTLYTSLCTLVKRVGKSVLVGNINMWVYRMETILHWQQQLN
			NIQITRVSGQAQPPPGSGSLHRDTGQTRQDFEFTPVTEESGLF
6680	1498	2951	PLCTLPLMPSALPGWAGERWEKQWPLA/PGPGTWQTPVGSISEE
			P\RKNEPDTHCPRGEARPEV*HLPKPHSPGSEGAEIQTSA*ALP
{			/nqvsppqpm+gaeengdqrggkeeageelhrsssgltaapgf?
			EVHRNLQTFPGLPSRGGGP/GGAGTQGSWAPGEQPP/SPLLPAS
			MQRSQAGLPGWEAGLVESPTHHIPALRPSGTNATGEAFPSTTCS
		ļ	SGP\PAPPGPTGLRPGGGSSSGGHG**PGLPVGKV\GALGAAQD
1			PQSQGRGPTQGTVGTEMLLSGLGSAKACPAARPAVP+LPSDPAS
			TIPKKGTRGFGEGPGVLQERNRWVVGRAQGFTSADAAGTAPPGV
1			*LPAPLSQPPGATEPQVRACGMAPPSPGTSGRLVANGRHPGPQV
		l	AQGCPPGAGCWGSQPRGSQRCPRTYTHSPLGHGRAPCPRRCWH*
	1		WQDPPSSPRTGCLPGIPARQAYSAPRTRSRPGIRTGRAAYGFIR
L <u>l</u>			FQGGGGG

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
[location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ŀ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
- }	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine
ì	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Ston
	amino acid	sequence	Codon, /=possible nucleotide deletion.
	sequence		\=possible nucleotide insertion)
6681	1169	511	INYIYYNQQQRAFHELK\EKLMSAPALGLPDLTKLFTLHVSERE
Ì		İ	KMTVGVLTQTVGPWSRPGAYLSKQLDGVSKGWPPCPRALAATAL
-			LAQEADELTLRQNLNRKSPHA\VVTLINTKGHH*LINARLTRVO
ļ			TLLCENPHKTIEVSNT/LNPATLLLVTRSPVKHNCLEVLDSVVS
ı		1	SRPNLRDHP*TSVDWELYVDGSGFANPCKVTLKKETSPAPVTPR
6682	109	1220	S
3332	103	1238	TVLCGAMQVSSLNEVKIYSLSCGKSLPEWLSDRKKRALQKKDVD
İ			VRRRIELIQDFEMPTVCTTIKVSKDGQYILATGTYKPRVRCYDT
		!	YQLSLKFERCLDSEVVTFEILSDDYSKIVFLHNDRYIEFHSQSG
			FYYKTRIPKFGRDFSYHYPSCDLYFVGASSEVYRLNLEQGRYLN
ļ	1		PLQTDAABNNVCDINSVHGLFATGTIEGRVECWDPRTRNRVGLL D\AP*TVSQQIQR*TSLPTISALKFN\GALTMAVGTTTGQVLLY
ļ			DLRSDKPLLVKDHQYGLPIKSVHFQDSLDLILSADSRIVKMWNK
			NSGKIFTSLEPEHDLNDVCLYPNSGMLLTANETPKMGIYYIPVL
<u></u>	<u> </u>		GPAPRWCSFLDNLTEELEENPESNE
6683	109	1238	TVLCGAMQVSSLNEVKIYSLSCGKSLPEWLSDRKKRALQKKDVD
1	!		VRRRIELIQDFEMPTVCTTIKVSKDGQYILATGTYKPRVRCYDT
			YQLSLKFERCLDSEVVTFEILSDDYSKIVFLHNDRYIRFHSOSG
1	•		FYYKTRIPKFGRDFSYHYPSCDLYFVGASSEVYRINT.ROGRVIN
	1		PLQTDAAENNVCDINSVHGLFATGTIEGRVRCWDPRTRNPVCLL
ŀ			DVAP*TVSQQIQR*TSLPTISALKFN\GALTMAVGTTTGOVILV
			DLRSDKPLLVKDHQYGLPIKSVHFODSLDLILSADSRIVKMWNK
			NSGKIFTSLEPEHDLNDVCLYPNSGMLLTANETPKMGIYYIPVL
6684	111	527	GPAPRWCSFLDNLTEELEENPESNE
1		J2 /	GLRGGTSRGRAGREPBFAAGVLCVVAGFCQSPCPPGGRGREAPA
			PP\SGRRHA*RPA*WLGGPGGDSGREEGGS/GELQRAMESKMG
			ELPLDINIQEPRWDQSTFLGRARHFFTVTDPRNLLLSGAQLEAS RNIVQNYR
6685	258	1473	KLLGDNFEGFCNKFELSDSENGSNS*QSPL\FDRLFDPDPQKVL
1 1			QGVIDMKNAVIGNNKQKANLIVLGAVPRLLYLLQQETSSTELKT
1	1		ECAVVLGSLAMGTENNVKSLLDCHIIPALLQGLLSPDLKFIEAC
1 1	Ì		LRCLRTIFTSPVTPEELLYTDATVIPHLMALLSRSRVTOEVICO
		ĺ	IFSHCCKGPDHQTILFNHGAVONIAHLLTSI.SVKVPMOAI.VCES
1 1			VLAFENPQVSMTLVNVLVDGELLPOIFVKMLORDKPIFMOLTCA
1 1			KCLTYMCRAGAIRTDDNCIVLKTLPCLVRMCSKERIJEERVEGA
1 1			ETLAYLIEPDVELQRIASITDHLIAMLADYFKYPSSVSAITDIK
1 1			RLDHDLKHAHELRQAAFKLYASLGANDEDIRKKVSLGEGRPPVI.
6686	310	927	TASRQGVTST
		761	DSVTFDDLAVDFTPKEWTLLDPTQRNLYRDVMLENYKNLATVGY
, ,		ŀ	QLFKPSLISWLEQEESRTVQRGDFQASEWKVQLKTKELALQQDV
	1	{	LGEPTSSGIQMIGSHNGGEVSDVKQCGDVSSEHSCLKTHVRTQN SENTFECYLYGYDELTLHVKTSTCFORSVFGUERVKG
	1	1	SENTFECYLYGVDFLTLHKKTSTGEQRSVFSHVWKKPSSLNPDV VCQKNRCTRKKKAF*LQLTLGKSFH*SIHT
6687	181	915	EAMLEAPYKKEEDEQQRKEVKKDYPSNTTSSTSNSGNETSGSST
			IGETSNRSRDRDRYRRRNSRSRSPGRQCRHRSRSWDRRHGSESR
ł			SRDHRREDRVHYRSPPLATGEPVDNLSPEERDARTVFCMQLAAR
j	1		IRPRDLEDFFSAVGKVRDVRIISDRNSRRSKGIAYVEFCEIQSV
[]			PLAIGLTGQRLLGVPIIVOASOAEKNRLAAMANNI.OKGNGGPMP
1 ccc 1			LYVGSLHFNITEDMLRGIFEPFGKV
6688	1025	1	AEVPNYPRVFHKCPDSCWRFKFOPIOLOPYILLSFSSEKDDYSE
	·]		SEPGLPR/SATARMATAAAPPNSSIDLPSDSGMGFISPAGDSLD
	}		LPSDGGTGFFSLAGDSSSTRLSSLAFISFSLSSVSVGSSAGTTS
	1	1	STSVGSVVAAFTSSSSSSTNRDVAGLDFSTVITSVSGSLVPSPR
ĺ	1	1	VAVICGSKGAGASGSASCSSRAGKTTEATAASSMPSGTSSFSTC
}	1	1.	TMSELEELFSLFSPAPLLSKLFTSSGSIAICCODSGPSDTGRIS
	<u>-</u> -		VCQLWLADSDTGKLSDCQEVVTVGDSGGLTCPELSLGRM*MSLL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ŀ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /-possible nucleotide deletion,
}	sequence		\=possible nucleotide insertion)
			SSAVIPGYSSSSDSRLNTVPTVDLLCPFQTKSST
6689	640	1299	SSSASYATSATSISDTAFSGSLKLKHGLLSALDSSSRTS*STSS
1	***		AEDSTFRICSPSVSDTSSDSSGSKDNVLILFSKVSI*SCFSLSS
1			FFSDSISFCFSSSSFCKR*FVSSKVSQNALLSSRLSNGPGGSSK
			QRNSLTARQLAMSL*ATKF*RNACNPNCLSSKKSAL*LSLNQRF
			GGSASRKPGNISPNSQKCSALSYCCNFVIKPREVSVSSENYPAF
6690	1	442	GTRGKMAATLGPLGSWQQWRRCLSARDGSRMLLLLLLLLGSGQGP
	_	112	QQVGAGQTFEYLKREHSLSKPYQGVGTGSSSLWNLMGNAMVMTQ
. [YIRLTPDMQSKQGALWNRVPCFLRDWELQVHFKIHGQGKKNL\H
			GDGLAIWYTKDRMOP
6691	287	1401	
0051	207	1401	LKTETSEEKARRYKDRPSQLNAVFQEQKKMIQAQESITLEDVAV
1	}		DFTWEEWQLLGAAQKDLYRDVMLENYSNLVAVGYQASKPDALFK
1			LEQGEQLWTIEDGIHSGACSDIWKVDHVLERLQSESLVNRRKPC
1			HEHDAFENIVHCSKSQFLLGQNHDIFDLRGKSLKSNLTLVNQSK
1			GYEIKNSVEFTGNGDSFLHANHERLHTAIKFPASQKLISTKSQF
1			ISPKHQKTRKLEKHHVCSECGKAFIKKSWLTDHQVMHTGEKPHR
!			CSLCEKAPSRKFMLTEHQRTHTGEKPYECPECGKAFLKKSRLNI
1			HQKTHTGEKPYICSECGKGFIQKGNLIVHQRIHTGEKPYICNEC
6692	178	939	/GKGFIQKTCLIAHQRFHTER
0052	170	939	WIKEGELSLWERFCANIIKAGPMPKHIAFIMDGNRRYAKKCQVE
			RQEGHSQGFNKLAETLRWCLNLGILEVTVYAFSIENFKRSKSEV
1	l, i		DGLMDLARQKFSRLMEEKEKLQKHGVCIRVLGDLHLLPLDLQEL
			IAQAVQATKNYNKCFLNVCFAYTSRHEISNAVREMAWGVEQGLL
l i			DPSDISESLLDKCLYTNRSPHPDILIRTSGEVRLSDFLLWQTSH
6693	178	939	SCLVFQPVLWPEYTFWNLFEAILQFQMNHSVLQK WIKEGELSLWERFCANIIKAGPMPKHIAFIMDGNRRYAKKCQVE
""	2,70	933	RQEGHSQGFNKLAETLRWCLNLGILEVTVYAFSIENFKRSKSEV
1			DCIMBLABOVECHI MERVEYI ONUCUGIDIN COLUMNIC STATES
{			DGLMDLARQKFSRLMEEKEKLQKHGVCIRVLGDLHLLPLDLQEL IAQAVQATKNYNKCFLNVCFAYTSRHEISNAVREMAWGVEQGLL
			DPSDISESLLDKCLYTNRSPHPDILIRTSGEVRLSDFLLWQTSH
			SCLVFQPVLWPEYTFWNLFEAILQFQMNHSVLQK
6694	292	813	SLLLHLAPPGAYTPSQPLSSVSTETASSVRQAAESRQHELPVR
! !		013	EVHSLGQILPQDGLTAEAGPPEAQDPWGSPGISLPAAHIGFAAA
			LAVGPSGCHTEP\FDEVWPSLFLGDAYAARDKSKLIQLGITHVV
1			NAAAGKFQVDTGAKFYRGMSLEYYGIEADDNPFFDLSVYFLP
6695	292	813	SLLLHLAPPGAYTPSQPLSSVSTETASSVRQAAESRQHELPVR
		010	EVHSLGQILPQDGLTAEAGPPEAQDPWGSPGISLPAAHIGFAAA
	j		LAVGPSGCHTEP\FDEVWPSLFLGDAYAARDKSKLIQLGITHVV
[[ļ		NAAAGKFQVDTGAKFYRGMSLEYYGIEADDNPFFDLSVYFLP
6696	i i	782	PRVRGRVGERWAFLSVPAAMSSEMEPLILLAWSYFRRKKFQLCAD
	· -	702	LCTQMLEKSPYDQAAWILKARALTEMVYIDEIDVDQEGIAEMML
	•		DENAIAQVPRPGTSLKLPGTNQTGGPSQAVRPITQAGRPITGFL
			RPSTQSGRPGTMEQAIRTPRTAYTARPITSSSGRFVRLGTASML
			TSPDGPFINLSRLNLTKYSQKPKLAKALIEYIFHHENDVKTALD
			LAALSTEHSQYKDWWWK/DQIEKCYYRVGMYRBABKQIKSS
6697	3	782	DDI PLODI NODAL DOCODYUMANINA CI COONYCONIO
	- 1	,04	PPLFLRRLNSRALRPGSRKVMAVVPASLSGQDVGSFAYLTIKDR
		İ	IPQILTKVIDTLHRHKSEFFEKHGEEGVEAEKKAISLLSKLRNE
	1		LQTDKPFIPLVEKFVDTDIWNQYLEYQQSLLNESDGKSRWFYSP
			WLLV\ECYMYRRIHEAI\IQSPPIDYFDVFKESKEQNFYGSQES
	ļ		IIALCTHLQQLIRTIEDLD\ENQLKDEFFKLLQISLWGEISVDL
6698	668	754	SL\SGGESSSQNTNVLNSLEDLKPFILLNDMEHLWSLLSNCK
6699	325	754	VGSCACAGSCKCKECKCTSCKKSECRAFP
5599	345	492	EGELP/PARRVLPRAMTASAQPRGRRPGVGVGVVVTSCKHPRCV
	İ		LLGKRKGSVGAGSFQLPGGHLEFGETWEECAQRETWEEAALHLK
LL			NVHFASVVNSFIEKENYHYVTILMKGEVDVTHDSEPKNVEPEKN

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A-Alanine, C-Cysteine, D-Aspartic Acid, B-
NO:	nucleotide	location	Glutamic Acid, F-Phenylalanine, G-Glycine,
Į	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
-	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
Į	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ſ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	1	\=possible nucleotide insertion)
			ESKRIIYNHAFFFQESKWSGGILQ
6700	1098	1392	TQCWRSSTPGMRTHFRTQP/RLECGQGFSQQENGHCMDTNECIQ
1			FPFVCPRDKPVCVNTYGSYRCRTNKKCSRGYEPNEDGTACVERT
L	<u></u>		LLLGLCNLLGK
6701	2	1485	AAAGPRTRVRRAAAFEGQPSPSPGLGPTSDKAAAPRTPKRRRLW
ľ			RQRQ/HPAMLCYVTRPDAVLMEVEVEAKANGEDCLNQVCRRLGI
		1	IEVDYFGLQFTGSKGESLWLNLRNRISQOMDGLAPYRLKLRVKF
1			FVEPHLILQEQTRHIFFLHIKEALLAGHLLCSPEQAVELSALLA
			QTKFGDYNQNTAKYNYEELCAKELSSATLNSIVAKHKELEGTSO
1			ASAEYQVLQIVSAMENYGIEWHSVRDSEGQKLLIGVGPEGISIC
1			KDDFSPINRIAYPVVQMATQSGKNVYLTVTKESGNSIVLLFKMI
			STRAASGLYRAITETHAFYRCDTVTSAVMMQYSRDLKGHLASLF
1			LNENINLGKKYVFDIKRTSKEVYDHARRALYNAGVVDLVSRNNO
1			SPSHSPLKSSESSMNCSSCEGLSCQQTRVLQEKLRKLKEAMLCM
1			VCCEEEINSTFCPCGHTVCCESCAAQLQVGESAAHFCLQPHLSL
			LLTGSRSQVLAR
6702	397	1971	PLAKFLKLDLVNVLCLPMEDVFLFYRTCFCSMGLGSSCHLSLPK
			RAEALLCSRKATVVRDLVAVRMAEEQEFTQLCKLPAQPSHPHCV
			NNTYRSAQHSQALLRGLLALRDSGILFDVVLVVEGRHIEAHRIL
			LAASCDYFKGMFAGGLKEMEQEEVLIHGVSYNAMCQILHFIYTS
		•	ELELSLSNVQETLVAACQLQIPEIIHFCCDFLMSWVDEENILDV
			YRLAELFDLSRLTEQLDTYILKNFVAFSRTDKYRQLPLEKVYSL
1 1			LSSNRLEVSCETEVYEGALLYHYSLEQVQADQISLHEPPKLLET
			VRFPLMEAEVLQRLHDKLDPSPLRDTVASALMYHRNESLQPSLQ
			SPOTELRSDFOCVVGFGGIHSTPS\MSSATRPKYLNPLLGEWKH
1			FTASLAPRMSNQGIAVLNNFVYLIGGDNNVQGFRAESRCWRYDP
1			RHNRWFQIQSLQQEHADLSVCVVGRYIYAVAGRDYHNDLNAVER
6703	45	1244	YDPATNSWAYVAPLKREVYAHAGATLEGKMYITCGRKGRIT
-/**	33	1244	GVGPRAAAMPLELELCPGRWVGGQHPCFIIAEIGQNHQGDLDVA
1		•	KRMIRMAKECGADCAKFQKSELEFKFNRKALERPYTSKHSWGKT
1			YGEHKRHLEFSHDQYRELQRYAEEVGIFFTASGMDEMAVEFLHE LNVPFFKVGSGDTNNFPYLEKTAK/TRGWHSVLRDVCGVQLNDE
			TSSWDVLGRVRTSKEKVLMVLVLDYSGRPMVISSGMQSMDTMKQ
1 1	l		VYQIVKPLNPNFCFLQCTSAYPLQPEDVNLRVISEYQKLFPDIP
			IGYSCHETGIAISVAAVALGAKVLERHITLDKTWKGSDHSASLE
			PGELAELVRSVRLVERALGSPTKQLLPCEMACNEKLGKSVVAKV
	ļ		KIPEGTILTMDMLTVKVGEPKGYPPEDIFNLVGKKVLVTVEEDD
, I	i		TIMEE
6704	82	1007	TMNTRNRVVNSGLGASPASRPTRDPQDPSGRQGELSPVEDQREG
	ļ	. • •	LEAAPKGPSRESVVHAGQRRTSAYTLIAPNINRRNEIQRIAEQE
	Į		LANLEKWKEQNRAKPVHLVPRRLGGSQSETEVRQKQQLQLMQSK
	į	•	YKQKLKREESVRIKKEAEEAELQKMKAIQREKSNKLEEKKRLQE
! I			NLRREAFREHQQYKTAEFL/RQTEHRIARQKCLSKCCLWPTILN
1 1			MGQKLGLQ\DSLKAEENRKLQKMKDEQHQKSELLELKRQQQEQE
į l	}		RAKIHQTEHRRVNNAFLDRLQGKSQPGGLEQSGGCWNMNSGNSW
			GI
6705	2	786	RLCRNSARVPCGWSASRSLGEGAGFIGPLRGPHPRAGGTGTSFT
l j	ļ		SYKRKGGIMSTIAAFYGGKSILITVATGFLGKELMEKLFRTSPD
!	ĺ	l	LKVIYILVRPKAGQTLQHRVFQILDSKLFEKVIEVRPNVHEKIR
]]			AIYADLNQNDFAISKEDMQELLSCTNIIFHCAATVRFDDTLRHA
		l	VQLNVTATRQLLLMASQMPKLBAFIHISTAYSNCNLKHIDEVIY
			PCPVEPKKIIDSLEW\LDDAIIDEITPKLIRDWPNIYTYTK
6706	130	531	FTHSSSSHSQEMLGKLNMLRNDGHFCDITIRVQDKIFRAHKVVL
		-	AACSDFFRTKLVGQAEDENKNVLDLHHVTVTGFIPLLEYAYTAT
	1		LSINTENIIDVLAAASYMQMFSVASTCSEFMKSSILWNTPNSQP
			EK

No: Despining conting	S	EQ	Predicted	Predicted end	Amino acid segment containing signal peptido
No:	- 1 :	ID	beginning	nucleotide	(Amalanine CoCycleine D. Reports 2-14
corresponding to first anino acid on, /sposible nucleotide insertion) 1143	N	io:		location	Glutamic Acid F-Phonylalanina Coddenia
Lofirst amino acid residue of amino acid sequence solve of acid sequence solve of acid sequence solve of acid sequence solve of acid sequence solve of acid sequence solve of acid sequence solve of acid sequence solve of acid sequence solve of acid sequence solve of acid sequence solve of acid sequence solve of acid sequence solve of acid sequence solve of acid sequence solve of acid sequence solve of acid sequence solve of acid sequence solve of acid sequence solve of acid sequence solve of acid sequence	- 1		location		HeHistidine Teleclousing V Israine,
to first anno acid residue of securine, manifo acid anno acid sidue of securine, manifo acid sequence			corresponding		LaLeucine Mamethionine Names
amino acid residue of amino acid sequence (amino ac	ı				P=Proline O-Glutamine P-n-1-1-
realdue of amino acid sequence coom, /=possible nucleotide deletion, /=possible nucleotide del	- 1		amino acid	1	S-Serine T-Thronning W-Walder
### Sequence Coden, y-possible nucleotide deletion, ide, y-possible nucleotide, y-possible	- 1				W-Trotophan V-Tunesin- William
Sequence	1			1	Codor (-possible musleshide deleti
1343 YWSGIGYELQHFHWRREHEEKGPETCGRIYESRSRWPCIS GWVWGWTAYNOSW GOQLRCVCCTSHSGOTRSSQCASKCGGOPPFK-NV SQAF-SRFCGLCNECGGCLILILGGGSSBWTDKHSCVENISH FFLSGN KTV-SSWERWYFAKYSKITSYGHESCKGRGP-PFK-NV SQAF-SRFCGLCNECGGCLILILGGGSSBWTDKHSCVENISH REWPSLLCEGGGHCYQGAVCREACABSEGIDASABEPHILGE FFLSGN KTV-SSWERWYFAKYSKITSYGHESCKGRGP-PFK-NV SQAF-SRFCGLCNECGGCGLUILLGGGSSBWTDKHSCVENISH TO-LDK-OFGYTQHFHCDSNLLCLIYNISPNLFSYSF-GVARYA C*RCHWYFERLLYHNCCDILLACL-PRQL-SSG GRENGTHAN C-C-RCL-SSG	- [\-nossible nucleotide deletion,
6708 115 1729 TVSSWERWYFAKTSRITSYCHENYSSSERRESCHENTER SORASKEN FFILSO KT'SSWERWYFAKTSRITSYCHSCKORGD'PDFKWYSORA'SRCCICCOCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	67	707		1343	Vuccious our distriction
FFILSO*KT*ISWENWYFAKISHISYCKIRGED*PIK*SQAP*SRCOLENPEGCEOLINEGCEOCHEORICGEOLINEGCSSWINNIGCVENNELLE SQAP*SRFCOLENPEGCEOCHEORICGEORYGEOCRAPGESCAPANA* C**RCHWYEWILLYNECOLILVAGEN*FIC*SSP*GVARYA* C**RCHWYEWILLYNECOLILVAGEN*FIC*SSP*GVARYA* C**RCHWYEWILLYNECOLILVAGEN*FIC*SSP*GVARYA* C**RCHWYEWILLYNECOLILVAGEN*FIC*SSP*GVARYA* C**RCHWYEWILLYNECOLILVAGEN*FIC*SSP*GOGGALO*UELUPF* GEI ISWWHPERFCKLALGSDCVBYTMESALTARDRUGVQDFVLL ENNTSEAD;*EUHRRFRERMINTYTIGPUNSVMPYHDIQUTUS* GAKKTDATKELQLYAFT*GPAPGGGAVAGRILLQSMPULAFBOQ** GAKKTDATKELQLYAFT*GPAPGGGAVAGRILLQSMPULAFBOQ** AKTLENNNSS*RFGKYMDVQPFBEADYMORYBRILLGSMPULAFBOQ** AKTLENNNSS*RFGKYMDVQPFBEADYMORYBRILLGSMPULAFBOQ** AKTLENNNSS*RFGKYMDVQPFBEADYMORYBRILLGUNSVLLEKSRVVMO** AKTLENNNSS*RFGKYMDVQPFBEADYMORYBRILLGUNSKLASKOV** VSSINDKSDBKVWRALTVIDFEBEVEDLIGIABAYUHLGNIH FAANESSNAQVTTENQLKYLTRILSVEGSTLLEALHHRITIAKS** RELLSPINLEGGAVARADALAKAVTSFTFTEURSLASKOV** ESPSMRSTTYLGLIDITYGFEVFGHS*FEGGCINTCMEKLQGUN** ESPSMRSTTYLGLIDITYGFEVFGHS*FEGGCINTCMEKLQGUN** ESPSMRSTTYLGLIDITYGFEVFGHS*FEGGCINTCMEKLQGUN** ESPSMRSTTYLGLIDITYGFEVFGHS*FEGGCINTCMEKLQGUN** ESPSMRSTTYLGLIDITYGFEVFGHS*FEGGCINTCMEKLQGUN** ESPSMRSTTYLGLIDITYGFEVFGHS*FEGGCINTCMEKLQGUN** ESPSMRSTTYLGLIDITYGFEVFGHS*FEGGCINTCMEKLQGUN** ESPSMRSTTYLGLIDITYGFEVFGHS*FEGGCINTCMEKLQGUN** ESPSMRSTTYLGLIDITYGFEVFGHS*FEGGCINTCMEKLQGUN** ESPSMRSTTYLGLIDITYGFEVFGHS*FEGGCINTCMEKLQGUN** ESPSMRSTTYLGLIDITYGFEVFGHS*FEGGCINTCMEKLQGUN** ESPSMRSTTYLGLIDITYGFEVFGHS*FEGGCINTCMEKLQGUN** ESPSMRSTTYLGLIDITYGFEVFGHS*FEGGCINTCMEKLQGUN** ESPSMRSTTYLGLIDITYGFEVFGHS*FEGGCINTCMEKLQGUN** ESPSMRSTTYLGLIDITYGFEVFGHS*FEGGCINTCMEKLQGUN** ESPSMRSTTYLGLIDITYGFEVFGHS*FEGGCINTCMEKLQGUN** ESPSMRSTTYLGLIDITYGFEVFGHS*FEGGCINTCMEKLQGUN** ESPSMRSTTYLGHA** ENEMPTYNTENDVARPROLAGUN** ESPSMRSTTYLGHA** ENEMPTYNTENDVARPROLAGUN** ESPSMRSTTYLGHA*** ENEMPTYNTENDVARPROLAGUN** ESPSMRSTTYLGHA*** ENEMPTYNTENDVARPROLAGUN** ESPSMRSTTYLGHA*** ENEMPTYNTENDVARPROLAGUN** ESPSMRSTTYLGHA*** ENEMPTYNTENDVARPROLAGUN** ESPSMRSTTYLGHA*** ENEMPTYNTENDVARPROLAGUN** ESPSMRSTTYLGHA*** ENEMPTYNTENDVARPROLAGUN** ESPSM	-			1343	CMURICUTARIOGUAGOS POR TOTAL CONTRACTOR CONT
SQAR*SRPCGLCNPCGHCGLDINLEGGSSPHTDHSCVENNLLC NERVPSILEGEPGHCYGOACREACHASPGAEPERICENE TD*LPR*GPGYIGHFHCDSNILCILINISPRIFSYSF*GVARYA TD*LPR*GPGYIGHFHCDSNILCILINISPRIFSYSF*GVARYA TD*LPR*GPGYIGHFHCDSNILCILINISPRIFSYSF*GVARYA C**CRHWYPEHLLANGCOLUNAC1**RRC1**SYSF*GVARYA GEILSWYMPHRPCKLALGSDGVAVTHGESALTARDRUGVQDPULL ENFTSBAAPIENLRRRERERLITYTIGFULGGAAGSPGGGMALQVELVPT GEILSWYMPHRPCKLALGSDGVAVTHGESALTARDRUGVQDPULL ENFTSBAAPIENLRRRERERLITYTIGFULGEACHAGAG GAGKTDATKALLGJUASTCAPQKGGAVBUHLQSNDYLEAPGA GAGKTDATKALLGJUASTCAPQKGGAVBUHLQSNDYLEAPGA AKTLRNDNSSRFGKYMDVQPDFKGAVUGGHLSYLLEKSKRVHQ NHGERNFHIFYGLEGGGEETTRRLGLERRPGLAFWLHGNIH FAANESNAGVYTTRQLKYTTLLSVEGSTLAHRKITAKG VSSINDKSDHKVVRKALTVIDFTEDBVEDLISIAASVLHLGNIH FAANESNAGVYTTRQLKYTTLLSVEGSTLAHRKITAKG EBLLSPINLEQAAYARDALAKAVYSRFFFKUVGKINGSLASKOV ESSPSWRSTTVIGLIDITYGFEVGINSFEGGFGKGKKKKEKKGRGAEK VSSINDKSDHKVVRKALTVILDFTEDBVEDLISIAASVLHLGNIH FAANESNAGVYTTRQLKYTLLSLUSGSTLHRKTITAKG EBLLSPINLEQAAYARDALAKAVYSRFFFKUVGKINGSLAGKAGK EBLLSPINLEQAAYARDALAKAVYSRFFFKUVGKINGSLAGKAGK EBLLSPINLEQAAYARDALAKAVYSRFFFKUVGKINGSLAGKAGK EBLLSPINLEQAAYARDALAKAVYSRFFFKUVGKINGSLAGKAGK EBLLSPINLEQAAYARDALAKAVYSRFFFKUVGKKGKKEKKGGGAEK TAAMEKKVSKGSREBEDLBALIAHQTILDAKRTYTUPLGCPP PSPRJNASLSVHERGEGGFRAGKKGKKEKKGGGAEK TAAMEKKVSKGSREBEDLBALIAHQTTLAKKTGKLOGGGGLWVGGGGAAGA FPHTKDLMVHLATTTRGVSTGGGGGGGGGAEKKGKKEKKGGGAEK TAAMEKKVSKGSREBEDLBALIAHQTTLAKKTGUTTSKLGSPGGTGGAGKKGKKEKKGGGAEK FPHTKDLMVHLATTTRGVSTGGGGGGGGGLWVGGGGFANGGAEK GOGANLTGLAFTLATTTSKLGSPGGTGTAGKKGTKKEKKGGGFANGGA FRIKMTNYRVESSSGGAARRARLALMGAFFATAAGVLVAGATIMHVI/YI WISSLTGHLHGGSRCGXTSAKKDDWATHAGATGAATGYALLLUSJAL GOGANLTGLAFTLLIMLGRRGGGGGLENATACHAGTAGKALLUSJAL GOGANLTGLAFTLLIMLGRRGGGGGALLAFAGAVLVAGATIMHVI/YI WISSLTGHLHGGSRCGXTSAKKDVALAMTALGPVHLAMTAA SELBFYGHTOVA VEPKRTNILIGGGGGGAAGAACLLKQVFAKDKTTFRFRK FEPGTGRFBLYKAGASLKSGLDLRSVVRLPGGENIDDHAUHV VDFNRTNILIGTARGSCCATSTGCWAGAGGGATLCHAGATGYALDHAUH VDFNRTNILIGTATGRAGGGGGALAGAACLLKQVFAKDKTTFRFRK FEPGTGRFBLAYGAAGAKGGGGGGALAGAACLLKQVFAKDKTTFRFRK FEPGTGRFBLAYGAAGAGGAAGAACLKGGGGAAGAACACLAGAGAGAAGAACACACACACACACACA	1				GMVVGWTAVNGSW*GGQLRCVCVCTSHSSDSTRSSQRASKCHS
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GEITAVVPEHPECKLÄLGSDVAYTMESATTARDRUGVODPVLL ENTTSEARFIENLITYTIGPULVSVNYPENDIOTYSE GAKKTDATKRILGLYAETCPAPORGAVARDRUGVODPVLL ENTTSEARFIENLITYTIGPULVSVNYPENDIOTYSE GAKKTDATKRILGLYAETCPAPORGAVARDRUGVENPULEAFON AKTLKRINDSSFRCKYMDVOPPFKGAVARDRULGSNPULEAFON AKTLKRINDSSFRCKYMDVOPPFKGAVARDRULGSNPULEAFON NHGENFHIFYGLLEGGEETLRRLGERNPQSYLYLVKGOCK VSSINDKSDWKVVRKALTVLIDFTEDBVEDLISTARAUTHENTIAK FANNESSNAGVTTERQLKYLTRILSVEGSTIKRALTHRKTIAKG EELLSPLANEGAAYARDALKAVYSRTFTWLVGKINRSLASKDV ESPSWRSTTVGLGLUTYGFBVCHNSFBGCINVCNEKLQOLFI ELTIKSEGEEYEARGIAWEPVQYNNKIICDLVEEKFKGII\SI LDE\ECTLEPGE FPHELLFPGGEEOFFFFLVSRRGLGFGKMCKKGKKEKKGRGAEK TAAKMEKKVSKRSRKEEEDLEALIAHFQTLDAKRTQVELFCFP SPRINASLSVHEKOBLILFGGEYTROGNTFLYNELYVYNIKK DTWTKVDIPSPPPRRCARQAVVVPGGGGGLWYFGEGPASPNGRG FYHYKDLUNHLATKTURGVKSTGGPSGSGHRWAMKGQLILF GGFRSTRDYIYYNDVAFFLDTFTWSKLSPSGTOFPTRSGCQ\ 195LFRAASSVYGGYSKGVKKDVKKTGTFTRSDMF FYHYKDLUNHLATKTURGVKSTGGPSGSGHRWAMKGQLILF GGFRSTRDYIYYNDVAFFLDTFTWSKLSPSGTOFPTRSGCQ\ 105LFRAASSVYGGYSKGVKKDVKKTGTFTRSDMF FYHYKDLUNGLASSVYGGYSKGVKKDVKKTGULGTFTRSDMF GFRANSLASSVYGGYSKGVKKDVKGVGGSGGRGHRANAKGLILF GGFRSTRDYIYYNDVAFFLDTFTWSKYLJAGAAYIVELI GGAASPGYGLLWVVWAMLAMALIQILSAKLOTATGKNLACQI RHYPRPVVWFYWQABIIAMATDLASFTGAAIGYTHGGFKKILGVSLL GGAASPGYGLLWVVWAMLAMAHIQILSAKGAAYIVELI FSQNNLAGLGKGMUYPELPTSSRVLLAAGAAYIVELI FSQNNLAGLGKGMUYPELPTSSRVLLAAGAAYIVELI FSQNNLAGLGKGMUYPELPTSSRVLLAAGAAYIVELI FSQNNLAGLGKGMUYPELPTSSRVLLAAGAAYIVELI FSQNNLAGLGKGMUYPELPTSSRVLLAAGAAYIVELI FSQNNLAGLGKGMUYPELPTSSRVLLAAGAAYIVELI FSQNNLAGLGKGMUYPELPTSSRVLLAAGAAYIVELI FSQNNLAGLGKGMUYPELPTSSRVLLAGAGAYAYIVELI FSQNNLAGRGGRGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	67	70B	115	1720	C*RCHWYFEWLLYNHCGDILVACL*RRQL*SSQ
ENFISEARFIENLRREFRENLITTIGGPULSVNYPRIOLITYSE GAGKTDATKELLGLYAETCPAPORGAVROELLGSNPULEAFON AKTLRNDASSFROKMUDYOPFKGAPVOGHILGSNPULEAFON AKTLRNDASSFROKMUDYOPFKGAPVOGHILGSNPULEAFON AKTLRNDASSFROKMUDYOPFKGAPVOGHILGSNPULEAFON AKTLRNDASSFROKMUDYOPFKGAPVOGHILGSNPULEAFON AKTLRNDASSFROKMUDYOPFKGAPVOGHILGSNPULEAFON NHGERNFHIFYQLLEGGEETLRRIGLERROSYLYLIKOGCAK VSSINDKSDAKVUTKOLLEGEETLRRIGLERROSYLYLIKOGCAK VSSINDKSDAKVUTKOLLEGETLRRIGLERROSYLYLIKOGCAK VSSINDKSDAKVUTKOLLEGETLRRIGLERROSYLYLIKOGCAK VSSINDKSDAKVUTKOLLEGETLRRIGLERROSYLYLIKOGCAK VSSINDKSDAKVUTKOLLEGETLRGETLRASULHIGHTKIIAK ELLSFLALEGETLAGALVAVSSTIFTKLUGKINTSLASKOU ESPSKRSTTVIGLLOTYFSFVORMSFCATHVOKKLOGGET ELITKSEGESPEAFGIAMEPVQYPNNKIICDLVEEKFKGII\SI LDE\ECLEPGE ENGINASLSVHEKORELLFGGETYROGKTFLYKELYVYNIKK DIWTKVDIPSPPPRRCARQAVVVPQGGGQLWVFGGEPASPNGSO FYHYKDLWHLAITKINGVKSTGGPSGRGHRWAMKGQILLF GGPRSTRDITYYNDVYAFRLDTFTWSLSPSGTOPPRSGCQ\ PSPSRINASLSVHEKORELLFGGETYROGKTFLYKELYVYNIKK DIWTKVDIPSPPPRRCARQAVVVPQGGGQLWVFGGEPASPNGSO FYHYKDLWHLAITKINGVKSTGGPSGRGHRWAMKGQILLF GGPRSTRDITYYNDVYAFRLDTFTWSLSFSGTOPPRSGCQ\ PSPSRINASLSVYGGYSKOKKKOVKKONKTROTRSDMF FYHYKDLWALHAITKINGVKSTGGPSGRGHRWAMKGQILLF GGPRSTRDITYNDVYAFRLUKJCHGPTRAGAIGFKLILGVSLL QGAVLTGIATPILIMLQRROQKPIEKVIGGLLLFVAAAYIVELI FEQUNIALGKOMUTPSILTSSAVELAGAYIYALIAYNIAGAYIVELI FEQUNIALGKOMUTPSILTSSAVELAGAYIYALIAYNIAGAYIYALI FEQUNIALGKOMUTPSILTSSAVELAGAYIYALIAYNIAGAYIYALI FEQUNIALGKOMUTPSILTSSAVELAGAYIYALIAYNIAGAYIYALI FEQUNIALIAYNIAGAYIYALIAYNIAGAYIYALIA FARISASPKTHIAAGASLASGDLRSVYALPGGENIDDHIAVHV VDFRNINILYGTMARGCSTSCHWAGGGRPLETPPTEGCTSDVE PHGQKRRTYFQVRAFGGOPGAGLAMAICCKOVFAKOKTYRPPKR FEROTOGRETSIYKAAGASLASGDLRSVYALPGGENIDDHIAVHV VDFRNINILYGTMARGCSTSCHLEGGTKKGYKVYPTPEI ARALLSAPKALLADHILSII GARGSGELYRGIAAGAKKKKUKGGGGRANLSYPVFKGURGDMEDOF ARALLSAPKALLADHILSIIIATGRSCHTAFFLUKDAGARITEVUL IRLDVOTKLKROQLKTSFFTVARGABLSGLDRSVAVPPFGCORDMAP MGFABGLQEIIARICHARGAYAVANAQOQ VFNSRFANSPASISIAGAGGRAGALFSTROOQ VFNSRFANSPASISIAGAGGRAGALFSTROOQ VVNSRFANSPASISIAGAGGARALGFOGLARANAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	"	•	113 .	1729	TVGSWSRSGRSPPVGRQLLLTGRGAQAAGSPQGGMALQVELVPT
OMMERYRGYSTYSEPPHLLAWDITVYRALRITERROQAWIISVES GAKKTDATRILGIANDATCHQARGAPUGGEILSYLLEKSKUVHQ NHGERRHIFYYQLLEGGEETLRRIGLERNQGSYLYIVKGQCKA VSSINDKSDRKVVRKALTVIDFITEDBYEOLLSIASVLHIGNIH FRANCESSNAQVITERQLKYLTRLISVEGSTLKEALITHKKIIAKG BELLSFLNIEQAAYRADALAKAYSERFTYKUVGKINKSLASKOV ESPSNRSTTVLGLLDIYGFEVFORNSFEGFCINYCNEKLQQLBT ELIILKSEGSEYLABGIABEPQVYRNKIICDLVEEKFKGII\SI LDE\ECLRGE FPHEHLFPSGERGFFSFLVSRRGLGFGKMGKKKKKKKKRGRAEK TARKMEKKVSKRSRKEEBDLBALIAHFQTLDAKRTQTVELPCP PSPRLNASLSVHPEKDELILIGGSYNGGKTFLVNELYVYNIK DYWTKUDIPSPPPRACRHQAVVVYGGGVWFGGEFASPNGG FYHYKDLMVLHLATKYMEGVKSTGGPSGESGRHWAMKRGLLLP GGFHSSTEDTIYYNDVAPANLDFTYNSKLSPSGTGPTPRSGCQ\ 1PSLPRAASSVYGGYSKQVKKDVDKGTRHSDMP FHHYRPVVWFYSSSGRARKMALMIAMIGILSAKLGIATGKNLASGI GARKSTEDTIYYNDVARNLAMFMIGKALGKUTAKKLASGI RBHYPRPVVWFYWQABIIAMATDLAEFTGRAIGFKLILGVSHL GGAVLTGTATFLILMURRGGKPELRVIGGLLLEVVAAAYIVELI FSQMLAQLGKGWIFSLPTSEAVFLAAGUV\GATIMPHVI/YI WSSLTCHLHGGSROQRYSATKWDVAIAMTIAGFVNLAIMARAA SELNFYGHTGVA SELNFYGHTGVA SELNFYGHTGVA 6711 3 347 VYECKTWTCKMSGLERNI*TMINTLHHYSVKLGHPDTLTHGEFK FSPMLAQLGKGWIFSLTSEAVFLAAGUV\GATIMPHTLIHGEFK FSPMCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	ſ				GETTRVVHPHRPCKLALGSDGVRVTMESALTARDRVGVQDFVLL
GAGKTDATKRILQLYAETCPAPQREGGAVEDRILQSNPVLEAFGN AKTURNDNSRFGFKYNDVQPDYKGGELISYLLEKSRVYHO NHGERNFHIFYOLLEGGEETTRRIGLERNPQSYLYLVKGQCAK VSSINDKSDWKVVRKALTVIJFTEDBVEDLISIASVLHIGNIH FAANEESNAQVTTENQLKVIRKILVSGSTLERALTHKKIAK EELISFINLEGAAYARDALAKAVYSRFFTWLVGKINRSLASKUV ESSPNNSTTVUGLIJ UTGEBVGINSEGPGCINYCNKKLOOLFI EIJIKSEGEEVEASGIAWEPVQYFNNKIICDLVEEKFKGII\SI LDE\ECLERGE PPHEHLFFSGERGFFSFLVSRRGLGFGKMGKKKKKKKGRGAEK TAAKHEKKVSKRSRKEEEDLALIHGGTLDAKKTQTVELFCEP PSPRLNASLSVHPEKDELILFGGSYNGGKTEINBELYVNIKK DTWTKVDIPSPPRRCAHGAVVVQGGGQLWYFGGEFASPNGGO FYHYKDLAVHLHATKYHKTGVKSTGGPGSRGKRWKAKKKYNIKKI GGFHESTRDYIYYNDVAFNLDFTTWSGKTEINFERLYVNIKK DTWTKVDIPSPPRRCAHGAVVVQGGGQLWYFGGEFASPNGGO FYHYKDLAVHLHATKYHKTGVKSTGGPGSRGKRWAMKRQLILF GGFHESTRDYIYYNDVAFNLDFTTWSGKSTENBERP FYHYKDLAVHLHATKYHKTGVKSTGGPGSRGKRWAMKRQLILF GGFHESTRDYIYYNDVAFNLDTTTWSGYTIPTSEGGTCA 158 980 RHKMTNYKVESSSGRARKRMALANGAFAFAAIGYIDFGNFATN IQAGASFGYQLLWVVWANILAMIQILEAKLGIATGKNILAGGI RDHYPRFVWFFWVGABAIAWATIGAFVALAMIALGI GGAVLTGIATFLILMQRRGQKPLEKVIGGLLLFVAAAYIVELI FSQPNLAQLGKGWITSPLFTEBAVFLAGAVL\GATIMPHI/YI WISSLTQHLKGGSRGGYTSATKWDAITTAGGFWLAIMATAA SSLINFYGHTGVA 6711 3 347 VYECKTWTCKMSQLERNI*TMINTLHHYSVKLGHPDTLINGEFK ELVRTDLIHILMSRNKNDQAI*HMEDLDTNAHMQIIFKELIML MAMLTWSYHDNMHDADYOGQGRPD 6712 118 578 PHGGKRTRYFQVRAFGQOFQAQLAMALCLKQVFAKDKTFFRKR FSPGTQRFELYKKAQASLKSGLDLRSVVRLPPGGNIDDHIAVHV VDFFNRINLIYGTMAERGS*TSCTWAGPTEYPTSECTSDVE PRITEMWRAQNKKKKSGGFQSMGLSYPVFRGIMKKGYKVPTPI QRKTIPYILDGKOVVAMARTGSGKTACPLLBWFERLKTHSAQTG ARAJILISPITELALTLKFYKELGKTAALLLGGDBMEDOF AALHENDDIIIATPGRLVHVAVSMSLKLQSVEYVYPDEADRLPF MGFARQLGEIIAR.PGGNTUFFSATLPKLLVSPRACLTEPUL GKCSTLJKFTKELGKTAALLLGGDBMEDOF AALHENDDIIIATPGRLVHVAVSMSLKLQSVEYVYPDEADRLPF MGFARGLGEIIAR.PGGRTYLFFRKELKTHALLHGNVRQOQTV VFVATKHABEYLTELLTTQRVSCAHIYSALDFTARRINLAKFTL GKCSTLJKTFTELLGTLFTRELGKFTARLLERPAGGATEFVUL GKCSTLJKTFTELLGTLFTRELGKFTAALLLEGDRADAQOQO GVGCGGGGUGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG		- 1			ENFTSEAAFIENLRRRFRENLIYTYIGPVLVSVNPYRDIQIYSR
AKTERNDMSSRFGKYNDVGPDERAGPVGGFILSYLLEKSRVVAG NHGERRHFHYGLLEGGEETLRHGSYLYLVKGQCAK VSSINDKSDMKVVRKALTVIDFTEDEVEDLLSIAASVLHLGNIH FAANESNAGVTTERGLKYLTRILSVEGSTLKEALTHRKIIAKG EBLLSPLANLEGAAYARDALAKAYSTFTWLVGKINRSLASKOV ESPSMRSTTVLGLLDIYGEVFQKNGFEGFCINYCNEKLGQLDFI ELILKSEGBEYLARGIAMEPVQYFNNKIICDLVEEKFKGII\SI LDE\ECLRPGE FPHEHLFFSGERGFFFFLVSRRGLGPGKMGKKKKKKKKGRGAEK TAAKMEKKVSKRSRKEEBLBALIAHFQTLDAKRTQTVELFCPP PSPRLNASLSVHPEKDELILIFGGEYNGGKTFLYNELYVYNIEK DTWTKVDIJPSPPPRACAHQAVVVPGGCHVFGGEPASPNGEQ FYHYKDLMVLHLATKTWEQVKSTGGSGRSGHRWAMKRGLILF GGPHSSTRDYIYNDVYAFNLDTTWSKLSPSGTGPTPRSGCQ\ 1781EPAASSYYGGSKGRVKKDWAFHSHMSM GGPHSSTRDYIYNDVYAFNLDTTWSKLSPSGTGPTPRSGCQ\ 1781EPAASSYYGGSKGRVKKDWAFHSHMSM GGPHSTRDYIYNDVYAFNLDTTWSKLSPSGTGPTPRSGCQ\ 1781EPAASSYYGGSKGRVKKDWAFHSHMSM 10GASSGYQLLWVVVVANIAMALMGIAKLGIAKLGIATGKNLAEQI RDHYPRPVVWFYWQABIIAMATDLAEFTGAAIGFKLILGVSLL QGAVLTGTAFFILLMQRRGGKFLEXVIGGLLLFVAAAYIVELI PSGPMLAGCKGWNIPSJTERSPTELAAGVL\GATIMPHI/YI WHSSLTCHLHGGSRQGTSATKWDVAIAMTIAGPVNLAIMATAA SSLNFYGHTGVA SSLNFYGHTGVA 6711 3 347 VTECKTWTCKMSQLERNI*TMINTLHHYSVKLGHPDTLIHGEFK ELVRTDLHNILMKENKNDQAI*HMBDLDTMAHMQIIFKELIML MAMITUSYHDNMINDAYPGQGHPA ELVRTDLHNILMKENKNDQAI*HMBDLDTMAHMQIIFKELIML WAMITUSYHDNMINDAYPGQGHPA VDFFNRINLIYGTMAERCS*TSCYWARPGRYETEWODERQYR PAKLSAPRYMALLMWIBSLI QARGSBEDGEPFTGAGDDAFARKLGPGRPYETFROBERQYT PAKLSAPRYMALLMBWISSLI GARGSBEDGEPFTGAGDDAFARKLGPGRPYETFROBERGYT ARALLISPTREILALTKHTKELIKTHYKLLGKFTLKTALILLGGDMEDGF AALHENDDIIIATFRELLHTKHTKLIKTFKLKLGKTELKTALILLGGDMEDGF AALHENDDIIIATFRELLHTKHTKLIKTFKLKLGVFPARAGLTEPUL IRLDVDTKLNEQLKTSFFLVREDTKAAVLLHLLHNVVRPQDQTV VFVATKHABEYLTTELLTTQRVSCAHIYSALDPTARKINLAKFTL GKCSTLIVTDLAARGIDIPLINNIYTHPKLLKTVERARGLTEPUL IRLDVDTKLNEQLKTSFFLVREDTKAAVLLHLLHNVVRPQDQTV VFVATKHABEYLTELLTTQRVSCAHIYSALDPTARKINLAKFTL GKCSTLIVTOLLARGIDIPLINNIYTHPELLERGLARVADNAQOQ VYRSRPAPSPBSIKRAEMBLUGGLHPLPSSRFEEBELGKRUR GQGQCGGGGUGUGGGGGGGGGGGGGGGGGGGGGGFGFFLFF	1				QHMEKYRGVSFYEEPPHLLAVADTVYRALRTERRDQAVMISVES
NHGERNFILITYQLLEGCEEETLRRLGLERNPGSYLYLVIKGQCAR VSSINKSDWKVVRKALTVIDTETEGDLSIASAVLHLGNIH FRANCESNAQVTEKQLKYLTRLLSVEGSTLREALITRKIIANG BELLSPLNEQAAYARDALARAVISRTFTKUKGLOSIF ELTLKSEGESVAGGIAWEPVQYRNKIICDLVEEKPKGII\SI ESPSWRSTTVIGLUITGEEVQGINSFEGFCINYCNRKLQGLFI ELTLKSEGESVEAGGIAWEPVQYRNKIICDLVEEKPKGII\SI LDE\ECCLPRGE PPHEHLFPSGERGFFSFLVSRRGLGFGKMCKKGKKEKKGRGAEK TAAKMEKKVSKRSRKEEEDLEALIAHFQTLDAKRTQTVELPCCPP FSPRLNASLSVHEEKDELLLRGGSYNGGKTELVNELYVANIKK DTWTKVDIPSPPRRCAHGAVVVQGGGGLWYGFGEFASPNGGO FFYHYKDLAVHLHAITKTHEGVKSTGGSGESGEHRWAMKRGLILF GGFHSSTRDYIYNDVAPANLDTFTWSKLSPSGTGPTFRSGCQ\ 1986PARSSVYGGYSKQVKKDDKGTHNSDMP FHYKDLAVHLHAITKTHEGVKSTGGSGESGEHRWAMKRGLILF GGFHSSTRDYIYNDVAPANLDTFTWSKLSPSGTGPTFRSGCQ\ 1986PARSSSYGGYSKQVKKDDKGTHNSDMP 1986PARSSSYGGYSKQVKKDDKGTHNSDMP 10AGASFGYGLLWVVWANLAMMIGILSAKLGIATGKNLASGI RHYTPRYVWFYWYGBIAAVAMAMIGILSAKLGIATGKNLASGI COAVLTGIATFILIMLQRRGGKPLERVIGGLLEPVAAAYIVELI FSCPHLAGLAKGMVIPSLTSEAVFILAGVULGALTMERVI'\T WHSSLTQHLHGGSRQQRTSATKHDVALAMTIAGFVNLAIMATTAA SSLINFYGHTGVA 6711 3 347 VTECKTMYCKMSGLERNI'TMINTLHHYSVKLGHPDTLTHGEFK ELVRTDLHNILMKENKNDQAF'HMBDLOTNAHMQIIFKELIML MAMITWSVHONMIDADYOPGOHRPG 6712 118 578 PHGQKRTRYFQVRAFGQOFQAQLAMALCLKQVFAKDKTFRRKR FEPGTQRFELYKKAQASLKSGLDLRSVVRLEPGGRIDDHIAVHV VDFFNRINIYGTMGRCS'TSCTWRQDERYEVTRMQDERQYRR PAKLSAPRYMALIMDWIRSLI 6712 118 578 PHGQKRTRYFQVRAFGQOFQAQLAMALCLKQVFAKDKTFRRKR FEPGTQRFELYKKAQASLKSGLDLRSVVRLEPGGRIDDHIAVHV VDFFNRINIYGTMGRCS'TSCTWRQDERYEVTRMQDERQYR PAKLSAPRYMALIMDWIRSLI 6713 2485 3 QAGGGBEDGEFFIQAEDDARARKLGGGFPYEYRMQDERQYR PAKLSAPRYMALIMDWIRSLI 1RLDVDTKLNEQLKTSFFLVFRSCHGKTAAULHLLHNVRPQDQTV VFVATKHRBEYLTELLTTQRVSCAHIYSALDFTARKINLAKFTL GKCSTLIVETNIAGGIFLIPLNONIYAFAKGLHLHENVRPQDQTV VFVATKHRBEYLTELLTTQRVSCAHIYSALDFTARKINLAKFTL GKCSTLIVETNIAGSTILLARPLKEPSOVA GVGCMLGRVPQSVVDEEDSGLOSTLEASLEIRGLARVADNAQO VVRSRPAPSPSIKRAKEMDLVGIGHHPLFSSRFEEBLGGERUGIFS GQCGCGGGUGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	1				GAGKTDATKRLLQLYAETCPAPQRGGAVRDRLLQSNPVLEAFGN
VSSINDKSDK/VPRRAIT/TOFFEDENEDLISIAASVLHIGHIH FAANESSNAQVITEROLKYLTELLS/SEGSTLREALTHRKI IAKG EELLSFINLEQAAYARDALAKAVYSRTFTKUVGKINRSLASKUV ESPSMRSTTYLGLLDIYGFEVFOHNSFEQFCINYCNSKLQQUFI ELTLKSEGGEYEAGE IAWEPUYFIKIICOLVEEKFKGII\SI LDE\ECLRPGE 6709 3 894 PPHEHLFPSGERGPFSFLVSRRGLGFGKMGKKKKKKKGRGAEK TAAKMEKKVSKRSRKEBEDLEALIAHFGTLDAKKTQTVELPCPP FSPRLNASLSVHPEKDELLIFGGEYFNGGKFFLVNELYYVNIKK DIWTKVDLWYLHLATKTMEQVKSTGGPSGRSCHRWVAMKRQLILF GCPHSSTRDYIYYDVYAPLDYFTWOGKFFLVNELYYVNIKK OFFRENTRYIYYDVVAPLDYFTWOKSTLSPSGTGFTPRSGCQ\ FYNYKDLWYLHLATKTMEQVKSTGGPSGRSCHRWVAMKRQLILF GCPHSSTRDYIYYDVVAPLDYFTWOKSTLSPSGTGFTPRSGCQ\ IPSLPRAASSVYGGYSKQRVKKDVDKGTRHSDMP IPSLPRAASSVYGGYSKQRVKKDVDKGTRHSDMP IPSLPRAASSVYGGYSKQRVKKDVLGISAKCIATKKNLSQLIL GGAVLTGIATPLILMLQRRGQKPLEKVIGGLLFVAAAVIVELI FSQFNLAQLGKGMVIPSLPTSSRVALAGVL\GATIMPHIYIT WHSSLTGHLHGGSRQQRYSSATKWDVAIAMTIAGFVNLAIMATAA SELNFYGHTGVA SELNFYGHTGVA SELNFYGHTGVA AMMLTWSYHDNMIDADYOGGQDRPG 6712 118 578 PHGGKRTRYFOVRAPGGPFOAGLAMALCLKGVFAKKKTELIML MAMLTWSYHDNMIDADYOGGQDAPACHCLKGVFAKKKTELIML VDFPRRINLIYGTMARGCS*TSCVMAGGFRYSYRQDERGYRE FSPGTGRSELYKKAQSKLSGLDLRSVVRLPPGGNIDDWIAVV VDFPRRINLIYGTMARGCS*TSCVMAGGFRYSYRQDERGYRE FSPGTGRSELYKKAQSKKSGLDLRSVVRLPPGGNIDDWIAVV VDFPRRINLIYGTMARGCS*TSCVMAGGFRYSYRQDERGYRE FSPGTGRSELYKKAQSKKSGLDLRSVVRLPPGGNIDDWIAVV VDFPRRINLIYGTMARGCS*TSCVMAGGFRYSYRQDERGYRE FSPGTGRSELYKAQSLKSGLLRSVFUKGYKVPTPI QRKTIPVILDGKDVVAMARTGSGKTACFLLPWFELKTHSAQTG ARALILSFTRELALQTLKKTFGLKTALLIGGRMEDGF ARALILSFTRELALQTLKKTFGLKTALLIGGRMEDGF ARALILSFTRELALQTLKKTFGLKTALLIGGRMEDGF ARALILSFTRELALQTLKKTFGLKTALLIGGRMEDGF ARALILSFTRELALQTLKKTTGRSCATHYSLLUPFARAGLTEPVL UFVATKHABYLTELLTTGVSCATHYSLLUPFARAGLTEPVL UFVATKHABYLTELLTTGVSCATHYSLLUPFARAGLTEPVL UFVATKHABYLTELLTTGVSCATHYSLLUPFARAGLTEPVL REGORGEDGEFELJFRGGGGTGLGFLLRSPLERGRAVADNAQQQ GKCSTLVTULAARGULFTLSPLUPTGRAAVLLHLLHNVVRPQDGCTV VFVATKHABYLTELLTTGVSCATHYSSELLERGLARVADNAQQQ GYCMMLGRVPOSVVDEDSGLGJSTLERSLELRGLARVADNAQQQ GYCMMLGRVPOSVVDEDSGLGJSTLERSLELRGLARVADNAQQQ GYCMMLGRVPOSVVDEDSGLGJSTLERSLELRGLARVADNAQQQ GYCMMLGRVPOSVVDEDSGLGJGSPSFRALGEVBEIPS	1	-			AKTUKNUNSSRFGKYMDVQFDFKGAPVGGHILSYLLEKSRVVHQ
FARNESNAQVITENQLKYLTRLLSVEGSTLREALTHEKTIAKG EELLSPLNLEQAAYARDALAKAYARTOHLAKAYATFIYLVUGKINRSLASKUV ESPSWRSTTVLGLLDIYGFEVFQHNSFEQFCINYCNEKLQQDFI ELITLKSEGEBYEAEGIAWEVQYFNNKIICDLVEEKFKGII\SI LDE\ECLERGE PPHEHLFPSGERGPFSFLVSRRGLGFGKMGKKKKKKKKGRGAEK TAAKMEKKVSKRSRKEBEDLEALIAHFGTLDAKTQTVELPCPP FSFRLMASLSVHPEKDELLLFGGEYFNGQKFFLVNELYVYNIKK DTWTKVDIPSPPRRCAHQAVVVPQGGGLWYFGGEFASPNGEQ FYHYKDLWHLHATKTHEQVKSTGSGRGHRWAWKRQLILF GGFHESTRDYIYYNDVYAFNLDTFTWSKLSFSGTGFTPRSGCQ\ 1FSLPRAASSVYGGYSKQRVKKUVKGTRHSDMP FHYKDLWHLHATKTHEQVKSTGFPFARGGYDFFRSGCQ\ 1FSLPRAASSVYGGYSKQRVKKUVKGTRHSDMP 1GAGASFGYQLLWVUVWANLMAMLIQILGAKLGIATGKNLAEQI RDHYPPVVVFYWVQABIIAMATDLAFFIGAAIGFKLILGVSLL QGAVLTGIATFILIMLQRRQQKFDAFLAYGALGYIFGENFATN 1QAGASFGYQLLWVUVWANLMAMLIQILGAKLGIATGKNLAEQI RDHYPPVVVFYWVQABIIAMATDLAFFIGAAIGFKLILGVSLL FSQPNLAQLGKGMVIPSLETSERVFLAAGVL\GATIMPHYI/YI WSSLIOTHINGBSCQRYSATKWDUAIAMTIAGPVNLAIMATAA SELNPYGHTGVA 6711 3 347 VYECKTMYCKNSQLERNI*TMINTLHYSVKLGHPDTLIHGEFK ELVRTDLINILMKSNKNDQAI*HMEDLDTNAHMQIIFKELIML MAMLTWSYHDNMIDADYGPQQHRRG 6712 118 578 PHGQXRTYPQVRAPGQOFQQAQLAMALCLKOYFAKKKFTFPRKR FSPGTQRFELYKKAQASLKSGLDLRSVVRLPPGENIDDHIAVHV VUPFNRINLIYGTMARRCS*TSCPVMAGGPRYEYRWQDERQYRR PAKLSAPRYAALLMDMISSLI 6713 2485 3 QARGSDSEDGEFFIQAEDDARAKKLGVFAKKFTFPTSECTSDVE PDTTEMWRAQNKKKKKSGGFGSMGLSYPVFGIMKKGYKVPPPI QRKTIPVILDGGDVVAMARTGSGKTACPFLLPMFERLKTHSAQTG AALHENDDIIATPGULAVENSLKLGSVETVVPDEADRLPE MGFAEQLQEIIARI-PGGGGTULTSRAGLTEPUL IRLDVDTKLINGQLKTSFFLVREDTKAAVLHLLHRVVRRQDDTV VFVATKHABYLTELLTTQRVSCAHIYSALDPTARKINLARFIL GKCSTLIVTULAARGLDTPLLDNVINYSFPAGGLFFLKRAGNTA GKCSTLIVTULAARGLDTPLLDNVINYSFPAGGLFFLKRAGNTA GKCSTLIVTULAARGLDTPLLDNVINYSFPAGGLFFLKRAGPUG VGVAMLGRVPOSVVDEDSGLGCLTHFLERSLELGGLARVANDAQOQ VYRSRPAPSPESIKRAKEMDLVGLGLHPLFSSRPEEELGKLRU VDSIKWYRSRATIFFINASSRDLCSQVMAKKARKROKRKARAFQC GCOGROCOCOCOCOCOCOCOCOCCOCOCOCCOCOCOCOCO					NHGEKNFHIFYQLLEGGEEETLRRLGLERNPQSYLYLVKGQCAK
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IRLDVDTKLNEQLKTSFFLVREDTKAAVLLHLLHNVVRPQDQTV VFVATKHHAEYLTELLTTQRVSCAHIYSALDPTARKINLAKFTL GKCSTLIVTDLAARGLDIPLLDNVINYSFPAKGKLFLHRVGRVA RAGRSGTAYSLVAPDEIPYLLDLHLFLGRSLTLARPLKEPSGVA GVDGMLGRVPQSVVDEEDSGLQSTLEASLELRGLARVADNAQOQ YVRSRPAPSPESIKRAKEMDLVGLGLHPLFSSRPEEEELQRLRL VDSIKNYRSRATIFEINASSRDLCSQVMRAKRQKDRKAIARFQQ GQQGRQEQQEGPVGPAPSRPALQEKQPEKEEEEPAGESVBDIFS			[į	MCEAROLOELIAN POGNOTAR POST
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GKCSTLIVTDLAARGLDIPLLDNVINYSFPAKGKLFLHRVGRVA RAGRSGTAYSLVAPDEIPYLLDLHLFLGRSLTLARPLKEPSGVA GVDGMLGRVPQSVVDEEDSGLQSTLEASLELRGLARVADNAQQQ YVRSRPAPSPESIKRAKEMDLVGLGLHPLFSSRPEEEELQRLRL VDSIKNYRSRATIFEINASSRDLCSQVMRAKRQKDRKAIARFQQ GQQGRQEQQEGPVGPAPSRPALQEKQPEKEEEERAGESVEDIFS	1		ļ		TREDADI KENEGEKTSEEPVREDTKAAVLLHLLHNVVRPQDQTV
RAGRSGTAYSLVAPDEIPYLLDLHLFLGRSLTLARPLKEPSGVA GVDGMLGRVPQSVVDEEDSGLQSTLEASLELRGLARVADNAQQQ YVRSRPAPSPESIKRAKEMDLVGLGLHPLFSSRPEEEELQRLRL VDSIKNYRSRATIFEINASSRDLCSQVMRAKRQKDRKAIARFQQ GQQGRQEQQEGPVGPAPSRPALQEKQPEKEEEEPAGESVEDIFS	I		1	ļ	VF VATAMHAEYLTELLTTQRVSCAHIYSALDPTARKINLAKFTL
GVDGMLGRVPQSVVDEEDSGLQSTLEASLELRGLARVADNAQQQ YVRSRPAPSPESIKRAKEMDLVGLGLHPLFSSRPEEEELQRLRL VDSIKNYRSRATIFEINASSRDLCSQVMRAKRQKDRKAIARFQQ GQQGRQEQQEGPVGPAPSRPALQEKQPEKEEEERAGESVEDIFS]		i		GRUSTEL VTDLAARGLDI PLLDNVINYSFPAKGKLFLHRVGRVA
YVRSRPAPSPESIKRAKEMDLVGLGLHPLFSSRPEEEELQRLRL VDSIKNYRSRATIFEINASSRDLCSQVMRAKRQKDRKAIARFQQ GQQGRQEQQEGPVGPAPSRPALQEKQPEKEEEERAGESVEDIFS	1	ŀ		1	KAGKSGTAYSLVAPDEIPYLLDLHLFLGRSLTLARPLKEPSGVA
VDSIKNYRSRATIFEINASSRDLCSQVMRAKRQKDRKAIARFQQ GQQGRQEQQEGPVGPAPSRPALQEKQPEKEEEERAGESVEDIFS	1				GVLGHLGRVFQSVVDEEDSGLQSTLEASLELRGLARVADNAQQQ
GQQGRQEQQEGPVGPAPSRPALQEKQPEKEEEERAGESVEDIFS	1	- 1			IVKSKPAPSPESIKRAKEMDLVGLGLHPLFSSRPEEEELQRLRL
GQQGRQEQQEGPVGPAPSRPALQEKQPEKEEEERAGESVEDIFS EVVGRKRORSGPNRGAKRRPEEARORDOEFVIDVPRKOFFSPRG		[VDS1KNYKSRATIFEINASSRDLCSQVMRAKRQKDRKAIARFQQ
L EVVGRKRORSGPNRGAKRRRERARORDORFVTDVDDKDFDCPDC	l		1		GUIGHQEQUEGPVGPAPSRPALQEKQPEKEEEERAGESVEDIFS
The state of the s	L		L		EVVGRKRQRSGPNRGAKRRREEARQRDQEFYIPYRPKDFDSERG

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
No:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
İ	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
1	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
ľ	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
	 		LCICCOCA EPOCA CANE DAMAGE TO A
			LSISGEGGAFEQQAAGAVLDLMGDEAQNLTRGRQQLKWDRKKKR
J]		FVGOSGQEDKKKIKTESGRYISSSYKRDLYQKWKQKQKID*S*L
			GRRRGILTRRRPRTEEVGEARPLAQAGCIPGPHAPRHPLQAESA LELKTKQQILKQRRRAQKAALSLQRWWPQAALCPQ
6714	169	1416	NNCOFT L DDDDADNAU L DGGGGD DA GWWPQAALCPQ
		1410	NNCQELLPPPPAPMAHIPSGGAPAAGAAPMGPQYCVCKVELSVS
1			GONLLDRDVTSKSDPFCVLFTENNGRWIEYDRTETAINNLNPAF
1	,		SKKFVLDYHFEEVQKLKFALFDQDKSSMRLDEHDFLGQFSCSLG
1			TIVSSKKITRPLLLLNDKPAGKGLITIAAQELSDNRVITLSLAG
1			RRLDKKOLFGKSDPFLEFYKPGDDGKWMLVHRTEVIKYTLDPVW
i			KPFTVPLVSLCDGDMEKPIQVMCYDYDNDGGHDFIGEFQTSVSQ
			MCEARDSVPLEFECINPKKQRKKKNYKNSGIIILRSCKINRDYS
1			PLDYILGGCQLMFTVGIDFTASNGNPLDPSSLHYINPMGTNEYL
1			SAIWAVGQIIQDYDSDKMFPALGFGAQLPPDWKVSHEFAINFNP TNPFCSGVDGIAQAYSACLP
6715	32	493	GPAGAESCEI UCI DAMUONI AGANICALIO
ł			GPAGAESGSLHCLPATVQALAGAAHSPHGGQPPRRGPLIGSGMP
	•		GKPKHLGVPNGRMVLAVSDGELSSTTGPQGQGEGRGSSLSIHSL PSGPSSPFPTEEQPVASWALSFERLLQDPLGLAYFTEFLKKEFS
			AENVTFWKACERFQQIPASDT
6716	1	176	
1		4.0	GAGGPAPRSFGSEEPRAALERDKMSARAAAKSTAMEETAIWEQ HTVTLHRVSLCCSK
6717	115	896	
1		***	LFAMSGFENLNTDFYQTSYSIDDQSQQSYDYGGSGGPYSKQYAG
1 1	į		YDYSQQGRFVPPDMMQPQQPYTGQIYQPTQAYTPASPQPFYGNN
	j j		FEDEPPLLEELGINFDHIWQKTLTVLHPLKVADGSIMNETDLAG PMVFCLAFGATLLLAGKIQFGYVYGISAIGCLGMFCLLNLMSMT
			GVSFGCVASVLGYCLLPMILLSSPAVIFSLQGMVGIILTAGIIG
			WCSFSASKIFISALAMEGQQLLVAYPCALLYGVFALISVF
6718	290	599	KQSSTVPGTILPSLKWHNSGLCKFPETGGKMTTFKEGLTFKDVA
i i			VIFTEEELGLLDPVQRNLYQDVMLENFRNLLSVGHHPFKHDVFL
1 1			LEKEKKLDIMKTATQ
6719	1	691	PTRPEEQDREDGKCHKMEMNPISGNLNCDPIAMSQCSSDHGCET
1 1	j j		DLDSDDDKIEKPNNFMKDSASQDNGLSRKISRKRVCSSDSDSSL
1 1			QVVKKSSKARTGLLRITRRCAATAANKIKLMSDVEDVSLENVHT
1 1			RSKNGRKKPLHLACTTAKKKLSDCEGSVHCEVPSEQYACEGKPP
1 1			DPDSEGSTKVLSQALNGDSDSEDMLNSEHKHRHTNIHKIDAPSK
			RKSSSVTSSG
6720	3	822	HEVAEEAGGTVYPQRGTMPGTKRFQHVIETPEPGKNELTGYEAA
, !		**	VPITEKSNPLTQDLDKADAENIVRLLGQCDAEIFQEEGQALSTY
j	1		QRLYSESILTIMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAF
1			LMSVSFNQLMKGLGQKPLYTYLIAGGDRSVVASREGTEDSALHG
	İ		IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP
1 [VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM
L l	ļ		SVVTLISE
6721	3	822	HEVAEEAGGTVYPQRGTMPGTKRFQHVIETPEPGKWELTGYEAA
[[İ	Í	VPITEKSNPLTQDLDKADAENIVRLLGQCDAEIFQEEGQALSTY
1 1			QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAF
[]			LMSVSFNQLMKGLGQKPLYTYLIAGGDRSVVASREGTEDSALHG
			IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP
1	j	j	VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM
			SVVTLISE
6722	1	390	RSWSKRTWQALPMAVLPLLLFLCGTPQAADNMQAIYVALGEAVE
	1	}	LPCPSPSTLHGDEHLSWFCSPAAGSFTTLVAQVQVGRPAPDPGK
		j	PGRESRLRLLGNYSLWLEGSKEEDAGRYWCAVLGQHHNYQNW
6723	173	659	VCQYCTARMADFGISAGQFVAVVWDKSSPVEALKGLVDKLQALT
1			GNEGRVSVENIKQLLQSAHKESSFDIILSGLVPGSTTLHSAEIL
	[ļ	AEIARILRPGGCLFLKEPVETAVDNNSKVKTASKLCSALTLSGL
			

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
i	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ì	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
Į	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ı	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion
ļ	sequence		\=possible nucleotide insertion}
			VEVKELQREPLTPBEVOSVREHLGHESDNL
6724	173	659	VCQYCTARMADFGISAGOFVAVVWDKSSPVRALKGLVDVLOALT
1	İ		GNEGRVSVENIKOLLOSAHKESSFDITI.SCI.VPGSTTI HEARTI
1	l		AEIARILRPGGCLFLKEPVETAVDNNSKVKTASKLCSALTLSGL
6725	356		VEVKELQREPLTPEEVOSVREHLGHESDNI.
0,23	356	722	RRRTPPVILATMDDDLMLALRLQEEWNLQEAERDHAQESLSLVD
ł			ASWELVDPTPDLQALFVOFNDOFFWGOLRAVRVKWSVDMTLCAG
6726	98	No.	ICSYEGKGGMCSIRLSEPLLKLRPRKDLVEVFFV
0720	, ,,	714	HLQKMERKINRREKEKEYEGKHNSLEDTDQGKNCKSTLMTLNVG
1 .		•	GYLYITQKQTLTKYPDTFLEGIVNGKILCPFDADGHYFIDRDGL
			LFRHVLNPLRNGELLLPEGFRENQLLAQEAEFFQLKGLAEEVKS
1			RWEKEQLTPRETTFLEITDNHDRSQGLRIFCNAPDFISKIKSRI
6727	1 .	831	VLVSKSRLDGFPEEFSISSNIIQFKYPIK
1	_ '	031	FRGMGDERPHYYGKHGTPQKYDPTFKGPIYNRGCTDYICCVFLL
1 1			LAIVGYVAVGIIAWTHGDPRKVIYPTDSRGEFCGQKGTKNENKP YLFYFNIVKCASPLVLLEFQCPTPQICVEKCPDRYLTYLNARSS
1			RDFEYYKQFCVPGFKNNKGVAEVLRDGDCPAVLIPSKPLARRCF
1 1			PAIHAYKGVLMVGNETTYEDGHGSRKNITDLVEGAKKANGVLEA
!	-		RQLAMRIFEDYTVSWYWDIISLGIAMAMSLLFIILLRFLAGIMG
			RGMIMGILVLGY
6728	486	935	FCSSWLRSLADSSLSWKMFLVGLTGGIASGKSSVIQVFQQLGCA
	į		VIDVDVMARHVVQPGYPAHRRIVEVFGTEVIJENGDIND KULGD
1 1	į.		LIFNOPDRROLLNAITHPEIRKEMMKETFKYFLREPRTSPROKK
6729			HVPSALKEADSLMRRDT
8/29	259	1191	VGLTGAQSGRTASMGRDQRAVAGPALRRWLLLGTVTVGFLAQSV
]			LAGVKKFDVPCGGRDCSGGCOCYPKKGGRGOPGPVGDOGVNGDB
i i	į		GLQGFPGLQGRKGDKGERGAPGVTGPKGDVGARGVSGFPCADGT
	ĺ		PGHPGQGGPRGRPGYDGCNGTOGDSGPOGPPGSEGFTGPDGDOG
[]	ļ		PKGQKGEPYALPKEERDRYRGEPGEPGLVGFQGPPGRPGHVGQM
1	ļ		GPVGAPGRPGPPGPPGPKGQQGNRGLGFYGVKGEKGDVGQPGPN
			GIPSDTLHPIIAPTGVTFHPDQYKGEKGSEGEPGIRGISLKGEE
6730	784	1015	
ļ Ē		1,013	NMVDYYEVLGLORYASPEDIKKAYHKVALKWHPDKNPENKEEAE RKFKEVAEAYBVLSNDEKRDIYDKYGTEGLNEF
6731	1	446	GIRKRLHGAVVPRVEVGCPWETRESEGVHLERPTSPLKNNDEGS
	1		LDIYAGLDSAVSDSASKSCVPSRNCLDLYEEILTEEGTAKEATY
1			NDLQVEYGKCQLQMKELMKKFKEIQTQNFSLINENQSLKKNISA
			LIKTARVEINRKDEEI
6732	102	1205	GRWQRRPPPPSPPLWCLQPGGGSDPQQLTQLRHCLSHSPQDTPW
	İ	ľ	AQRQVCYTAATTQAAAPATRNCLPDHSGHRPTPPRSHRHHRQEN
	ĺ		LGSIKPSSRSTKATSTTMAGDGRRAEAVREGWGVVVTDDADTDE
			GRGRLAPQNGGSSDAPAYRTPPSRQGRREVRFSDEPPEVYGDFE
-			PLVAKERSPYCKRTRLEEFRSDSAKEEVRESAYYIRSDODDODD
ļ		}	PORTEEMKTRRTTRLOOOHSEOPPLOPSPVMTRRGLEDSHEEP
1		ĺ	DEASSQTDLSQTISKKTVRSIOEAPAVSEDLVIRI,RRDDT.DVDD
i		i	YEATSVQQKVNFSEEGETEEDDQDSSHSSVTTVKARSRDSDESG
6733	613		DKTTRSSSQYIESFW
J , J J	012	1311	RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK
	j		KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDI.T
		ļ	QLLSIMEGELQAREDVIHMLKTEKTKPEVLEAHYGSAEPEKVID
		Į.	VLHRDAILAQEKSIGEDVYEKPISELDRLEEKOKETYRRMI.EQI.
- 1	1	1	LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEOERERLKK
6734	189		LLEQEKAYQARKE
1	-	331	SAAMFPVFSGCFQELQEKNKSLELVSFEEVAVHFTWEEWQDLDD
			AQRTLYRDVMLETYSSLVSLGHCITKPEMIFKLEQGAEPWIVEE

Deginning nucleotide location corresponding corresponding cofirst amino acid residue of amino acid sequence se	SEQ	Predicted	Predicted end	Amino acid cocreeb
No: nucleotide location corresponding to first cofirst amino acid residue of residue of amino acid sequence se	ID	beginning		Amino acid segment containing signal peptide
Cocation Corresponding Coffice Contemponding Coffice C	NO:	nucleotide	t	Glutamic Acid F-Ob
corresponding to first amino acid residue of amino acid residue of amino acid residue of amino acid sequence amino acid sequence amino acid sequence (Approline, Geolulamine, Rahysinine, Servine, Tethreonine, Weylaine, Weinkund, *Stop Codon, /-possible nucleotide intelled deletion (Approximate amino acid sequence) (Approximate acid sequence) (Approximate acid sequence) (Approximate acid sequence) (Approximate acid sequence) (Approximate acid sequence) (Approximate acid sequence) (Approximate acid sequence) (Approximate acid sequence) (Approximat	1	location	1	Halistidine Talkolousine W tarrier
amino acid residue of amino acid residue of amino acid sequence sequence sequence 6735 280 558 Karrine, Taffirencine, Vavlaine, Wattyptophan, Yatyxosine, Xauknown, *stop TMANEAGSKNOYSICHRISUSCOWNIV TMANEAGSKNOYSICHRISUSCOWNIV SARRAGVINISSPELKOVENOSTERPERKEREPOTOREELINEA 6736 195 808 MYNELSGSKNOYDOPPEGDINDMVANYVDFFREVENTEPOTOREELINEA KSRRAGVINISSPELKOVENOSTERPERKEREPOTOREELINEA KSRRAGVINISSPELKOVENOSTERPERKEREPOTOREELINEA KSRRAGVINISSPELKOVENOSTERPERKEREPOTOREELINEA KSRRAGVINISSPELKOVENOSTERPERKEREPOTOREELINEA KSRRAGVINISSPELKOVENOSTERPERKEREPOTOREELINEA KSRRAGVINISSPELKOVENOSTERPERKEREPOTOREELINEA KSRRAGVINISSPELKOVENOSTERPERKEREPOTOREELINEA KSRRAGVINISSPELKOVENOSTERPERKEREPOTOREELINEA KSRRAGVINISSPELKOVENOSTERPERKEREPOTOREELINEA KSRRAGVINISSPELKOVENOSTERVENOSTERVENOSTERVINISTET KOGET MYNELSPERSERPENDERALDERPERKEREPOTOREELINEA KRAKELEESESTIVENDENOSTERVENOSTERVINISSELPATH REKRESLEINHENBERGVENOSTERVINISSELPATH REKRESLEINHENBELTERPENBERGENATIONET REKRESLEINHENBERGVENOSTERVINISSELPATH REKRESLEINHENBELTERPENBERGENATIONET REKRESLEINHENBERGVENOSTERVINISSELPATH REKRESLEINHENBERGVENOSTERVINISSELPATH REKRESLEINHE				LeLeucine Menethionine Negative
residue of amino acid sequence		to first	1	P=Proline O-Glutamine P-Amei-in-
amino acid sequence codon, /-possible nucleotide deletion, /-possible nucleotide deletion, /-possible nucleotide deletion, /-possible nucleotide deletion, /-possible nucleotide insertion) FININLISCOSKRYON/SOICHRESUNG/SUNGKY 6735 280 558 SERRAGY/FONNPELKGY/FONNKOKYFEPEKKY/FONNFELKGY/FONNFELKGY/FONNKOKYFEPEKKY/FONNFELKGY/FONNKOKYFEPEKKY/FONNFELKGY/FONNKOKYFEPEKKY/FONNFELKGY/FONNKOKYFEPEKKY/FONNFELKGY/FONNKOKYFEPEKKY/FONNFELKGY/FONNKOKYFEPEKKY/FONNKOKYFEPEK	- 1	amino acid	residue of	S=Serine, TeThreonine, Wayaline,
sequence sequence sequence sequence TIMIRISGSKRQVFSGICHRSLVSLOSVHIV TIMIRISGSKRQVFSGICHRSLVSLOSVHIV SSS SERRAVTYMSNIPPIKGVFNKNETHPEKKFEGTQRFELHKRA QASLMAGIDRLAVQLPPGGILNDWVAVKVVDFFRRVHLIYGTI NGGCT SSSPYLIRRIESERIKTAGSGVBARVVVCYRRRIDISTILIMLAD KHARLIEBESSTTVEADLIDKOKHQLARRELPLSRQVBSLAATH IRGKCSVALLMSTERVLSVLDKDENDVFYSLVTDPSLKTLLADKA KHARLIEBESSTTVEADLIDKOKHQLARRELPLSRQVBSLAATH IRGKCSVALLMSTERVLSVLDKDENDVFYSLVTDPSLKTLLADKA KHARLIEBESSTTVEADLIDKOKHQLARRELPLSRQVBSLAATH IRGKCSVALLMSTERVLSVLDKDENDVFYSLVTDPSLKTLLADKA KHARLIEBESSTTVEADLIDKOKHQLARRELPLSRQVBSLAATH IRGKCSVALLMSTERVLSVLDKDENDFYSLVTDPSLKTLLADKA KHARLIEBESSTTVEADLIDKOKHQLARRELPLSRQVBSLAATH IRGKCSVALLMSTERVLSVLDKDENDFYSLVTDSSLKTLLADKA KHARLIEBESSTTVEADLIDKOKHQLARRELPLSRQTDV BERKRSLDINEBPSCVALDSTOKTOKA REPTOKOLQHISDRBNIDDLAMEFPRSDERVRSTIFLSKGTDV BERKRSLDINEBPSGILAKVISSSSKALTRIDSTVSLCH REPTOKOLQHISDRBNIDDLAMEFPRSDERVRSTIFLSKGTDV BERKRSLDINEBPSGILAKVISSSSTIFLDDSTVSQPNLKTIK CVALAITYHKRUPPGGILAKVISSSTYBLDDSTVSQPNLKTIK ROPERRYCQPSTRAVITSRAMDHEDOKNIDETPSKENTPSKSTIFLSKGTDV BERKRSLDINEBPSGILAKVISSTVBOHARVIDVCQILATITABSPALIS CACAGOPARREVGARATALPVRASSGSMAPSGILAVPLAVLVLLL ROPERRYCQPSTRAVITDRINEBLEDGDOMISPTAPRSPALIS GARBERVARLEKHLIMLLEGGSVYKLJKKLAFTEKKCALLANG ANKESSESSISTERLIATVADLYSGSVYBLIKKVGDRHISAHKP VLAARSDSWSLANLSSTKELDLSDANPEVTMIRMRITYDDELEF REDDVFLITEMALANSPOLOLLBROKKVGLKKLAFTEKKCALLANG ANKESSESSISTERLIATVADLYSGSVYBLIKKVGDRHISAHKP VLAARSDSWSLANLSSTKELDLSDANPEVTMIRMRITYDDELEF REDDVFLITEMALANSPOLOLLBROKKVGLKKLAFTEKKCALLANG ANKESSESSISTERLATVADLYSGCVYBLIKKVGDRHISAHKP VLAARSDSWSLANLSSTKELDLSDANPEVTMIRMRITYDDELEF REDDVFLITEMALANSPOLOLLBROKKVGLKKLAFTEKKCALLANG ANKESSESSISTERLATVADLYSGCVYBLIKKVGDRHISAHKP VLAARSDSWSLANLSSTKELDLSDANPEVTMIRMRITYDDELEF REDDVFLITEMALANSPOLOLLBROKKVALKKOLOVERNITYDELEF REDDVFLITEMALANSPOLOLLBROKKVALKKOLOVERNITYDELEF REDDVFLITEMALANSPOLOLLBROKKVALKKOLOVERNITYDELEF REDDVFLITEMALANSPOLOLLBROKKINGVARNITYDESCUL VLANSNSPHELISTROMANSTREDDCTARMITYDESCUL LOCHTANGVARNITYDESCUL BROKKVALKSCORPERP VLEHERARSTANDSCORPARTITYDE SILANDAV VLANSNSPHELISTROMAN STORE	j	residue of		WeTryptophan Vermoning Vermoning
A-possible nucleotide insertion	İ	amino acid	sequence	Codon. /=possible nucleotide deleter
6735 2880 558 KSRRADVTKSINSTPLKOVTNOKUTSPEKKFEGTÖRFELKKRA OASLINAGIDURLAVOLPPGGDINDWAWKVVDFFRRVALTYGTI NGGCT 6736 195 808 MYSELMFKEDFYNIKGUTNOKUTSPEKKFEGTÖRFELKKRA OASLINAGIDURLAVOLPPGGDINDWAWKVVDFFRRVALTYGTI NGGCT SSSMYLIKRIELERIKTAGSOWEAKVVOCTRARDISTILIMLAD KHAKELERESETTVEADLIDKOKHOLKERELPLSKOYESLATI IRGKCSVALLINSTERVLSVLDEDEDTYPSLVTDPSLKTLLADKO KHAKELERESETTVEADLIDKOKHOLKERELPLSKOYESLATI IRGKCSVALLINSTERVLSVLDEDEDTYPSLVTDPSLKTLLADKO BIRWGDRYOADIPBERLDETTYPSLVTDPSLKTLLADKO BIRWGDRYOADIPBERLDETTYPSLVTDPSLKTLLADKO BIRWGDRYOADIPBERLDETTYPSLVTDPSLKTLLADKO BIRWGDRYOADIPBERLDETTYPSLVTDPSLKTLLADKO BIRWGDRYOADIPBERLDETTYPSLVTDPSLKTLLADKO BIRWGDRYOADIPBERLDETTYPSLVTDPSLKTLLADKO RECKALATYHIKRDPBORNLLDITPONHPLELSESTPJTOK BIRWGDRYOADIPBERLDETTYPSLVTDBSLKTLLADKOTTOR BERKSLDTHUBPROQIAKKTSCSTIFLDDSTVSORNKTIK CVALATYHIKRDPBORNALDIPBERDETTYSLTDSKTOTO BERKSLDTHUBPROQIAKKTSCSTIFLDDSTVSORNKTIK CVALATYHIKRDSVAKYTPDISLABELDGOMNEPTYPDKIN PERGATIFFORTISAGKTORD GOVERNATION BERKSLDTHUBPROQIALERUM DOSTAGERANDO TERMINATION BERKSLDGARTALDVERNADO TERMINATION TERMINATION BERKSLDGARTALDVERNADO TERMINATION TERMINATION BERKSLDGARTALDVERNAD SANDAN TERMINATION TERMINATION BERKSLDGARTALDVERNATION TERMINATION TERMINATION TERMINATION BERKSLDGARTALDVERNATION TERMINATION		sequence	_	\=possible nucleotide insertion)
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GASIMAGLDIRLAVGLPPGEDLINDWAVAWUVDFPRRVNLTYGTI XDGCT XD	6735	280	558	KSRRAGVTKMSNPRLKOVENKDYTEDDVDVZEDOTODDRAWY
6736 195 808 MYSCLEPKEEPRIKSIGLININFILKKISSVLPLITDYVYFEN SSSNPYLIRRIEELKKTASGNVEAVVUYPRRRDISMTLIHAD KHAKEIEESSTYVARDLINKOKHOLKHRELPISRGYYSSLEATH IRGKCSVALLMETESVLSYLDKEDTPFYSLVYDSEKTELATH IRGKCSVALLMETESVLSYLDKEDTPFYSLVYDSEKTELATH IRGKCSVALLMETESVLSYLDKEDTPFYCYPAVL 6737 150 1209 PVIMPLHFSPDIVERSCOVSSFYLERRAMSRIESYRPDITDLS REDTGCNIQHISDRENIDDLINMEPRISDEPRASTIFLERSGTOV REKRASLFIHMEPGQIARKYSGSTIFLDBOTYSGPNIKTIK CVALATYHIKNRDPDGMALDIFDERLHBLSKSEVPPDYDKIN PEQKQIYRFYGHTSFAGQUIARCATVITVYLERLITYARIDIC ANMERVUGAILLASKWADQAVANVUYQILKDITVERHITARIDIC ANMERVUGAILLASKWADQAVANVUYQILKDITVERHITARIDIC ANMERVUGAILLASKWADQAVANVUYQILKDITVERHILSPEDPLSRE RAHKLEAISELCEDKYVDLRRSAKRSASADNLTLERWSPAIIS CACAEOPARBEVARATALPVRRASGEMAPSGSLAVPLAVVILLIM MGAPWHGRRSNVRVITDERWEELLEDDMHIEPYARWCPACQAIL WGAPWHGRRSNVRVITDERWEELLEDDMHIEPYARWCPACQAIL WGAPWHGRRSNVRVITDERWEELLEDDMHIEPYARWCPACQAIL WGAPWHGRRSNVRVITDERWEELLEDDMHIEPYARWCPACQAIL WGAPWHGRRSNVRVITDERWEELLEDDMHIEPYARWCPACQAIL WGAPWHGRRSNVRVITDERWEELLEDDMHIEPYARWCPACQAIL WGAPWHGRRSNVRVITDERWEELLEDDMHIEPYARWCPACQAIL WGAPWHGRRSNVRVITDERWEELLEDDMHIEPYARWCPACQAIL WGAPWHGRRSNVRVITDERWEELLEDDMHIEPYARWCPACQAIL WGAPWHAGRISNVRVITDERWEELLEDDMHIEPYARWCPACQAIL WGAPWHGRRSNVRVITDERWEELLEDDMHIEPYARWCPACQAIL WGAPWHAGRISNVRVITDERGEVKKOPKLARTERWCALLAAQ ANKESSSES ISRLAIVADLYEOQOYSDLIKKVGURHISAHKY VLAARSDSWSLANLSSTKELDLSDANPEVITMIRRITTDELEF REDDVFLITEMKLANRFQQLILERRECKWOWSLAVINVRNCTRFYQ TABELMASTLMNYCAEITASHWVSEVEGOVYSDLIKKVGURHISAHKY VLAARSDSWSLANLSSTKELDLSDANPEVITMIRRITTDELEF REDDVFLITEMKLANRFQQLILERRECKWOWSLAVINVRNCTRFYQ TABELMASTLMNYCAEITASHWVSEVEGOVYSDLIKKVGURHISAHKY VLAARSDSWSLANLSSTKELDLSDANPEVITMIRRITTDELEF REDDVFLITEMKLANRFQQLILERRECKWOWSLAVINVRNCTRFYQ TABELMASTLMNYCAEITASHWVSEVEGOVYSDLIKKVGURHISAHKY VLAARSDSWSLANLSSTKELDLSDANPEVITMIRRITTDELEF REDDVFLITEMKARTHOYABELLANGAWARTHARNYTORDELTARAY VLAARSDSWSLANLSSTRELDDPASMAANTATLARYTORDETTARAY VLAARSDSWSLANLSSTRELDPASTYNAANTATLARYTORDETTARAY VLAARSDSWSLANLSSTRELDPASTYNAANTATLARYTORDETTARAY VLAARSDSWSLANLSSTRELDPASTYNAANTATLARYTORDETTARAY VLAARSDSWSLANLSSTRELDPAST	İ			OASLNAGLDLRLAVOLPPGEDLNDWYAVKKOPERIPRI TYOTT
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RHAKEIBESSTYVRADLIDNOKHOLOKRIELPISROYSSLATTI IRGGCSVALLBETSVLSVLDKEDTPYSVDOSLATVLADKO BIRVGGRYQADIPEMILEGTPYCVPAVL PYINPLIPSPEDOTYPSSCCVSSSPKLRRAHISRLESYRPDTULS REDTGCNLQHISDRENIDLINEPRESHPRASTIFLEKSGTDV REKKELPINHIPPGGIRKYSSCSTIFLDDSTVSOPNLKYTIK CVALAIYHHINKREPOGRMULDITPENHIPPLSKSEVPPDYDKIN PERGIYHPVRTLFSAQLITAECAIVTLVTLERLLITYAEDICT ANMERIVLGAILAGKVUNDQAWNUNDVOLUKDITVEDNMBLE ROFLELLOPNINVPSSVYAKYYPDLRSLARANLISPEDLINSRE ROFLELLOPNINVPSSVYAKYYPDLRSLARANLISPEDLINSRE ROFLELLOPNINVPSSVYAKYYPDLRSLARANLISPEDLINSRE ROFLELLOPNINVPSSVYAKYYPDLRSLARANLISPEDLINSRE ROFLELLOPNINVPSSVYAKYYPDLRSLARANLISPEDLINSRE ROFLELLOPNINVPSSVYAKYYPDLRSLARANLISPEDLINSRE ROFLELLOPNINVPSSVYAKYYPDLRSLARANLISPEDLISPEDLISRE ROFLELLOPNINVPSSVYAKYYPDLRSLARANLISPEDLISPEDLISRE ROFLERSTCOPKYKOLOKRIARSANLISPEDLISPEDLISRE ROFLERSTCOPKYKOLOKRIARSTKELLEGOWNIEPYAPWCPACORI UGAPRHTHGRRSNVRVITDEWRRALLEGOWNIEPYAPWCPACORI VLARSDSSENISPENLEHLENGSYVALCKKLASTERCCALLANO ANKESSSESFISRLLAIVADLYSEGYSDLKIKVOERRISAHRF VLAARSDSWALANLESTKELLDSDAVVENTURRITYTDELEF REDDYFLIELMKLANRPOLOLLERECEGOWNELVANRNCIRPYQ TABELMASTLANVYCAEIIASHWSBYEGOWNIENSHARHT VLAARSDSWALANLESTKELDSDANNETYMTMLRRITYTDELEF REDDYFLIELMKLANRPOLOLLERECEGOWNIENSHKRITTELEF REDDYFLIELMKLANRPOLOLLERECEGOWNIENSHKRITTELEF REDDYFLIELMKLANRPOLOLLERECEGOWNIENSHKRITTELEF REDDYFLIELMKLANRPOLOLLERECEGOWNIENSHKRITTELEF REDDYFLIELMKLANRPOLOLLERECEGOWNIENSHKRITTELEF REDDYFLIELMKLANRPOLOLLERECEGOWNIENSHKRITTELEF REDDYFLIELMKLANRPOLOLLERECEGOWNIENSHKRITTELEF REDDYFLIELMKLANRPOLOLLERECEGOWNIENSHTSHTOTTELEF REDDYFLIELMKLANRPOLOLLEREDSPONITATAGDENISHAH VLARASBUSHANLSTKELDSDANNTSPOTYGEDOCTARI WOLKSRNLOCORIPONAPHITSTOTYMOLRENISHTENTYFORM PAEGLERTVOLOPSOVALABUVEYPORSMILAANAVORTUPPSCLL PALGILIGEGEFELARRGLIFLAGOOCVVNNLTGGIGDEVTO DIKTOHNEGLIPEPSVITTSHIDPDASTMANVSTLVPFSCLL PALGILIGEGEFELARRGLIFLAGOOCVVNNLTGGIGDEVTO DIKTOHNEGLIPEPSVITTSHIDPDASTMANVSTLVPFSCLL PALGILIGEGEFELARRGLIFLAGOOCVVNNLTGGIGDEVTO DIKTOHNEGLIPEPSVITTSHIDPDASTMANVSTLVPFSCLL PALGICTRTVOHODSOVALABUVEYPORSMILAANAVORTUPPENDL 6744 95 1343 RTPARRECGOEVERSPRONDSCHER	1		[SSSNPYLIRRIERINKTASCNVEAKUCEVERRETENTENTENT
1109 1209 PVINPLHYSPOTYURSCKYTSLYNDSKIETKILADKO 1209 PVINPLHYSPOTYURSCKYSSSPKLRRNAISRLESYRDDTUS. ERKKSLPINNIHPPGOLIRKYSSCSTIPLOSTVSOPPLKYTIK CVALATYTH INRDPDGOLIRKYSSCSTIPLODSTVSOPPLKYTIK ROPIELLOPHIN NYSSVYTAKYYTYDLESLARINLISPPLEPISRE RAHKLEAISRICCBUYKOLIRRSARKSASADNITIPRNSPAIIS CACAEOPARAEVGAATALPAVANSGEMAPSIATURDNIEL GARWHORRSNIVAVITOENRRELLEGOMMIEPYARMOCHACOMI QPENBSFARMEGELEVINIARVOUTEOPLGASADYLTVALIA GARWHORRSNIVAVITOENRRELLEGOMMIEPYARMOCHACOMI QPENBSFARMEGELEVINIARVOUTEOPLGASADYLTVALIA KOGEFRIVOGPRIKKOPTINISDKERKSIEPVSSWE REDDVILLEUKALANINISTELDISDANDEVITMILKRIVITDELEF REDDVILLEUKALANINISTELDISDANDEVITMILKRIVITDELEF REDDVILLEUKALANINISTERIOLISPANIVAVINICIRFYQ TABELNASTIMNYCAEIIASHWSSVEGVINIAU ANNESSSESTISRILLATVADLYEGGYSDLKIKVGORHISAHKF VLAARSDSWSLANLISTRELLDISDANDEVITMILKRIVITDELEF REDDVILLEUKALANINISTERIOLISPANIVAVINICIRFYQ TABELNASTIMNYCAEIIASHWSSVEGVINIAU ANNESSSESTISRILLATVADLYEGGYSDLKIKVGORHISAHKF VLAARSDSWSLANLISTRELLDISDANDEVITMILKRIVITDELEF REDDVILLEUKALANINISPOTYOSDEVITATAGYDHTVRFWOA HSGICTRYCHODSGVARLEVTPORSMIAAAVQFVUSGORIHM VLAARSDSWSLANLISTRELLASHIDPDASTWAAVANISTUOPTSCLL PLAIGILQEGEFSLARGILFILACQONCYVWILTGGIGDEVTQ LIPKKILP BORNEHPINISPOTYONSINAAAVQFVURGURMITTGGEDCTARI WDLRSRNLQCORITOVARPINOVCHIPNOGELIVAGGAHIM WDLRSRNLQCORITOVARPINOVCHIPNOGENITITGGEDCTARI WDLRSRNLQCORITOVARPINOVCHIPNOGENITITGGEDCTARI WDLRSRNLQCORITOVARPINOVCHIPNOGENITITGGEDCTARI WDLRSRNLQCORITOVARPINOVCHIPNOGENITITGGEDCTARI WDLRSRNLQCORITOVARPINOVCHIPNOGENITITGGEDCTARI WDLRSRNLQCORITOVARPINOVCHIPNOGENITITGGEDCTARI WDLRSRNLQCORITOVARPINOVCHIPNOGENITITGGEDCTARI WDLRSRNLQCORITOVARPINOVCHIPNOGENITITGGEDCTARI WDLRSRNLQCORITOVARPINOTOCHIPNOSOMALERD PREGGETKPKYRE	1	ļ		KHAKEIERESETTVRADI.TDKOKHOLKUPRI EL CROVEGI DAMI
6737 150 1209 PVINPLHSFODTURSECUSSBYKERRANSFILESYRPDTDLS REDIGCNLOHISDRENIDLAMPERSONPRASTIPLESCOTOUR REDIGCNLOHISDRENIDLAMPERSONPRASTIPLESCOTOUR REDIGCNLOHISDRENIDLAMPERSONPRASTIPLESCOTOUR REPRISELT INTHPPOGIARKYSSCSTIPLESCOTOUR REPRISELT REPRISELTE ACUTAVITELLIFIC ANNERIVLGAILLASKWOODQAWWANDVOILKOITVEDNURSEE ROPLELLOFININPSSVYAKYYPDLIRSLABANLISPEPLENISE ROPLELLOFININPSSVYAKYYPDLIRSLABANLISPEPLENISE ROPLELLOFININPSSVYAKYYPDLIRSLABANLISPEPLENISE ROPLELLOFININPSSVYAKYYPDLIRSLABANLISPEPLENISE ROPLELLOFININPSSVYAKYYPDLIRSLABANLISPEPLENISE ROPLELLOFININPSSVYAKYYPDLIRSLABANLISPEPLENISE ROPLERSFROMEDLESVILAKVYTELEPSPEPLISE ROPLERSFROMEDLESVILAKVYTELEPSPEPLISE ROPLERSFROMEDLESVILAKVYTELEPSPEPLISE VLAARSDSWALANLISTELDLISANPSVYALOKKLABTERRCALLAAQ ANKESSESFISHLALAVADLYEEQCYSDLKIKVEDRHISAHF VLAARSDSWALANLISSTELDLISANPSVYALOKKLABTERRCALLAAQ ANKESSESFISHLALAVADLYEEQCYSDLKIKVEDRHISAHF VLAARSDSWALANLISSTELDLISANPSVYALOKKLABTERRCALLAAQ ANKESSESFISHLALAVADLYEEQCYSDLKIKVEDRHISAHF VLAARSDSWALANLISSTELDLISANPSVYALOKKLABTERRCALLAAQ ANKESSESFISHLALAVADLYEEQCYSDLKIKVEDRHISAHF VLAARSDSWALANLISSTELDLISANPSVYALOKKLABTERRCALLAAQ ANKESSESFISHLALAVADLYEEQCYSDLKIKVEDRHISAHF VLAARSDSWALANLISSTELDLISANPSVYALOKKLABTERRCALLAAQ ANKESSESFISHLALAVADLYEEQCYSDLKIKVEDRHISAHF VLAARSDSWALANLISSTELDLISDANPSVYALOKKLABTURGTETVQ FREDOVFLITEMKLAARROLQLIERGECKGWISLVAVRICTRYQ VLAARSDSWALANLISSTELDLISDANPSVATIORITISHTISHTYFEEL REDOVFLITEMKLAARROLQLIERGECKGWISLVAVRICTRYQ FREDOVFLITEMKLARROLQLIERGECKGWISLVAVRICTRYQ FREDOVFLITEMKLARROLQLIERGECKGWISLVAVRICTRYQ BERGICTRYCHOODSCVALARVYDESMILAAVQPVIGGVOHTERM VOLKSRINLOCALIFORMYTISHTYPTESCLL PLAIGILQEGEFELARROLIFICACCINCVVINITIGGIGDETTQ LIPKKIP BOOGRAFICHTONICAL PROPERTIONIC				IRGKCSVALLNETESVI.SVI.DKEDTERVSI IVDDGI VALI ADVO
1209 PVINPLHFSPGDIVRESCUSS PKLRRNAHGRLESYRPDTDLS REDRIGGIUGHISDREN DIDLIME PHPSOH PRASTIFLSKOOTDV RERKKSLFINHIPPOQIARKYSSCSTIFLDDSTVSQPRIKYTIK CVALAIYHI KRRPDOGRHLLDI PDENLHIBLSKSEVPDTDKHR PERKQIYREVATLFSAAQLTIRCAIVTUVILERLLITVAE DICP ANMKRIVLGAILLASKWIDDQAVINUVDYQILIDITVEDNINELE RQFIELLIQHNINVPSSVAKYYFDLERSAMINLSPPLEPLSRE RAHKLEAISRICEBKYKDLRRSARKRSASADNLTTPRISPLISE RAHKLEAISRICEBKYKDLRRSARKRSASADNLTTPRISPLISE RAHKLEAISRICEBKYKDLRRSARKRSASADNLTTPRISPLISE RAHKLEAISRICEBKYKDLRRSARKRSASADNLTTPRISPLISE RAHKLEAISRICEBKYKDLRRSARKRSASADNLTTPRISPLISE RAHKLEAISRICEBKYKDLRRSARKRSASADNLTTPRISPLISE RAHKLEAISRICEBKYKDLRRSAGEMAPSGSLAVPLAVIVLIL WGAPWTHGRRSNVRVITDENNRBLLEGDWINIFYAPMCPACONL QPENBSPABWGEDLEVNIAKVDVTEQPGLSGRFITTALPTIYLY KOLGEFREYOGPRTKKDINFISDENBETSVSNP ANKESSSESFISHLAIVADLYEGGYBLIKVUDRHISPHYDY VLAARSDSWSLANLSSTKELDLSDANPEVTMTMLRWIYTDELEF REDDVFLITEMKLANRPQLOLLRRCEKGVMLLVAVNNCIRFYQ TABELNASTLMNYCAEILASHWYSUEVGWKAL 6740 3 631 SWEDWABEEVAKLEKHIMLLRGEVKLOKKLAETEKKCALLAAO ANKESSSESFISHLAIVADLYEGGYBKYNKAL 6741 141 960 PLITIPPSSSFISHALDSTKELDLSDANPEVTMTMLRWIYTDELEF REDDVFLITEMKLANRPGLOLLRRCEKGWMLVAVNNCIRFYQ TABELNASTLMNYCAEILASHWYSUEVGWKAL 6742 141 960 PLITIPPSSRARGHTMNTSPGTVGSDPVILATAGYDHTVFFWOA HSGICTRIVCHODSQVNALEVTDRSMINAAVQPVSLGYCHTRM YDLNSNNENDIISYDGVNKNIASVGFHEDGRMYTTGGEDCTARI WDLRSRILOCQRIFCVNAPINCVCLHPAGILVGDOSGAIHIW DLKTRHUCQRIFCVNAPINCVCLHPAGILVGDOSGAIHIW DLKTRHUCQRIFCVNAPINCVCLHPAGILVGDOSGAIHIW DLKSRILOCQRIFCVNAPINCVCLHPAGILVGDOSGAIHIW DLKSRILOCQRIFCVNAPINCVCLHPAGILVGDOSGAIHIW DLKSRILOCQRIFCVNAPINCVCLHOPALIVGDGGOLHTRM YDLSNNENDIISYDGVNKNIASVGFHEDGRWYTGGEDCTARI WDLSSRILOCQRIFCVNAPINCVCCHTORGIDDEVTQ LIPKKIP PLAGIGLIGEGEFSLARGLIFLACQONCYVNALTGGIDDEVTQ LIPKKIP BULSGRILOCORF FONDAINCVCHTORGIDDEVTQ LIPKKIP DLKGRILOCORF FONDAIN PINCVCCHPROLITOGIDDEVTQ LIPKKIP WHISTODKSLHLEGDPNPSAAPTSTCAFMPKRISISKQLASVK ARKCSDLEKAIATTALIFRNSDBOGKLEKAIAKDLLOTOFN FAGGGETKPCYREILSELDBHTENKLDFEDFMITLLSTIVMSDL LLDNIR 6744 95 1343 PRPARNCAGCENLIGNENGSFALGSGARGGEPAVRALERD RQVVSTVGYMBEVGDOHRABLKELFPSFDTTGTGSLGGEELF DLCMISLEEVARPOPCCSL				BIRVGPRYOADIPEMILEGTERCVEAUT.
REDTGCNLQHISDRENIDDLANE PRESCHPRASTIPLEKSCTOV REKRKSLETHNIHPSCQ LARKYSISCTI LIDBTVSOPRIKYTIK CVALAIYYHIKNRDPOGNMLLDI PDENLHPLSKSEVPPDUDKIN PEQKQIYRFVRTLFSAQLIAECAIVTLVYLEKLITVAELDICP ANNKRIVUGAILLASKVMDDQAVMNUVYQILKDITVEDNINELE RQFLELLQPHINVPSSVYAKYYFDLRSLARBANLSPPLEPLSRE RAHKLEAISRICCENKYRDLRSRAKRSADAULTDPRNSPARIS CACAEQBARAEVGATALDVRRASGEMAPSGSLAVPLAVLVLLL WGABWHGRISNVRVITDENNRELLEGDMHIFT/AMCPACQNI QPENESFAEMGEDLEVNIAKVDVTEQFGJSGRFIITALPTIYCC KDGEFRRYQGPRTKKDFINFISDKEMKSIEPVSSMP 6739 3 631 SWPDMAEEVAKLEKHIMLRGEVYKLKAEFTEKRCALLAAQ ANKESSESFISRLLAIVADLYEGEQVSDLXIKVGDRHISAHKP VLAARSDSWSLANLSSTKELDLSDANPEVTMTMLRWIYTDBLEF REDDVFLTELMKLANRFQLQLLERECEKGVMSLVNVNNCIRFYQ TABELINASTLMNYCASILASHWYSEVEGVNKAL SWPDMAEEVAKLEKHIMLRGEVYKLKAEFTEKRCALLAAQ ANKESSESFISRLLAIVADLYEGEQVSDLXIKVGDRHISAHKP VLAARSDSWSLANLSSTKELDLSDANPEVTMTMLRWIYTDBLEF REDDVFLTELMKLANRFQLQLLERECEKGVMSLVNVNNCIRFYQ TABELNASTLMNYCASILASHWYSEVEGVNKAL VLAARSDSWSLANLSSTKELDLSDANPEVTMTMLRWIYTDBLEF REDDVFLTELMKLANRFQLQLLRECEKGVMSLVNVNNCIRFYQ TABELNASTLMNYCASILASHWYSEVEGVNKAL VLAARSDSWSLANLSSTKELDLSDANPEVLATTAGYDHTVRFWQA HSGICTRTVQHQDSQVNALEVTPDRSMIAAAQVPSLGYQHIRM VDLNSINNPNITISYDGVNKATLASVGPHEDGRMYTGGEDCTARI WDLKSRNLQCQRIFQVNAPINCVCLHPNQAELIVGQOSGAHHW DLKTHNPNDNPITISYDGVNKATLASVGPHEDGRMYTGGEDCTARI WDLKSRNLQCQRIFQVNAPINCVCLHPNQAELIVGQOSGAHHW DLKTHNPGLIPEPEVSITSAHIDPDASYMAAVNSTLVPFSCLL LIPKKIP DLKTRILQCGFFSLARRGLLFLACQGNCYVMLTGGIODEVTQ LIPKKIP DLKTRILQCGFFSLARRGLLFLACQGNCYVMLTGGIODEVTQ LIPKKIP DLKTRINGCFFSLARRGLLFLACQGNCYVMLTGGIODEVTQ LIPKKIP DLKTRINGCFFSLARRGLLFLACQGNCYVMLTGGIODEVTQ LIPKKIP ARSTODESCHLEGDPNPSAAPTSTCAPRKMPKRISISKQLASVK ALRKCSDLEKATATTALIPRNSSDSDGKLEKATAKDLLQTOFRN PAEGGETKRYRELISELDEHTENKLDFEDFMITLLISTTVMSDL LONIR: CRASSTORM PARAGRETURG FFOR FFOR FFOR FFOR FAEGGETKRYRELISELDEHTENKLDFEDFWDFTGSLGGGELT DLCHMSLEEVAPVLQGTLLQDNLLGRWPDCKEALLLLISRT LSNEBHCGPPOCSLEAPGRYCHEDGSSPHKTGSLGGGETGSLGGEDETT DLCHMSLEEVAPVLQGTLLQDNLLGRWPDCKEALLLLISRT LSNEBHCGPPOCSLEAPGRYCHEGGESHKMTGSLGGGETGSLGGEDFWP	6737	150	1209	PVIMPLHESPGDIVEPSCCVSSSPKI, PPNAUGPI, PCVB PDTPPT C
REKRKSLFINHIPGGJARKYSIGSTIFLDBSTYGOPRLKYTIK CVALAITYHIKNRIPGGORMLLDIFDENIBLEKSERUPPDUKKIN PEOKOTYRFVRTLESAAQLTABCATVTLYVLERLLTYAEIDICP ANNKETULGAILLASKVMDDQAVWNDYYGJIDTYEDNIBLE ROFLELLGFNINVPSSVYAKYYFDLRSLARANNLSFPLEPLSRE RAHKLBAISRICEBKYKDLRSRAKRSASADNLTLPRNSPAIIS CACAEQPARBVGARATLDVRMSGESHAVJENJULDTKDENNBLE RAHKLBAISRICEBKYKDLRSRAKRSASADNLTLPRNSPAIIS CACAEQPARBVGARATLDVRMSGESHAGSGIAVTLAVULDL WGAPWTHGRSRINVRVITDENNRELLEGDWINIFYRPWCPACONL (DEBUSFARWGDLEVINIAKDVYTEGDSGRFIITALPTIYHC KDGEFRRYGGPRTKKOFINFISDKEMKSIEPVSSWF ANNESSESFISRLAINADLYSEGVSKYLKVEDRHISAHKP VLAARSDSWSLANLSSTKELDLSDANPEVTMTMLRHYTTDELEF REDDVFLIETMIKLANPFQLOLLRERCEBLKYKVEDRHISAHKP VLAARSDSWSLANLSSTKELDLSDANPEVTMTMLRHYTTDELEF REDDVFLIETMIKLANFPQLOLLRERCEBVSLKVUDRHISAHKF VLAARSDSWSLANLSSTKELDLSDANPEVTMTMLRHYTTDELEF REDDVFLIETMIKLANFPQLOLLRERCEWSLLKVUDRHISAHKF VLAARSDSWSLANLSSTKELDLSDANPEVTMTMLRHYTTDELEF REDDVFLIETMIKLANFPQLOLLRERCEWSLLVWORMISAHKF VLAARSDSWSLANLSSTKELDLSDANPEVTMTMLRHYTDELEF REDDVFLIETMIKLANFPGOLOLLRERCEWSLLVWORMISAHKF VLAARSDSWSLANLSSTKELDLSDANPEVTMTMLRHYTDELEF REDDVFLIETMIKLANFPGOLOLLRERCEWSLLVWORMISAHKF VLAARSDSWSLANLSSTKELDLSDANPEVTMTMLRHYTDELEF REDDVFLIETMIKLANFPGFOTVGSDVLKIKVGDRHISAHKF VLAARSDSWSLANLSSTKELDLSDANPEVTMTMLRHYTDELEF REDDVFLIETMIKLANFPGFOTVGSDVLKIKVGDRHISAHKF VLANRSDSWSLANLSSTKELDLSDANPEVTMTMLRHYTYDELEF REDDVFLIETMIKLANFPGFOTVGSDVLKIKVGDRHISAHKF VLANRSDSWSLANLSSTRELDLSDANPEVTMTMLRHYTYDELEF REDDVFLIETMIKLANFPGFOTVGSDVLKKVGDRHISAHKF VLANRSDSWSLANLSSTRELDLSDANPEVTMTMLRHYTYDELEF REDDVFLIETMIKLANFPGFOTVGSDVLKKVGDRHISAHKF VLANRSDSWSLANLSSTRELDLSDANPEVTMTMLRHYTYDELEF REDDVFLIETMIKLANFPGFOTVGSDVLKKVGNLLVWORMITSFOT TABELNASTIMNYCASITASHWSEVEGVNKAL PITLIPFSRARAGHTWNTSFOTVGSDVLKKVGNLLVWGNCIRFVQA HGGICTRTVQHQDSQVNALEVTPDRSMIAAAVQVSLGYGHTRM YDLNSNNIPPSIISTDGVNKHIASVGFHEGRWMYTGGEDCTARI WOLKSRILQCGFFVSARFSULFRCGURWYTUTGGEDCTARI WOLKSRILQCGFFVSARFSTALGHLWNDSGGGLEVMYTUTGGEDCTARI WOLKSRILQCGFFVSARFSSPNKASSFALQSAGGGLANVALIKRD DLKTNILGCGFFSLARGLIFTHNINGDSDSGKLEKATAKDLLGTOFN PAEGGETKPYREILSELDBHTENKLDFEDFMITLLSTVMSDL LIPKKIP HIGTORIC		}		REDTGCNLQHISDRENIDDLNMEFNPSDHDRASTIFISYSOTOV
CVALATYYHIKRADPOCRMLIDIFDENHIPLISKSEVPPDUKKIN PECKQITPEVRILESAAOLTAECHIVTYJERLICITYAEROLTOE ANMERIVIGAILLASKVMDDOAVWNUDYCQILKDITVEDMINELE ROFLELLGYNINVPSSVYAKYYPDLISLASAMINISPPLEPLSRE RAHKLBAISRICEUKYKDLRESARKESASADNILTDENKSPAIIS CACACEORARAEVGAATALPYRMASGEMAPSGEMAPSLAVPLAVLVULD WGAPWTHGRENNIVITUTDENMELLASSGEMAPSLAVPLAVLVULD WGAPWTHGRENNIVITUTDENMELLASSGEMAPSLAVPLAVLVULD WGAPWTHGRENNIVITUTDENMELLASSGEMAPSCHAVPLAVLVULD KDGEFRYGGPRIKKOPINFISDKEWKSIEPVSWF 6739 3 631 SWEDMAEEEVAKLEKHIMILINGEVYKLOKKLASTERKECALLAAQ ANKESSESFISRLAIVADLYEQEGYSDLKIKVGORHISAHKP VLAARSDSNISANISSTKELDLSDANPEVTHTMLRRITYTDELEF REDDVFLITELMKLANRPOLOLLEBRCEKGVMSLVAVRNCIRPYQ TABELMASTKENNISSTKELDLSDANPEVTHTMLRRITYTDELEF REDDVFLITELMKLANRPOLOLLEBRCEKGVMSLVAVRNCIRPYQ TARELMASTKENNISSTKELDLSDANPEVTHTMLRRITYTDELEF REDDVFLITELMKLANRPOLOLLEBRCEKGVMSLVAVRNCIRPYQ TARELMASTKENNISSTKELDLSDANPEVTHTMLRRITYTDELEF REDDVFLITELMKLANRPOLOLLEBRCEKGVMSLVAVRNCIRPYQ TARELMASTKENNISSTKELDLSDANPEVTHTMLRRITYTDELEF REDDVFLITELMKLANRPOLOLLEBRCEKGVMSLVAVRNCIRPYQ HSGICTRTVQHODSQUNALEVTPDRSMIAAAVQPVSLGYGHIRM YDLMSNNNNISSTKELDLSDANPEVTHTMLRRITYTDELEF REDDVFLITELMSTKALDHINDRITYTDELEF REDDVFLITELMSTKALDHINDRITYTORGEDCTARII WOLRSRNLQCQRIFQVNALEVTPDRSMIAAAVQPVSLGYGHIRM YDLMSNNNNISSTKELDLSDAGRAWASTLVAVRTUPFSCLL PLAIGILQEGEFESLARRGLIFILACQCNCTVWMITGGIGDEVTQ LIPKKIP UDLKTHNBOLIPPSSARAGHTMNTSPGTVGSDPVILATAGYDHTVRFWQA HSGICTRTVQHQDSQVNALEVTPDRSMIAAAVQPVSLGYGHIRM YDLNSNNNPIISYDGVNNIASVGFHEDGRWYTTGGEDCTARII WOLRSRNLQCQRIFQVNNIASVGFHEDGRWYTTGGEDCTARII WDLKTHHBOLIPPSSARAGHTWNTSPGTVGSDPVILATAGYDHTVRFWQA LIPKKIP UDLKTHBOLIPPSSARAGHTWNTSPGTVGSDPVILATAGYDHTVRFWQA LIPKKIP UDLKTHBOLIPPSSARAGHTWNTSPGTVGSDPVILATAGYDHTVRFWQA LIPKKIP ARGGETKPRYRRISSEDDEKLEKAIRGLIFLGCGGGGTAHIW DLKTHBEGLIPPSSARAGHTWNTSPGTVGSDPVILATAGYDHTVRFWQA LIPKKIP DLKTHLBEGLIPPSSTSARAFRIFLIFLACQGRCVVWNITGGIGGDEVTQ LIPKKIP ARGGETKPRYRRISSEDDERTENKLDFCFTBMILLISTTVMSDL LONIR:	1			REKRKSLFINHHPPGOIARKYSSCSTIFLDDSTVSOPNLKYTTV
PECKQIYRFVRILEGIADLECAIVTLVIJERLITAELDICP ANMERIUGAILLASKWUDDOAWUNDYQILKDITVEDNNELE ROFLELLOPNINVPSSVYAKYYPDLRSLARANNISPPLEPELSRE RAHKLEAISRICEDKYMDLRSRARKSASADNILTPRWSPAIIS CACAEQRARAEVGAATALPVWAMSGEMAPSGILAVPLAVLVLLU WCAPWTHGRRSNVRVITDEBWRRLLEGDWM EPYAPPCPACONI OPEWSPFARWGDLEVMIARVUTTOPGHSGRIFITALPTITHC KDGEFRRYQGPRIKKDFINFISDKEWKSIEPVSSWF 6739 3 631 SWPDMAEEEVAKLEKHIMLLRGEYVKLOKKAETEKRCALLAAO ANKESSSEFISRLAIVADLVEGSYDLKIKVOGHAISAKKP VLAARADSWSLANLSSTKELDLSDANPEVTHTMLRWIYTDELEF REDDVFLTELMKLANRFQLQLLRERCEKGVMSLVNVRNCIRFYQ TAEELNASTLMNYCAEIIASHWVSEVGVNKAL ANKESSSEFISRLAIVADLVEGSQYSDLKIKVGGMFISAKKF VLAARSDSWSLANLSSTKELDLSDANPEVTHTMLRWIYTDELEF REDDVFLTELMKLANRFQLQLLRERCEKGVMSLVNVRNCIRFYQ TAEELNASTLANNYCAEIIASHWVSEVGVNKAL ANKESSSESFISRLAIVADLVEGSQYSDLKIKVGGMFISAKKF VLAARSDSWSLANLSSTKELDLSDANPEVTHTMLRWIYTDELEF REDDVFLTELMKLANRFQLQLLRERCEKGVMSLVNVRNCIRFYQ TAEELNASTLANNYCAEIIASHWVSEVGVNKAL FREDDVFLTELMKLANRFQLQLLRERCEKGVMSLVNVRNCIRFYQ TAEELNASTLANNYCAEIIASHWVSEVGVNKAL HSGICTRTVGKOBSQUNALEVTPDRAMAANVSTLVPFSCLL PLANGILQEGFFSLARRGLLFLACQGNCYVWNLTGGIGDEVTQ LIPKKIP DLKTCHNBOLIPPEVSITSAHIDPDASYMAAVNSTLVPFSCLL PLANGILQEGFFSLARRGLLFLACQGNCYVWNLTGGIGDEVTQ LIPKKIP WDLKSTNILQCQRIFQVNNILASVGPHEGRWMYTGGEDCTARI WDLKSTNILQCQRIFQVNNILASVGPHEGRWMYTGGEDCTARI WDLKSTNILQCQRIFQVNNILASVGPHEGRWMYTGGEDCTARI WDLKSTNILQCGRIFQVNNILASVGPHEGRWMYTGGEDCTARI WDLKSTNILQCGRIFQVNNILASVGPHEGRWMYTGGEDCTARI WDLKSTNILQCGRIFQVNNILASVGPHEGRWMYTGGEDCTARI WDLKSTNILQCGRIFQVNNILASVGPHEGRWMYTGGEDCTARI WDLKSTNILQCGRIFQVNNILASVGPHEGRWMYTGGEDCTARI WDLKSTNILQCGRIFQVNNILASVGPHEGRWMYTGGEDCTARI WDLKSTNILQCGRIFQVNNILASVGPHEGRWMYTGGEDCTARI WDLKSTNILQCGRIFQVNNILASVGPHEGRWMYTGGEDCTARI WDLKSTNILQCGRIFQVNNILASVGPHEGRWMYTGGEDCTARI WDLKSTNILQCGRIFQVNNILASVGPHEGRWMYTGGEDCTARI WDLKSTNILQCGRIFQVNNILASVGPHEGRWMYTGGEDCTARI WDLKSTNILQCGRIFQVNNILASVGPHEGRWMYTGGEDCTARI WDLKSTNILGCGRIFGVNYMORSERIAGRADLLQTQFRN PAEGGETKPKYREILSELDBHTENKLDFECTARI WDLKSTNILGCGRIFGVNYMORSERIACH LIPKKIP 412 MRSTQDKSTNICAGCEVLSRFSSPNKASSPALQSAGGGLPAVRALRED DLCHMLSLEEVAPVLQGTLLQDLLLGRVHPOFFEALILLISST UNIVER	ŀ			CVALAIYYHIKNRDPDGRMLLDIFDENLHDISKSEUPPDVDKUN
AMMERIUGALLASKWHODQAWNUNDYGLIKDITUEDMINELE RQFIELLGYNINVPSSYVAKYYYDLIKALAMINILSPPLEVLSRE RAHKLRAISRICEDKYKOLRRSARKRSASADNLTLPRWSPAIIS CACAEQPARAEVGARTALDYWASGEMAPSGENAPPLAVLVULLU WGAPWTHGRRSINVRVITDEMWRELLEGOWMIEPYAPKCPACOMI OPEWESFABWGEDLEVWIAKVDVTEOPGISGRYFITALPTIYHC KOGERTYGRATKUNDFINISOKRKSIGRYFITALPTIYHC KOGERTYGRAFTKUNDFINISOKRKSIGRYITALPTIYHC KOGERTYGRAFTKUNDFINISOKRKSIGPYSSTW VLAARSDSWILAMUSSYKELDLSDANPEVTHTMLRWIYTDELEF REDDVPLITELMKLANRPOLQLLRBRCEKGVWSLWVURNCIRFYQ TABELMASTIANYCAETIASHWYSECWINKAL ANKESSESFISRLAIVADLYEQGYSDLKIKVGORHISAHKF VLAARSDSWILAMUSSYKELDLSDANPEVTHTMLRWIYTDELEF REDDVPLITELMKLANRPOLQLLRBRCEKGVWSLWVURNCIRFYQ TABELMASTIKHNYCAETIASHWYSECWINKAL VARARSDSWILAMUSSYKELDLSDANPEVTHTMLRWIYTDELEF REDDVPLITELMKLANRPOLQLLRBRCEKGVWSLWVURNCIRFYQ TABELMASTKHNYCAETIASHWYSECWINKAL VARARSDSWILAMUSSYKELDLSDANPEVTHTMLRWIYTDELEF REDDVPLITELMKLANRPOLQLLRBRCEKGVWSLWVURNCIRFYQ TABELMASTKHNYCAETIASHWYSECWINKAL VARARSDSWILAMUSSYKELDLSDANPEVTHTMLRWIYTDELEF REDDVPLITELMKLANRPOLQLLRBRCEKGVWSLWWNCNCIRFYQ TABELMASTKHLDLOSHITASHWYDOLLRBRCEKGVWSLWWNCNCIRFYQ HIGHTYVQHQOSQUNALEVTPORSMIAAAVQPVSLGYQHIRM YDLNSNNENPI 1SYDGVNNI IASVGENGAETAHIW DLKTHOHROLI PEPESVITSAHIDPDASYMAAVNSTLVPPSCLL PHAIGILQEGFFESLARRGLLFLACQGNCYVWNLTGGIGDEVTQ LIPKTKIP DLKTKIP PHAIGILQEGFFSLARRGLLFLACQGNCYVWNLTGGIGDEVTQ LIPKTKIP DLKTKIP DLKTKIP DLKTKIP PHAIGILQEGFFSLARRGLLFLACQGNCYWNLTGGIGDEVTG LIPKTKIP LIPKTKIP NHSTODKSHLEGOPPSSAPTSTCAPRWPRRISISKQLASVK ALRKCSDLEKAIATTALIFRNSSDSGKLEKAIAKDLLQTOFFN PAEGGETKPKYRRILSELDBEHTENKLDFEDFWILLISITUMSDL LONIR 1 412 NHSTODKSLHLEGDPNPSSAPTSTCAPRWPRRISISKQLASVK ALRKCSDLEKAIATTALIFRNSSDSGKLEKAIAKDLLQTOFFN PAEGGETKPKYRRILSELDBEHTENKLDFEDFWILLISITUMSDL LONIR 6744 95 1343 RTPARNRCAGCEVLSRFSSPNKASSPALGSAGGIDAWRALRD DLCHMLSLEEVAPVLQQTLLQULLGRWFPDFFRENLILLISBT LSNEEHPGEPOCSLEAPPREPESSVEEFFE		1		PEQKQIYRFVRTLFSAAOLTAECAIVTLVYLERILTVAETDICE
RQFLELLQYNINVPSSVYAKYPFLRSLARANNLSPPLEPLSRE RAHKLRAISRLCEDKYKDLRSDAKKRSASADNLTLPRWSPAIIS CACAEQPARAEVGAATALPVRWASGEMAPSGSLAVFLAVLVULLL WGAPWTHGRRSNVRVITDENWRELLEGDWNIEFYAFWCPACONL OPENBESFABWGGLEVNIAKUVTGPOLGGRFI ITALPTIYHC KDGEFRRYGGPRIKOFINFISDKENKSIEFVSSWF SWPPMMAEBEVAKLEKHLMLLRGEYVKLQKKLAEFTEKRCALLAAQ ANKESSSESFISRLAIVADLYRCGGYSDLKIKVGCRHSAAKF VLAARSDSWSLANLSSTRELDLSDANPEVYMTHLRWIYYDBLEF REDDVITLEMKLANRFQLQLIARRCCKGYMSLVNYNRCIRPYQ TABELMASTLMNYCAEIIASHWUSEVEGVIKAL ANKESSSESFISRLLAIVADLYRCGGYSDLKIKVGGRHSAAKF VLAARSDSWSLANLSSTRELDLSDANPEVYMTHLRWIYYDBLEF REDDVITLEMKLANRFQLQLIARRCCKGYMSLVNYNRCIRPYQ TABELMASTLMNYCAEIIASHWUSEVEGVIKAL FREDDVITTELMKLANRFQLQLIARRCCKGYMSLVNYNRCIRPYQ TABELMASTLMNYCAEIIASHWUSEVEGVIKAL FREDDVITTELMKLANRFQLQLIARRCCKGYMSLVNYNRCIRPYQ TABELMASTLMNYCAEIIASHWUSEVEGVIKAL FREDDVITTELMKLANRFQLGLIARRCCCHARGCHTMYTHFWQA HSGICTRTVQRQSQVAALEVTDRSMIAAAVQPVSLGYGHIRM YOLNSNNNPNISSOGVAALEVTDRSMIAAAVQPVSLGYGHIRM YOLNSNNNPNISSOGVAALEVTDRSMIAAAVQPVSLGYGHIRM YOLNSNNNPNISSOGVAALEVTDRSMIAAAVQPVSLGYGHIRM YOLNSNNNPNISYGDVAAPINCUCHPNQAELIVGDGGAHHW DLKTDHNGOLIPPEEVSITSAHDPDASYMAAVNSTLVPFSCLL PHAIGILQEGFESLARRGLIFLACQGNCYVWNLTGGIGDEVTQ LIPKTKIP DLKTDHNGOLIPPEEVSITSAHDAAQQPVSLGYGHIRM WDLRSRNLQCQRIFQVNAPINCUCHPNQAELIVGDGGAHHW DLKTDHNSOLIPPEEVSITSAHDAAQQPVSLGYGHIRM WDLRSRNLQCQRIFQVNAPINCUCHPNQAELIVGDGGAHHW DLKTDHNSOLIPPEEVSITSAHDAAQQPVSLGYGHIRM WDLRSRNLQCQRIFQVNAPINCUCHPNQAELIVGDGGAHHW DLKTDHNSOLIPPEEVSITSAHDDASYMAAVNSTLVPFSCLL PLAIGILQEGFESLARRGLLFLACGGNCYWNLTGGIGDEVTQ LIPKTKIP DLKTMINGOLIPPEEVSITSAHDDASYMAAVNSTLVPFSCLL PLAIGILQEGFESLARRGLLFLACGGNCYWNLTGGIGDEVTQ LIPKTKIP DLKTMINGOLIPPEEVSITSAHDDASYMAAVNSTLVPFSCLL PLAIGILQEGFESLARRGLLFLACGGNCYWNLTGGIGDEVTQ LIPKTKIP DLKTMIPBOLIPPEEVSITSAHDDASYMAAVNSTLVPFSCLL PLAIGILQEGFESLARRGLLFLACGGNCYWNLTGGIGDEVTQ LIPKTKIP DLKTMIPBOLIPPEEVSITSAHDERDASYMAPORTLVPFGCCTARI WDLRSRNLQCQRIFGVWARGARGGGAGGLPAVRALRED ARKCSDLEKKARGLEDHTENNLDFEDFWILLLSITWSDL LQNIR 6744 95 1343 RTPARNRCAGCEVLSRFSSPNKASSFALQSAGGLPAVRALRED DCKMLSEEHPQEPDCSLERQPKYVRGGRYGGRAGGEPAVRALRED DCKMLSEEHPQEPDCSLERQPKYVRGGR	1	·		ANWKRIVLGAILLASKVWDDQAVWNVDYCQILKDITVRDMVRLE
6738 148 653 CACAGOPARAEUAPVRASGEMAPSGELAVPLAVULLI WARPWTHGRRSNVRVITDENWRBLLEGDMNIEFYAFWCPACONI QPEMESFARWGEDLEVNIAKVDVTEQPGLGGRITTALPTITHC KOGEFRYQGPRIKKOFINFISDKEWKSIEFYSSWF 6739 3 631 SWPPMAEEVAKLEKHLMLLRGEYVKLQKKLAETEKRCALLAAQ ANKESSESFISRLLAIVADLYBCEQYSDLKIKVGDRHISAKKF VLAARSDSWSLANLSSTKELDLSDANPEVTMTHLRWIYTDELEF REDDVFLTELMKLANRFQLOLLRBRCEKGWMSLVNVRNCIRFYQ TABELMASTLMHYCAEIIASHWYSEVEGVNKAL 6740 3 631 SWPDMAEEEVAKLEKHLMLRGEYVKLQKKLAETEKRCALLAAQ ANKESSESFISRLLAIVADLYBCEQYSDLKIKVGDRHISAKKF VLAARSDSWSLANLSSTKELDLSDANPEVTMTHLRWIYTDELEF REDDVFLTELMKLANRFQLQLLRBRCEKGWMSLVNVRNCIRFYQ TABELMASTLMHYCAEIIASHWYSEVEGVNKAL 6741 141 960 PITLPFSSRARGHTMNTSPGTVSDPVILATAGYDHTVRFWQA HSGICTRTVQHQDSQVNALEVTPDRSMIAAAVQPVSLGYQHIRM YDLNSNNPNPIISYDGVNKNIASVGFHEDRMWYTGSEDCTARI WDLRSRNLQCQRIFQVNAPINCVCHPNQAELIVGDQSGAIHIW DLKTDHNSQLIPBEVSITSAHLDPDASWAAVNSTLUPPSCLL PFAIGILQGGEFESLARRGLLFLACGGNCYVWNLTGGIGDEVTQ LIPKTKIP 6742 141 960 PITLPFSSRARGHTMNTSPGTVGSDPVILATAGYDHTVRFWQA HSGICTRTVQHQDSQVNALEVTPDRSMIAAAVQPVSLGYQHIRM YDLNSNNPNPIISYDGVNKNIASVGFHEDGRWYTTGEGDCTARI WDLRSRNLQCQRIFQVNAPINCVCHPNQAELIVGDQSGAIHIW DLKTDHNSQLIPBEVSITSAHLDPDASWAAVNSTLUPPSCLL PFAIGILQGEGFESLARRGLLFLACGGNCYVWNLTGGIGDEVTQ LIPKTKIP 6742 141 960 PITLPFSSRARGHTMNTSPGTVGSDPVILATAGYDHTVRFWQA HSGICTRTVQHQDSQVNALEVTPDRSMIAAAVQPVSLGYQHIRM YDLNSNNPNPIISYDGVNKNIASVGFHEDGRWMYTGGEDCTARI WDLRSRNLQCQRIFQVNAPINCVCHPNQAELIVGDQSGAIHIW DLKTDHNSQLIPBEPSITSAHLDDASWAAVNSTLUPPSCLL PFAIGILQGEGFESLARRGLLFLACQGNCYVWNLTGGIGDEVTQ LIPKTKIP MHSTQDKSLHLEGDPNPSAAPTSTCAPRMPKRISISKQLASVK ALRKCSDLEKAIATTALIFRNSSDSDGKLEKAIAKDLLQTOFRN PAEGGETTPKYREILSELDEHTENKLDFDFDTUTGSLQGEUT DLCHMLSLEEVAPVLQQTLLQDNLLGRVHPQDFKAALIRDD RQVWSTVGYGMDEVEQDQHBARLKELPPSFDTUTGSLQQEELT DLCHMLSLEEVAPVLQQTLLQDNLLGRVHPQOFRAALILLISRT LSNEBHPQPPDCSLBAQPKYVRGGRYYGRGLPGFRSLEFFESEGUEFFWP	1			RQFLELLQFNINVPSSVYAKYYFDLRSLARANNI.SFDLEDI.SDE
CACAGORARAEVGARTALPVRWASGEWAPSGILAVPLAU-ULLL GAPWHIGKRSNVRVITDENNRBLLEGDWMIEFYAPWCPACONL QPEWESFAEWGEDLEVNIAKUDTTEQPGLSGRITITALPTITHC KDGEFRRYGGPRIKGDFINFISDKEWKSIEPVSWF SWEPDMAEERVALEHHALLERGEVYKLOFKLAETEKRCALLAAO ANKESSESFISRLLAIVADLYEQEGYSDLKIKVGDRHSAHKP VLAARSDSWSLANLSSTKELDLSDANPEVYMTHLRWIYTDELEF REDDVFLITELMKLANRFQLOLLERRCEKGYMSLVNVRNCIRFYQ TABELMASTLMNYCAEIIASHWUSEVEGVNKAL 6740 3 631 SWEPDMAEEEVAKLEKHLALLERGEVYKLOKKLAETEKRCALLAAO ANKESSESFISRLLAIVADLYEGEGVSDLKIKVGGRHSAHKF VLAARSDSWSLANLSSTKELDLSDANPEVTMTMLRWIYTDELEF REDDVFLITELMKLANRFQLQLLERRCEKGMSLVNVRNCIRFYQ TABELMASTLMNYCAEIIASHWUSEVEGVNKAL 6741 141 960 PILTEPFSSRARGHTMNTSFOTVGSDFVILATAGYDHTVRFWQA HSGICTRTVQHQDSQVNALEVTDRSMLAAVQPVSLGYGHIRM WDLKSTNLQCQRIFQVNAPINCVCLHPNQAELIVGDGSGAIHIW DLKTDHNSQLIPBEVSITSAHIDPDASYMAAVNSTLVPFSCLL PLAIGILQEGFFSLARRGLLFLACGGNCYVWNLTGGIGDEVTQ LIPKTKIP 6742 141 960 PILTEPFSSRARAGHTMNTSFOTVGSDFVILATAGYDHTVRFWQA HSGICTRTVQHQDSQVNALEVTPDRSMIAAAVQPVSLGYGHIRM YDLNSNNPNPIISYDGVNKNIASVGFHEDGRMMYTGGEDCTARI WDLRSRNLQCQRIFQVNAPINCVCLHPNQAELIVGDGSGAIHIW DLKTDHNSQLIPBEVSITSAHIDPDASYMAAVNSTLVPFSCLL PLAIGILQEGFFSLARRGLLFLACGGNCYVWNLTGGIGDEVTQ LIPKTKIP BARSTQLGCRIFTQVNAPINCVCLHPNQAELIVGDGSGAIHIW DLKTDHNEQLIPBEVSITSAHIDPDASYMAAVNSTLVPFSCLL PLAIGILQEGFFSLARRGLLFLACGGNCYVWNLTGGIGDEVTQ LIPKTKIP AMSTQDKSLHLEGDPNPSAAPTSTCAPRMPKRISISKQLASVK ALRKCSDLERAIATTALIFRNSSDSDGKLEKAIAKDLLQTOFRN FAEGGETTPKYREILSELDEHTENKLDFDFDTMILLSITVMSDL LONIR 6744 95 1343 RTPARNRCAGCEVLSFFSSPNKASSFALQSAGGLPAVRALRED RQKVSTVGYGMDEVECDOHBARLKELFPSSPDTTGTGSLGQEELIT DLCHMSLESVAPVLQQTLLQDNLLGRVHFDQFKEALILLISRT LSNEHFPQEPCSLBAQPRYVNGGRYYGRSLEFFSEGOLEFFWMP				RAHKLEAISRLCEDKYKDLRRSARKRSASADNLTLPRWSDAILS
### ### ### ### ### ### ### ### ### ##	6738	148	653	CACAEQPARAEVGAATALPVRWASGEMAPSGSLAVPLAVLVLLL
GPEMESFAEMGEDLEVNIAKVDVTEOPGLSGRFITTALPTIYHC KDGEFRRYQOFRKKDFINFISDKEWKSIEPVSSWF 3 631 SWPDMAEEEVAKLEKHLMLRGEYVKLQKKLAETERGCALLAQ ANKESSSESFISRLLAIVADLVEQEGYSDLKIKVGDRHISAHKP VLAARSDSWSLANLSSTKELDLSDANPEVTMTMLRWIYTDELEF REDDVFLTELMKLANRFQLQLLRERCEKGVMSLVAVRORCIRPYQ TABELMASTLMNYCAEIIASHWYSEVEGYNKAL 6740 3 631 SWPDMAEEEVAKLEKHLMLRGEYVKLQKKLAETEKGCALLAAQ ANKESSSESFISRLLAIVADLYEQEGYSDLKIKVGDRHISAHKF VLAARSDSWSLANLSSTKELDLSDANPEVTMTMLRWIYTDELEF REDDVFLTELMKLANRFQLQLLRERCEKGVMSLVAVRNCIRPYQ TABELMASTIMNYCAEIIASHWYSEVEGYNKAL 6741 141 960 PLTLPFSSRARAGHTMNTSPGTVGSDPVILATAGYDHTVRFWQA HSGICTRTVQHQDSQVNALEVTPDRSMLAAAVQPVSLGYQHIRM VDLNSNNPNPIISYDGVNKNIASVGFHEDGRWMYTGGEDCTARI WDLRSRNLQCQRIFQVNAPINCVCLHPNQAELIVGDQSGAIHIW DLKTDHNSQLIPEPEVSITSAHIDPDASYMAAVNSTLVPPSCLL PLAIGILLGEGEFESLARRGLLFLACQGNCYVWNLTGGIGDEVTQ LIPKTKIP 6742 141 960 PLTLPFSSRARAGHTMNTSPGTVGSDPVILATAGYDHTVRFWQA HSGICTRTVQHQDSQVNALEVTPDRSMIAAAVQPVSLGYCHIRM YDLNSNNPNPIISYDGVNKNIASVGFHEDGRWMYTGGEDCTARI WDLRSRNLQCQRIFQVNAPINCVCLHPNQAELIVGDQSGAIHIW DLKTDHNSQLIPEPEVSITSAHIDPDASYMAAVNSTLVPPSCLL PLAIGILQEGEFESLARRGLLFLACQGNCYVWNLTGGIGDEVTQ LIPKTKIP 6743 1 412 WHSTQDKSLHLEGDPNPSAAPTSTCAPRKWPKRISISKQLASVK ALRKCSDLEKAIATTALIFRNSSDSDGKLEKAIAKDLLQTQFRN PAEGGETTPKYREILSELDEHTENKLDFEDFMILLSITVMSDL LQNIR 6744 95 1343 RTPARINRCAGCEVLSRFSSPNKASSPALQSAGGGLBAVRALRED RQKVSTVQYGMDEVEQDQHERALKELFDSSCTTGTGSLGGELT DLCHMLSLEEVAPVLQQTLLQDNLLGRVHPQPKEALILLISRT LSNEEHPQEPDCSLBAQPKYVRGGRSLJEEFGSSVEEFFE VTVIEPLDEEARPSHIPAGDCSEHWTTORSEEVARGSCEPFWP				WGAPWTHGRRSNVRVITDENWRBLLEGDWMIEFYAPWCPACONI.
6739 3 631 SWPDMAEEVSKLEKHINLISKEKSIEPUSSWP SWPDMAEEVSKLEKHINLIGETYKLQKYLQKKLAETEKRCALLAAQ ANKESSESFISRLLAIVADLYEQEQYSDLKIKVCDRHISAHKP VLAARSDSWSLANLSSTKELDLSDANPEVINTMLRWIYTDELEF REDDVFLTELMKLANRFQLQLLBERCEKGVMSLVNVRNCIRFYQ TAEELNASTLMNYCAEIIASHWYSEVESVNKAL 6740 3 631 SWPDMAEEVAKLEKHIMLLRGEYVKLQKKLAETEKRCALLAAQ ANKESSESFISRLAIVADLYEQEQYSDLKIKVGDRHISAHKF VLAARSDSWSLANLSSTKELDLSDANPEVINTMLRWIYTDELEF REDDVFLTELMKLANRFQLQLLBERCEKGVMSLVNVRNCIRFYQ TAEELNASTLMNYCAEIIASHWYSEVEGVNKAL 6741 141 960 PLTLPFSSRARAGHTMNTSFGTVGSDPVILATAGYDHTVRFWQA HSGICTRTVQHQDSQVNALEVTPDRSMIAAAVQPVSLGYQHIRM YDLNSNNPNPIISYDGVNNIASVGFHEDGRMWYTGGEDCTARI WDLRSRNLQCQRIFQVNAPINCVCLHPNQAELIVGDQSGAIHIW DLKTDHNBQLIPBPEVSITSAHIDPDASYMAAVNSTLVPPSCLL PLAIGILQEGFESLARRGLLFLACQGNCYVWNLTGGIGDEVTQ LIPKTKIP 6742 141 960 PLTLPFSSRARAGHTMNTSPGTVGSDPVILATAGYDHTVRFWQA HSGICTRTVQHQDSQVNALEVTPDRSMIAAAVQPVSLGYQHIRM YDLNSNNPNPIISYDGVNNIASVGFHEDGRMWYTGGEDCTARI WDLRSRNLQCQRIFQVNAPINCVCLHPNQAELIVGDQSGAIHIW YDLNSNNPNPIISYDGVNNIASVGFHEDGRMWYTGGEDCTARI WDLRSRNLQCQRIFQVNAPINCVCLHPNQAELIVGDQSGAIHIW DLKTDHNBQLIFEPEVSITSAHIDPDASYMAAVNSTLVPPSCLL PLAIGILQEGEFESLARRGLLFLACQGNCYVWNLTGGIGDEVTQ LIPKTKIP 6743 1 412 MHSTQDKSLHLEEGDPNPSAAPTSTCAPRKWPKRISISKQLASVK ALRKCSDLEKAIATTALIFRNSSDSDGKLEKAIAKDLLQTQFRN PAEGQETKPKVREILSELDEHTENKLDFEDFMILLLSITVMSDL LQNIR: 6744 95 1343 RTPARNRCAGCEVLSRFSSPNKASSFALQSAGGGLPAVRALRRD RQKVSTVGYGMDEVEQDQHBARLKELFDSFDTTGTGSLGQEELT DLCHMLSLEEVAPVLQQTLLQDNLLGRVPTPQFKEALILLISRT LSNEEHPQEPDCSLEAQPKYVRGGRYGRGSLEPEGESVEEFPE VTVTUEPLDEEARPSHIPARGOSSEHKKTORSSEFYEAEGGLRFMP	ŀ			QPEWESFAEWGEDLEVNIAKVDVTEOPGLSGREITTALDTIVUC
SWPDMAEBEWAKLEKHMILIRQEYVKLQKKLAETEKRCALLANQ ANKESSESFISRLIAIVADLYEQEQYSDLKIKVORHISAHKP VLAARSDSSIANLSSTKELDLSDANPEVITMIRWIYTDELEF REDDVFLTEIMKLANRFQLQLLRERCEKGWASLUNVRNCIRFYQ TABELNASTIMMYCAE II ASHWUSEVEGVNKAL 6740 3 631 SWPDMAEEEVAKLEKHLMILRGEYVKLQKKLAETEKRCALLANQ ANKESSESFISRLLAIVADLYEQEQYSDLKIKVGDRHISAHKF VLAARSDSWSLANLSSTKELDLSDANPEVITMIRWIYTDELEF REDDVFLTELMKLANRFQLQLLRERCEKGWASLUNVRNCIRFYQ TABELNASTIMMYCAE II ASHWUSEVEGVNKAL 6741 141 960 PLILPFSSRARAGHTMNTSPGTVGSDPVILATAGYDHTVRFWQA HSGICTRTVQHQDSQVNALEVYPDRSMLAAAVQPVSLGYQHIRM YOLNSNNPNPISTYDGVNKNIASVGFHEDGRWMYTGGEDCTARI WDLRSRNLQCQRIFQVNAPINCVCLHPNQAELIVGDQSGAIHIW DLKTHNRGLIPEPEVSITSAHDPDASYMAAVNSTLVYPSCLL PLAIGILQEGEFESLARRGLLFLACQGNCYVWNLTGGIGDEVTQ LIPKTKIP 6742 141 960 PLTLPFSSRARAGHTMNTSPGTVGSDPVILATAGYDHTVRFWQA HSGICTRTVQHQDSQVNALEVTPDRSMIAAAVQPVSLGYQHIRM YDLNSNNPNPISYDGVNKNIASVGFHEDGRWMYTGGEDCTARI WDLRSRNLQCQRIFQVNAPINCVCLHPNQAELIVGDQSGAIHIW DLKTDHNEQLIPEPEVSITSAHIDPDASYMAAVNSTLVPFSCLL PLAIGILQEGEFESLARRGLLFLACQGNCYVWNLTGGIGDEVTQ LIPKTKIP 6743 1 412 MHSTQDKSLHLEGDPNSSAPTSTCAPRKMPKRISISKQLASVK ALRKCSDLEKAIATTALIFRNSSDBGKLEKAIAKDLLQTQFRN PAEGGETKPKYREILSELDEHTENKLDFEDFNILLISITVMSDL LQNIR: 6744 95 1343 RTPARNRCAGCEVLSRFSSPNKASSFALQSAGGGLPAVRALRD RQKVSTVQYGMDEVEQDQHBARLKELFDSFDTTGTGSLGQBELT DLCHMLSLEEVAPVLQQTLLQDNLLGRVFPQFKEALILLISRT LSNEEHPQEPDCSLEAQPKYVRGGRYGRGSLEPETEFGESVEEFPE	6730			KDGEFRRYQGPRTKKDFINFISDKEWKSIEPVSSWF
ANKESSESFISILLAIVADLYEQEGYSDLKIKYGDRHISAHKP VLAARSDSWLANLSSTKELDLSDANPEVTMTMLRWIYTDELEF REDDVFLTELMKLANRFQLQLLRERCEKGYMSLVNVRNCIRFYQ TABELNASTLMNYCAEIIASHWISEVEGYNKAL 6740 3 631 SWPDMAEEEVAKLEKHLMLRQEYVKLOKKLAETEKRCALLAAQ ANKESSESFISILLAIVADLYEQEGYSDLKIKVGDRHISAHKF VLAARSDSWSLANLSSTKELDLSDANPEVTMTMLRWIYTDELEF REDDVFLTELMKLANRFQLQLLRERCEKGYMSLVNVRNCIRFYQ TABELNASTLMNYCAEIIASHWVSEVEGYNKAL 6741 141 960 PLTLPFSSRARAGHTMNTSPGTVGSDFVILATAGYDHTVRFWQA HSGICTRTVQHQDSQVNALEVTPDRSMLAAAVQPVSLGYQHIRM YDLNSNNNPPIISYDGVNKNIASVGFHEDGRWMYTGGEDCTARI WDLRSRNLQCQRIFQVNAPINCVCLHPNQAELIVGDQSGAIHIW DLKTDHNEQLIPPEVSITSAHIDPDASYMAAVNSTLVPPSCLL PLAIGILQEGEFESLARRGLLFLACQGNCYVWNLTGGIGDEVTQ LIPKTKIP 6742 141 960 PLTLPFSSRARAGHTMNTSPGTVGSDPVILATAGYDHTVRFWQA HSGICTRTVQHQDSQVNALEVTPDRSMLAAAVQPVSLGYQHIRM YDLNSNNPNPIISYDGVNKNIASVGFHEDGRWMYTGGEDCTARI WDLRSRNLQCQRIFQVNAPINCVCLHPNQAELIVGDQSGAIHIW DLKTDHNEQLIPPEVSITSAHIDPDASYMAAVNSTLVPPSCLL PLAIGILQEGEFESLARRGLLFLACQGNCYVWNLTGGIGDEVTQ LIPKTKIP DLKTDHNEQLIPPEVSITSAHIDDDASYMAAVNSTLVPFSCLL PLAIGILQEGEFESLARRGLLFLACQGNCYVWNLTGGIGDEVTQ LIPKTKIP 6743 1 412 MHSTQKSLHLEGDPNPSAAPTSTCAPRKWPKRISISKQLASVK ALRKCSDLEKATATTALIPRNSDSDGKLEKAIAKDLLQTQFRN PAEGQETKPKYREILSELDEHTENKLDFEDFMILLISTTVMSDL LQNIR 6744 95 1343 RTPARNCAGCEVLSRFSSPNKASSFALQSAGGLPAVRALRRD RQKVSTVGYGMDEVSQDQHBARLKELFDSFDTTGTGSLSQEELT DLCHMLSLEEVAPVLQQTLLQDNLLGRVHFDQFKEALILLISRT LSNEHPPQEPDCSLEAQPKYVRGRKYGRSDEVEREGOLRFWNP	0/39	3	631	SWPDMAEEBVAKLEKHLMLLRQEYVKLQKKLAETEKRCALLAAO
REDDVFTTELMKLANRFQLQLLRERCEKGWMSLVNVRNCIRFYQ TABELINASTLMNYCAEIIASHWVSEVEGVNKAL SWFDMAEEEVAKLEKHIMLLRQEYVKLQKKLAETEKCRALLAAQ ANKESSSESTISRLLAIVADLYEQEQYSDLKIKVGDRHISAHKF VLAARSDSWSLANLSSTKELDEDANPEVTHTMLRRIYTDELEF REDDVFLTELMKLANRFQLQLLRERCEKGWMSLVNVRNCIRFYQ TABELNASTLMNYCAEIIASHWVSEVEGVNKAL 6741 141 960 PLTLPFSSRARGHTMNTSPGTGSDPVILATAGYDHTVRFWQA HSGICTRTVQHQDSQVNALEVTPDRSMIAAAVQPVSLGYQHIRM YDLNSNNPNPIISYDGVNKNIASVGFHEDGRWMYTGGEDCTARI WDLRSRNLQCQRIFQVNAPINCVCLHPNQABLIVODQSGAIHIW DLKTDHNEQLIPPEPVSITSAHIDPDASYMAAVNSTLVPFSCLL FLAIGILQEGEFESLARRGLLFLACQGNCYVWNLTGGIGDEVTQ LIPKTKIP 6742 141 960 PLTLPFSSRARAGHTMNTSPGTVGSDPVILATAGYDHTVRFWQA HSGICTRTVQHQDSQVNALEVTPDRSMIAAAVQPVSLGYQHIRM YDLNSNNPNPIISYDGVNKNIASVGFHEDGRWMYTGGEDCTARI WDLRSRNLQCQRIFQVNAPINCVCLHPNQAELIVGDQSGAIHIW DLKTDHNEGLIPEPEVSITSAHIDPDASYMAAVNSTLVPFSCLL PLAIGILQEGFFESLARRGLLFLACQGNCYVWNLTGGIGDEVTQ LIPKTKIP 6743 1 412 MHSTQDKSLHLEGDPNPSAAPTSTCAPRKMPKRISISKQLASVK ALRKCSDLEKAIATTALIFRNSDSDGKLEKAIAKDLLQTQFRN FAEGQETKPKYREILSELDEHTENKLDFEDFMILLESITVMSDL LQNIR 6744 95 1343 RTPARNRCAGCEVLSRFSSPNKASSFALQSAGGCLPAVRALRRD RQKVSTVGYGMDEVEQDQHBRRLKELFDSFDTTGTGSLGQGELT DLCHMLSLEEVAPVLQQTLLQDNLLGRVHFDQFKEALILLISRT LSNEEHPQEPDCSLBAQPKYVRGKRYGRSLPEFGESVEEFPE VTVIEPLDEEARPSHIPAGDCSENKKTORSEEVEAFGGOLFRWPD				ANKESSSESFISRLLAIVADLYEOEOYSDLKIKVGDRHISAHKR
6740 3 631 SWPDMAEEVAKLEKHIMLLRQEYVKLQKKLAETEKRCALLAAQ ANKESSESFISRILAIVADLYRQEQYSDLKIKVGGRHISAHKF VLAARSDSWSLANLSSTKELDLSDANPEVTMTMLRWIYTDELEF REDDVFLITELMKLANRFQLQLLRERCEKGWMSLVNVRNCIRFYQ TABELNASTLMNYCAEIIASHWVSEVEGVNKAL 6741 141 960 PLTLPFSSRARGHTMNTSPGTVGSDPVILATAGYDHTVRFWQA HSGICTRTVQHQDSQVNALEVTPDRSMIAAAVQPVSLGYQHIRM YDLNSNNPNPIISYDGVNKNIASVGFHEDGRWMYTGGEDCTARI WOLKSRNLQCQRIFQVNAPINCVCLHPNQAELIVGDQSGAIHIW DLKTDHNEQLIPEPEVSITSAHIDPDASYMAAVNSTLVPFSCLL FLAIGILQEGEFESLARRGLLFLACQGNCYVWNLTGGIGDEVTQ LIPKTKIP 6742 141 960 PLTLPFSSRARAGHTMNTSPGTVGSDPVILATAGYDHTVRFWQA HSGICTRTVQHQDSQVNALEVTPDRSMIAAAVQPVSLGYQHIRM YDLNSNNPNPIISYDGVNKNIASVGFHEDGRWMYTGGEDCTARI WDLRSRNLQCQRIFQVNAPINCVCLHPNQAELIVGDQSGAIHIW DLKTDHNEQLIPEPEVSITSAHIDPDASYMAAVNSTLVPFSCLL PLAIGILQEGEFESLARRGLLFLACQGNCYVWNLTGGIGDEVTQ LIPKTKIP 6743 1 412 MHSTQDKSCHLEGDPNPSAAPTSTCAPRKWPKRISISKQLASVK ALRKCSDLEKAIATTALIFRNSSDSDGKLEKAIAKDLLQTGFRN FAEGGETKRKYREILSELDEHTENKLDFEDFMILLLSITVMSDL LQNIR 6744 95 1343 RTPARNRCAGCEVLSRFSSPNKASSFALQSAGGGLPAVRALRED RQKVSTVGYGMDEVEQDQHBARLKELFDSFDTTGTGSLGQEELT DLCHMLSLEEVAPVLQQTLLQDNLLGRVHFDQFKEALILLISRT LSNEEHPQEPDCSLBAQPKYVRGKRYGRSIPEFQESVEEFPE VTVIEPLDEEARPSHIPAGDCSEHKKTORSEEVEAEGGLRFWNP	1 1			VLAARSDSWSLANLSSTKELDLSDANPEVTMTMLRWIYTDELEF
6741 SWPDMAEEEVAKLEKHMLLRQEYVKLQKKLAETEKRCALLAAQ ANKESSESFISRLLAIVADLYEGGCYSDLKIKVGDRHISAHKF VLAARSDSWSLANLSSTKELDLSDANPEVTMTMILRWIYTDELEF REDDVFLTELMKLANRFQLQLLRERCEKGYMSLVMVRNCIRFYQ TAEELNASTLMNYCAEIIASHWVSEVEGVKKAL 6741 141 960 PLTLPFSSRARAGHTMNTSFGTVGSDPVILATAGYDHTVRFWQA HSGICTRTVQHQDSQVNALEVTPDRSMIAAAVQPVSLGYQHIRM YDLNSNNPNPIISYDGVNKNIASVGFHEDGRWMYTGGEDCTARI WDLKSRNLQCQRIFQVNAPINCVCLHPNQAELIVGDQSGAIHIW DLKTDHNEQLIPEPEVSITSAHIDPDASYMAAVNSTLVPFSCLL PLAIGILQEGEFESLARRGLLFLACQGNCYVWNLTGGIGDEVTQ LIPKTKIP 6742 141 960 PLTLPFSSRARAGHTMNTSPGTVGSDPVILATAGYDHTVRFWQA HSGICTRTVQHQDSQVNALEVTDRSMIAAAVQPVSLGYQHIRM YDLNSNNPNPIISYDGVNKNIASVGFHEDGRWMYTGGEDCTARI WDLRSRNLQCQRIFQVNAPINCVCLHPNQAELIVGDQSGAIHIW DLKTDHNEQLIPEPEVSITSAHIDPDASYMAAVNSTLVPFSCLL PLAIGILQEGEFESLARRGLLFLACQGNCYVWNLTGGIGDEVTQ LIPKTKIP 6743 1 412 MHSTQDKSLHLEGDPNPSAAPTSTCAPRKMPKRISTSKQLASVK ALRKCSDLEKAIATTALIFRNSSDSDGKLEKAIAKDLLQTQFRN FAEGQETKPKYREILSELDEHTENKLDFEDFMILLSITVMSDL LONIR 6744 95 1343 RTPARNRCAGCEVLSRFSSPNKASSFALQSAGGGLPAVRALRRD RQKVSTVGYGMDEVEQDQHEARLKELFDSFDTTGTGSLGQEELT DLCHMLSLEEVAPVLQQTLLQDNLLGRVHFDQFKEALILLISRT LSNEEHPQEPDCSLEAQPKYVRGGKRYGRSLPEFQESVEEFPE VTVIEPLDEEARPSHIPAGDCSEHWKTORSSEYEARSGLEFWNP				REDDVFLTELMKLANRFQLQLLRERCEKGVMSLVNVRNCIRFYQ
ANKESSESFISLLAIVADLYEQEQYSDLKIKVGDRHISAHKF VLAARSDSWSLANLSSTKELDLSDANPEVTMTMLRWITTDELEF REDDVFLTELMKLANRFQLQLLRERCEKGYMSLVNVRNCIRFYQ TABELNASTLMNYCAEIIASHWYSEVEGVNKAL 6741 141 960 PITLPFSSRARGHTMNTSPGTVGSDPVILATAGYDHTVRFWQA HSGICTRTVQHQDSQVNALEVTPDRSMIAAAVQPVSLGYQHIRM YDLNSNNPNPIISYDGVNKNIASVGFHEDGRWMYTGGEDCTARI WDLRSRRHQCQRIFQVNAPINCVCLHPNQAELIVGDQSGAIHIW DLKTDHNEQLIPPEPEVSITSAHIDPDASYMAAVNSTLUPFSCILL PLAIGILQEGEFESLARRGLLFLACQGNCYVWNLTGGIGDEVTQ LIPKTKIP 6742 141 960 PITLPFSSRARAGHTMNTSPGTVGSDPVILATAGYDHTVRFWQA HSGICTRTVQHQDSQVNALEVTPDRSMIAAAVQPVSLGYQHIRM YDLNSNNPNPIISYDGVNNNIASVGFHEDGRWMYTGGEDCTARI WDLRSRNLQCQRIFQVNAPINCVCLHPNQAELIVGDQSGAIHIW DLKTCHNEGLIPPEVSITSAHIDPDASYMAAVNSTLVPFSCILL PLAIGILQEGEFESLARRGLLFLACQGNCYVWNLTGGIGDEVTQ LIPKTKIP DLKTCHNEGLIPPEVSITSAHIDPDASYMAAVNSTLVPFSCILL PLAIGILQEGEFESLARRGLLFLACQGNCYVWNLTGGIGDEVTQ LIPKTKIP ALRCSDLEKAIATTALIFRNSSDSDGKLEKAIAKDLLQTOFFNN FAEGGETKPKYREILSELDEHTENKLDFEDFMILLSITVMSDL LQNIR 6744 95 1343 RTPARNRCAGCEVLSRFSSPNKASSFALQSAGGGLPAVRALRRD RQKVSTVGYGMDEVEQDQHBARLKELFDSFDTTGTGSLGQEELT DLCMMLSLEEVAPVLQQTLLQDNLLGRVHFDQFKEALILLILSRT LSNEEHFQEPDCSLEAQPKYVRGGKRYGRRSLPBFQESVEEFFPE VTVIEPLDEEARPSHIPAGDCSEHWKTORSSEFYEARGOLRFWNP	6740		(3)	TAEELNASTLMNYCAEIIASHWVSEVEGVNKAL
VLAARSDSWSLANLSSTKELDLSDANPEVTMTMLRWIYTDELEF REDDVFLTELMKLANRPQLQLLRERCEKGVMSLVDVRRCIRFYQ TAEELNASTLMNYCAEIIASHWVSEVEGVNKAL PLTLPFSSRARAGHTMNTSPGTVGSDPVILATAGYDHTVRFWQA HSGICTRTVQHQDSQVNALEVTPDRSMIAAAVQPVSLGYQHIRM YDLNSNNPNPIISYDGVNKNIASVGFHEDGRWMYTGGEDCTARI WDLKTDHNEQLIPEPEVSITSAHIDPDASYMAAVNSTLVPFSCLL PLAIGILQEGEFESLARRGLLFLACQGNCYVWNLTGGIGDEVTQ LIPKTKIP PUTLPFSSRARAGHTMNTSPGTVGSDPVILATAGYDHTVRFWQA HSGICTRTVQHQDSQVNALEVTPDRSMIAAAVQPVSLGYQHIRM YDLNSNNPNPIISYDGVNKNIASVGFHEDGRWMYTGGEDCTARI WDLRSRNLQCQRIFQVNAPINCVCLHPNQAELIVGDQSGAIHIW DLKTDHNEQLIPEPEVSITSAHIDPDASYMAAVNSTLVPFSCLL PLAIGILQEGEFESLARRGLLFLACQGNCYVWNLTGGIGDEVTQ LIPKTKIP 6743 1 412 MHSTQDKSLHLEGDPNPSAAPTSTCAPRKMPKRISISKQLASVK ALRKCSDLEKAIATTALIFRNSSDSDGKLEKAIAKDLLQTQFRN FAEGQETKPKYREILSELDEHTENKLDFEDFMILLISITVMSDL LQNIR 6744 95 1343 RTPARNRCAGCEVLSRFSSPNKASSFALQSAGGGLPAVRALRRD RQKVSTVGYGMDEVEQDQHEARLKELFDSFDTTGTGSLGQEELT DLCHMLSLEEVAPVLQCTLLQDNLLGRVHRDQFKEALILLISRT LSNEEHPQEPDCSLBAQPKYVRGRKRYGRRSLPEFGESVEEFPE VTVIEPLDEEARPSHIPAGDCSEHWKTQRSEEYEAGGOLRFWNP	""		631	SWPDMAEEEVAKLEKHLMLLRQEYVKLQKKLAETEKRCALLAAQ
REDDVFL'EELMKLANRFQLQLLRERCEKGVMSLVNVRNCIRFYQ TAEELNASTLMNYCAEIIASHWVSEVEGVMKAL PHTIPFSSRARAGHTMNTSFGTVGSDFVILATAGYDHTVRFWQA HSGICTRTVQHQDSQVNALEVTPDRSMIAAAVQPVSLGYQHTRM YDLNSNNPNPIISYDGVNKNIASVGFHEDGRWMYTGGEDCTARI WDLKSRNLQCQRIFQVNAPINCVCLHPNQAELIVGDQSGAIHIW DLKTDHNEQLIPEPEVSITSAHIDPDASYMAAVNSTLVPFSCLL PLAIGILQEGEFESLARRGLLFLACQGNCYVWNLTGGIGDEVTQ LIPKTKIP 6742 141 960 PLTLPFSSRARAGHTMNTSPGTVGSDPVILATAGYDHTVRFWQA HSGICTRTVQHQDSQVNALEVTPDRSMIAAAVQPVSLGYQHIRM YDLNSNNPNPIISYDGVNKNIASVGFHEDGRWMYTGGEDCTARI WDLRSRNLQCQRIFQVNAPINCVCLHPNQAELIVGDQSGAIHIW DLKTDHNEQLIPEPEVSITSAHIDPDASYMAAVNSTLVPFSCLL PLAIGILQEGEFESLARRGLLFLACQGNCYVWNLTGGIGDEVTQ LIPKTKIP 6743 1 412 MHSTQDKSLHLEGDPNPSAAPTSTCAPRKMPKRISISKQLASVK ALRKCSDLEKAIATTALIFRNSSDSDGKLEKAIAKDLLQTQFRN FAEGGETKPKYRTEILSELDEHTENKLDFEDFMILLLSITVMSDL LQNIR 6744 95 1343 RTPARNRCAGCEVLSRFSSPNKASSFALQSAGGGLPAVRALRRD RQKVSTVGYGMDEVEQDQHBARLKELPDSFDTTGTGSLGQEELT DLCHMLSLEEVAPVLQQTLLQDNLLGRVHFDQFKEALILLLSRT LSNEEHPQEPDCSLBAQPKYVRGGKRYGRRSLPEFQESVEEFPE VTV1EPLDEEARPSHIPAGDCSEHWKTORSEEYEAEGOLRFWNP	1 1			ANKESSSESFISRLLAIVADLYEQEQYSDLKIKVGDRHISAHKF
TAEELNASTLMNYCAEIIASHWUSEVEGVNKAL 960 PLTLPFSSRARAGHTMNTSPGTVGSDPVILATAGYDHTVRFWQA HSGICTRTVQHQDSQVNALEVTPDRSMIAAAVQPVSLGYQHIRM YDLNSNNPNPIISYDGVNKNIASVGFHEDGRWMYTGGEDCTARI WDLRSRNLQCQRIFQVNAPINCVCLHPNQAELIVGDQSGAIHIW DLKTDHNEQLIPEPEVSITSAHIDPDASYMAAVNSTLVPFSCLL PLAIGILQEGEFESLARRGLIFLACQGNCYVWNLTGGIGDEVTQ LIPKTKIP 6742 141 960 PLTLPFSSRARAGHTMNTSPGTVGSDPVILATAGYDHTVRFWQA HSGICTRTVQHQDSQVNALEVTPDRSMIAAAVQPVSLGYQHIRM YDLNSNNPNPIISYDGVNKNIASVGFHEDGRWMYTGGEDCTARI WDLRSRNLQCQRIFQVNAPINCVCLHPNQAELIVGDQSGAIHIW DLKTDHNEQLIPEPEVSITSAHIDPDASYMAAVNSTLVPFSCLL PLAIGILQEGEFESLARRGLLFLACQGNCYVWNLTGGIGDEVTQ LIPKTKIP 6743 1 412 MHSTQDKSLHLEGDPNPSAAPTSTCAPRKMPKRISISKQLASVK ALRKCSDLEKAIATTALIFRNSSDSDGKLEKAIAKDLLQTQFRN FAEGGETKPKYREILSELDEHTENKLDFEDFMILLSITVMSDL LQNIR 6744 95 1343 RTPARNRCAGCEVLSRFSSPNKASSFALQSAGGGLPAVRALRRD RQKVSTVGYGMDEVEQDQHBARLKELPDSFDTTGTGSLGQEELT DLCHMLSLEEVAPVLQQTLLQDNLLGRVHFDQFKEALILLISRT LSNEEHPQEPDCSLBAQPKYVRGGKRYGRRSLPEFQESVEEFPE VTVIEPLDEEARPSHIPAGDCSEHWKTORSEEYEAEGOLRFWNP]			VEAAKSDSWSLANLSSTKELDLSDANPEVTMTMLRWIYTDELEF
PITLPFSSRARAGHTMNTSPGTVGSDPVILATAGYDHTVRFWQA HSGICTRTVQHQDSQVNALEVTPDRSMIAAAVQPVSLGYQHIRM YDLNSNNPNPIISYDGVNKNIASVGFHEDGRWMTTGGEDCTARI WDLRSRNLQCQRIFQVNAPINCVCLHPNQAELIVGDQSGAIHIW DLKTDHNEQLIPBFEVSITSAHIDPDASYMAAVNSTLVPFSCLL PLAIGILQEGEFESLARRGLLFLACQGNCYVWNLTGGIGDEVTQ LIPKTKIP PUTLPFSSRARAGHTMNTSPGTVGSDPVILATAGYDHTVRFWQA HSGICTRTVQHQDSQVNALEVTPDRSMIAAAVQPVSLGYQHIRM YDLNSNNPNPIISYDGVNKNIASVGFHEDGRWMYTGGEDCTARI WDLRSRNLQCQRIFQVNAPINCVCLHPNQAELIVGDQSGAIHIW DLKTDHNEQLIPEPEVSITSAHIDPDASYMAAVNSTLVPFSCLL PLAIGILQEGEFESLARRGLLFLACQGNCYVWNLTGGIGDEVTQ LIPKTKIP PLAIGILQEGEFESLARRGLLFLACQGNCYVWNLTGGIGDEVTQ LIPKTKIP AHSTQDKSLHLEGDPNPSAAPTSTCAPRKMPKRISISKQLASVK ALRKCSDLEKATATTALIFRNSSDSDGKLEKAIAKDLLQTQFRN FAEGQETKPKYREILSELDEHTENKLDFEDFMILLSITVMSDL LQNIR 6744 95 1343 RTPARNRCAGCEVLSRFSSPNKASSFALQSAGGLPAVRALRRD RQKVSTVGYGMDEVEQDQHEARLKELFDSFDTTGTGSLGQEELT DLCHMLSLEEVAPVLQQTLLQDNLLGRVHFDQFKEALILILSRT LSNEEHFQEPDCSLEAQPKYVRGGKRYGRSLPEFGESVEEFPE VTVIEPLDEEARPSHTPAGDCSEHWKTQRSEEYEAEGOLRFWNP				TAFFI WASTI MARKE ANRIQUELRERCEKGVMSLVNVRNCIRFYQ
### ### ##############################	6741	141	960	DI TI DESCRIDA CUTANA CONTRACTOR DE LA C
### POLINSNPNPIISYDGVNKNIASVGFHEDGRWMYTGGEDCTARI ####################################	1 4		500	HEGICTET OUDBOOK THAT THE PROPERTY OF THE PROP
### ### ##############################	1			VOLNSWNDNDI I SYDCUNYNTA CYGRUDDON WYDIARM
DLKTDHNEQLIPEPEVSITSAHIDPDASYMAAVNSTLVPFSCLL PLAIGILQEGEFESLARRGLLFLACQGNCYVWNLTGGIGDEVTQ LIPKTKIP 6742 141 960 PLTLPFSSRARAGHTMNTSPGTVGSDPVILATAGYDHTVRFWQA HSGICTRTVQHQDSQVNALEVTPDRSMIAAAVQPVSLGYQHIRM YDLNSNNPNPIISYDGVNKNIASVGFHEDGRWMYTGGEDCTARI WDLRSRNLQCQRIFQVNAPINCVCLHPNQAELIVGDQSGAIHIW DLKTDHNEQLIPEPEVSITSAHIDPDASYMAAVNSTLVPFSCLL PLAIGILQEGEFESLARRGLLFLACQGNCYVWNLTGGIGDEVTQ LIPKTKIP ALRKCSDLEKAIATTALIFRNSSDSDGKLEKAIAKDLLQTQFRN FAEGQETKPKYREILSELDEHTENKLDFEDFMILLSITVMSDL LQNIR 6744 95 1343 RTPARNRCAGCEVLSRFSSPNKASSFALQSAGGGLPAVRALRRD RQKVSTVGYGMDEVQDQHBARLKELFDSFDTTGTGSLGQEELT DLCHMLSLEEVAPVLQCTLLQDNLLGRVHFDQFKEALILILISRT LSNEEHFQEPDCSLBAQPKYVRGGKRYGRRSLPEFQESVEEFPE VTVIEPLDEEARPSHIPAGDCSEHWKTORSEEYEAEGOLRFWNP				WDL RSPNI OCOPI FOUND DINGUGI HDNOS PROTECTION
PLAIGILQEGEFESLARRGLLFLACQGNCYVWNLTGGIGDEVTQ LIPKTKIP 6742 141 960 PUTLPFSSRARAGHTMNTSPGTVGSDPVILATAGYDHTVRFWQA HSGICTRTVQHQDSQVNALEVTPDRSMIAAAVQPVSLGYQHIRM YDLNSNNPNPIISYDGVNKNIASVGFHEDGRWMYTGGEDCTARI WDLRSRNLQCQRIFQVNAPINCVCLHPNQAELIVGDQSGAIHIW DLKTDHNEQLIPEPEVSITSAHIDPDASYMAAVNSTLVPFSCLL PLAIGILQEGEFESLARRGLLFLACQGNCYVWNLTGGIGDEVTQ LIPKTKIP 6743 1 412 MHSTQDKSLHLEGDPNPSAAPTSTCAPRKMPKRISISKQLASVK ALRKCSDLEKAIATTALIFRNSSDSDGKLEKAIAKDLLQTQFRN FAEGQETKPKYREILSELDEHTENKLDFEDFMILLSITVMSDL LQNIR 6744 95 1343 RTPARNRCAGCEVLSRFSSPNKASSFALQSAGGGLPAVRALRRD RQKVSTVGYGMDEVEQDQHEARLKELFPSFDTTGTGSLGQEELT DLCHMLSLEEVPLQQTLLQDNLLGRVHFDQFKEALILILISRT LSNEEHFQEPDCSLEAQPKYVRGGKRYGRRSLPEFQESVEEFPE VTVIEPLDEEARPSHIPAGDCSEHWKTORSEEYEARGOLRFWNP	1 1			DLKTDHNEOLIDEDEVSTTSAUTDDDAGVWAADDOW
6742 141 960 PLTLPFSSRARAGHTMNTSPGTVGSDPVILATAGYDHTVRFWQA HSGICTRTVQHQDSQVNALEVTPDRSMIAAAVQPVSLGYQHIRM YDLNSNNPNPIISYDGVNKNIASVGFHEDGRWMYTGGEDCTARI WDLRSRNLQCQRIFQVNAPINCVCLHPNQAELIVGDQSGAIHIW DLKTDHNEQLIPEPEVSITSAHIDPDASYMAAVNSTLVPFSCLL PLAIGILQEGEFESLARRGLLFLACQGNCYVWNLTGGIGDEVTQ LIPKTKIP MHSTQDKSLHLEGDPNPSAAPTSTCAPRKMPKRISISKQLASVK ALRKCSDLEKAIATTALIFRNSSDSDGKLEKAIAKDLLQTQFRN FAEGQETKPKYREILSELDEHTENKLDFEDFMILLLSITVMSDL LQNIR 6744 95 1343 RTPARNRCAGCEVLSRFSSPNKASSFALQSAGGLPAVRALRRD RQKVSTVGYGMDEVEQDQHEARLKELFDSFDTTGTGSLGQEELT DLCHMLSLEEVAPVLQQTLLQDNLLGRVHFDQFKEALILILISRT LSNEEHFQEPDCSLEAQPKYVRGGKRYGRRSLPEFQESVEEFPE VTVIEPLDEEARPSHIPAGDCSEHWKTORSEEYEARGOLRFWNP	1 1			PLAIGILOEGEFESI APPGILEI A COGNOVIENT TOGLODEUM
HSGICTRTVQHQDSQVNALEVTPDRSMIAAAVQPVSLGYQHIRM YDLNSNNPNPIISYDGVNKNIASVGFHEDGRWMYTGGEDCTARI WDLRSRNLQCQRIFQVNAPINCVCLHPNQAELIVGDQSGAIHIW DLKTDHNEQLIPEPEVSITSAHIDPDASYMAAVNSTLVPFSCLL PLAIGILQEGEFESLARRGLLFLACQGNCYVWNLTGGIGDEVTQ LIPKTKIP MHSTQDKSLHLEGDPNPSAAPTSTCAPRKMPKRISISKQLASVK ALRKCSDLEKAIATTALIFRNSSDSDGKLEKAIAKDLLQTQFRN FAEGQETKPKYREILSELDEHTENKLDFEDFMILLLSITVMSDL LQNIR 6744 95 1343 RTPARNRCAGCEVLSRFSSPNKASSFALQSAGGLPAVRALRRD RQKVSTVGYGMDEVEQDQHEARLKELFDSFDTTGTGSLGQEELT DLCHMLSLEEVAVLQQTLLQDNLLGRVHFDQFKEALILILISRT LSNEEHFQEPDCSLEAQPKYVRGGKRYGRRSLPEFQESVEEFPE VTVIEPLDEEARPSHIPAGDCSEHWKTORSEEYEARGOLRFWNP				LIPKTKIP
HSGICTRTVQHQDSQVNALEVTPDRSMIAAAVQPVSLGYQHIRM YDLNSNNPNPIISYDGVNKNIASVGFHEDGRWMYTGGEDCTARI WDLRSRNLQCQRIFQVNAPINCVCLHPNQAELIVGDQSGAIHIW DLKTDHNEQLIPEPEVSITSAHIDPDASYMAAVNSTLVPFSCLL PLAIGILQEGEFESLARRGLIFLACQGNCYVWNLTGGIGDEVTQ LIPKTKIP MHSTQDKSLHLEGDPNPSAAPTSTCAPRKMPKRISISKQLASVK ALRKCSDLEKAIATTALIFRNSSDSDGKLEKAIAKDLLQTQFRN FAEGQETKPKYREILSELDEHTENKLDFEDFMILLSITVMSDL LQNIR 6744 95 1343 RTPARNRCAGCEVLSRFSSPNKASSFALQSAGGGLPAVRALRRD RQKVSTVGYGMDEVEQDQHEARLKELFDSFDTTGTGSLGQEELT DLCHMLSLEEVAPVLQQTLLQDNLLGRVHFDQFKEALILLISRT LSNEEHFQEPDCSLBAQPKYVRGGKRYGRRSLPEFQESVEEFPE VTVIEPLDEEARPSHIPAGDCSEHWKTORSEEYEARGOLRFWNP	6742	141	960	
#DLNSNNPPPIISYDGVNKNIASVGFHEDGRWMYTGGEDCTARI #DLRSRNLQCQRIFQVNAPINCYCLHPNQAELIVGDQSGAIHIW DLKTDHNEQLIPEPEVSITSAHIDPDASYMAAVNSTLVPFSCLL PLAIGILGEGEFESLARRGLLFLACQGNCYVWNLTGGIGDEVTQ LIPKTKIP ##STQDKSLHLEGDPNPSAAPTSTCAPRKMPKRISISKQLASVK ALRKCSDLEKAIATTALIFRNSSDSDGKLEKAIAKDLLQTQFRN FAEGQETKPKYREILSELDEHTENKLDFEDFMILLSITVMSDL LQNIR ###STPARNRCAGCEVLSRFSSPNKASSFALQSAGGGLPAVRALRRD RQKVSTVGYGMDEVEQDQHBARLKELFDSFDTTGTGSLGQEELT DLCHMLSLEEVAPVLQQTLLQDNLLGRVHFDQFKEALILLILSRT LSNEEHFQEPDCSLBAQPKYVRGGKRYGRRSLPEFQESVEEFPE VTVIEPLDEEARPSHIPAGDCSEHWKTORSEEYEARGOLRFWNP			ļ	HSGICTRTVQHQDSOVNALEVTPDRSMTADAVODVGI GVOVTBY
## WDLRSRNLQCQRIFQVNAPINCVCLHPNQAELIVGDQSGAIHIW DLKTDHNEQLIPEPEVSITSAHIDPDASYMAAVNSTLVPFSCLL PLAIGILQEGEFESLARRGLLFLACQGNCYVWNLTGGIGDEVTQ LIPKTKIP 6743 1 412 MHSTQDKSLHLEGDPNPSAAPTSTCAPRKMPKRISISKQLASVK ALRKCSDLEKAIATTALIFRNSSDSDGKLEKAIAKDLLQTQFRN FAEGQETKPKYREILSELDEHTENKLDFEDFMILLLSITVMSDL LQNIR 6744 95 1343 RTPARNRCAGCEVLSRFSSPNKASSFALQSAGGGLPAVRALRRD RQKVSTVGYGMDEVEQDQHBARLKELFDSFDTTGTGSLGQEELT DLCHMLSLEEVAPVLQQTLLQDNLLGRVHFDQFKEALILILISRT LSNEEHFQEPDCSLBAQPKYVRGGKRYGRRSLPEFQESVEEFPE VTVIEPLDEEARPSHIPAGDCSEHWKTORSEEYEARGOLRFWNP	1 1	1		YDLNSNNPNPIISYDGVNKNIASVGFHEDGRWMYTGGEDCTARI
DLKTDHNEQLIPEPEVSITSAHIDPDASYMAAVNSTLVPFSCLL PLAIGILQEGEFESLARRGLIFLACQGNCYVWNLTGGIGDEVTQ LIPKTKIP 6743 1 412 MHSTQDKSLHLEGDPNPSAAPTSTCAPRKMPKRISISKQLASVK ALRKCSDLEKAIATTALIFRNSSDSDGKLEKAIAKDLLQTQFRN FAEGQETKPKYREILSELDEHTENKLDFEDFMILLLSITVMSDL LQNIR 6744 95 1343 RTPARNRCAGCEVLSRFSSPNKASSFALQSAGGGLPAVRALRRD RQKVSTVGYGMDEVLQDDHEARLKELFDSFDTTGTGSLGQEELT DLCHMLSLEEVPLQQTLLQDNLLGRVHFDQFKEALILILISRT LSNEEHFQEPDCSLEAQPKYVRGGKRYGRRSLPEFGESVEEFPE VTVIEPLDEEARPSHIPAGDCSEHWKTORSEEYEARGOLRFWNP		İ		WDLRSRNLQCQRIFOVNAPINCVCLHPNOAELIVGDOSGA THIW
PLAIGTLQEGEFESLARRGLIFLACQGNCYVWNLTGGIGDEVTQ LIPKTKIP MHSTQDKSLHLEGDPNPSAAPTSTCAPRKMPKRISISKQLASVK ALRKCSDLEKAIATTALIFRNSSDSDGKLEKAIAKDLLQTQFRN FAEGQETKPKYREILSELDEHTENKLDFEDFMILLLSITVMSDL LQNIR 6744 95 1343 RTPARNRCAGCEVLSRFSSPNKASSFALQSAGGGLPAVRALRRD RQKVSTVGYGMDEVEQDQHEARLKELFDSFDTTGTGSLGQEELT DLCHMLSLEEVAPVLQQTLLQDNLLGRVHFDQFKEALILILISRT LSNEEHFQEPDCSLEAQPKYVRGGKRYGRRSLPEFGESVEEFPE VTVIEPLDEEARPSHIPAGDCSEHWKTORSEEYEARGOLRFWNP	1 1			DLKTDHNEQLIPEPEVSITSAHIDPDASYMAAVNSTIADESCIT.
6743 1 412 MHSTQDKSLHLEGDPNPSAAPTSTCAPRKMPKRISISKQLASVK ALRKCSDLEKAIATTALIFRNSSDSDGKLEKAIAKDLLQTQFRN FAEGQETKPKYREILSELDEHTENKLDFEDFMILLLSITVMSDL LQNIR 6744 95 1343 RTPARNRCAGCEVLSRFSSPNKASSFALQSAGGGLPAVRALRRD RQKVSTVGYGMDEVEQDQHEARLKELFDSFDTTGTGSLGQEELT DLCHMLSLEEVAPVLQQTLLQDNLLGRVHFDQFKEALILILSRT LSNEEHFQEPDCSLEAQPKYVRGGKRYGRRSLPEFQESVEEFPE VTVIEPLDEEARPSHIPAGDCSEHWKTORSEEYEARGOLRFWNP]			PLAIGILQEGEFESLARRGLLFLACOGNCYVWNLTGGIGDEVTO
##STQURSTHLEGDPNPSAAPTSTCAPRKMPKRISISKQLASVK ALRKCSDLEKAIATTALIFRNSSDSDGKLEKAIAKDLLQTQFRN FAEGQETKPKYREILSELDEHTENKLDFEDFMILLLSITVMSDL LQNIR 6744 95 1343 RTPARNRCAGCEVLSRFSSPNKASSFALQSAGGGLPAVRALRRD RQKVSTVGYGMDEVEQDQHBARLKELFDSFDTTGTGSLGQEELT DLCHMLSLEEVAPVLQQTLLQDNLLGRVHFDQFKEALILILSRT LSNEEHPQEPDCSLBAQPKYVRGGKRYGRRSLPEFGESVEEFPE VTVIEPLDEEARPSHIPAGDCSEHWKTORSEEYEAEGOLRFWNP	F-6313-4			LIPKTKIP
ALRKCSDLEKAIATTALIFRNSSDSDGKLEKAIAKDLLQTQFRN FAEGQETKPKYREILSELDEHTENKLDFEDFMILLLSITVMSDL LQNIR 6744 95 1343 RTPARNRCAGCEVLSRFSSPNKASSFALQSAGGGLPAVRALRRD RQKVSTVGYGMDEVEQDQHEARLKELFDSFDTTGTGSLGQEELT DLCHMLSLEEVAPVLQQTLLQDNLLGRVHFDQFKEALILLLSRT LSNEEHFQEPDCSLEAQPKYVRGGKRYGRRSLPEFGESVEEFFE VTVIEPLDEEARPSHIPAGDCSEHWKTORSEEYEAEGOLRFWNP	0/43	1	412	MHSTQDKSLHLEGDPNPSAAPTSTCAPRKMPKRISISKOLASVV
FAEGGETKPKYREILSELDEHTENKLDFEDFMILLLSITVMSDL LQNIR 6744 95 1343 RTPARNRCAGCEVLSRFSSPNKASSFALQSAGGGLPAVRALRRD RQKVSTVGYGMDEVEQDQHEARLKELFDSFDTTGTGSLGQEELT DLCHMLSLEEVAPVLQQTLLQDNLLGRVHFDQFKEALILLISRT LSNEEHFQEPDCSLBAQPKYVRGGKRYGRRSLPEFQESVEEFPE VTVIEPLDEEARPSHIPAGDCSEHWKTORSEEYEARGOLRFWNP	j 1	1	Ì	ALRKCSDLEKAIATTALIFRNSSDSDGKLEKAIAKDIJOTOFPN
6744 95 1343 RTPARNRCAGCEVLSRFSSPNKASSFALQSAGGGLPAVRALRRD RQKVSTVGYGMDEVEQDQHEARLKELFDSFDTTGTGSLGQEELT DLCHMLSLEEVAPVLQQTLLQDNLLGRVHFDQFKEALILILSRT LSNEEHFQEPDCSLEAQPKYVRGGKRYGRRSLPEFQESVEEFPE VTVIEPLDEEARPSHIPAGDCSEHWKTORSEEYEARGOLRFWNP] [ŀ		FAEGQETKPKYREILSELDEHTENKLDFEDFMILLISITUMSDI.
RIPARNKCAGCEVLSRFSSBNKASSFALQSAGGGLPAVRALRRD RQKVSTVGYGMDEVEQDQHBARLKELFDSFDTTGTGSLGQEELT DLCHMLSLEEVAPVLQQTLLQDNLLGRVHFDQFKEALILILISRT LSNEEHFQEPDCSLBAQPKYVRGGKRYGRRSLPEFQESVEEFPE VTVIEPLDEEARPSHIPAGDCSEHWKTORSEEYEARGOLRFWNP	1			LONIR
RQKVSTVGYGMDEVEQDQHEARLKELFDSFDTTGTGSLGQEELT DLCHMLSLEEVAPVLQQTLLQDNLLGRVHFDQFKEALILILGRT LSNEEHFQEPDCSLEAQPKYVRGGKRYGRRSLPEFQESVEEFFE VTVIEPLDEEARPSHIPAGDCSEHWKTORSEEYEAEGOLRFWNP	0/44	95		RTPARNRCAGCEVLSRFSSPNKASSFALOSAGGGLPAVRAT.PDD
DLCHMLSLEEVAPVLQQTLLQDNLLGRVHFDQFKEALILILSRT LSNEEHFQEPDCSLBAQPKYVRGGKRYGRRSLPEFQESVEEFFE VTVIEPLDEEARPSHIPAGDCSEHWKTORSEEYEAEGOLRFWNP		į		RQKVSTVGYGMDEVEQDQHBARLKELFDSFDTTGTGSLGORELT
LSNEEHFQEPDCSLEAQPKYVRGGKRYGRRSLPEFQESVEEFPE VTVIEPLDEEARPSHIPAGDCSEHWKTORSEEYEAEGOLRFWNP				DLCHMLSLEEVAPVLQQTLLQDNLLGRVHFDOFKEALILILSRT
VTVIEPLDEEARPSHIPAGDCSEHWKTORSEEYEAEGOLRFWNP	} .			LSNEEHFQEPDCSLBAQPKYVRGGKRYGRRSLPEFOESVEEFPE
DDLNASQSGSSPPQDWIEEKLQEVCEDLGITRDGHLNRKKLVSI			1	VTVIEPLDEEARPSHIPAGDCSEHWKTORSEEYEAEGOLRFWNP
	<u> </u>			DDLNASQSGSSPPQDWIEEKLQEVCEDLGITRDGHLNRKKLVSI

SEQ	Predicted	Predicted end	I hmino paid company
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
-	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine.
i	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ļ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion.
	sequence		\=possible nucleotide insertion)
1			CEQYGLQNVDGEMLEEVFHNLDPDGTMSVEDFFYGLFKNGKSLT
İ			PSASTPYRQLKRHLSMQSFDESGRRTTTSSAMTSTIGFRVFSCL
1		l	DDGMGHASVERILDTWQEEGIENSQEILKALDFGLDGNINLTEL
6745	<u> </u>	588	TLALENELLVTKNSIHQACI
3713	1	388	TFRDQGWAQRRRWLLGCASWESWEAAIAAGPGLPSSTARQQNNP
			AAGTECFAAVWARGTAMGSVLSTDSGKSAPASATARALERRRDP
1	1		ELPVTSFDCAVCLEVLHQPVRTRCGHVFCRSCIATSLKNNKWTC PYCRAYLPSEGVPATDVAKRMKSEYKNCAECDTLVCLSEMRAHI
1			RTCQKYIDKYGPLQELEETA
6746	110	492	GATGAMAESAPARHRRKRRSTPLTSSTLPSQATEKSSYFQTTEI
1			SLWTVVAAIQAVEKKMESQAARLQSLEGRTGTAEKKLADCEKMA
J.			VEFGNQLEGKWAVLGTLLQEYGLLQRRLENVENLLRNRN
6747	247	484	EAVTFKDVAVVFTEEELGLLDLAQRKLYRDVMLENFRNLLSVGH
			QPFHRDTFHFLREEKFWMMDIATQREGNSVYAGVC
6748	201	665	MTTFKEAVTFKOVAVVFTEEBLGLLDPAQRKLYRDVMLENFRNL
			LSVGNQPFHQDTFHFLGKEKFWKMKTTSQREGNSGGKIOIEMET
			VPEAGPHEEWSCQQIWEQIASDLTRSQNSIRNSSQFFKEGDVPC
l			QIEARLSISXVQQXPYRCNECKQ
6749	95	719	RREVKGGDGVCPRARGSPQSQQFPSCAGGGEGLQQSGEALDGAM
			SAGGPCPAAAGGGPGGASCSVGAPGGVSMFRWLEVLEKEFDKAF
1 1			VDVDLLLGEIDPDQADITYEGRQKMTSLSSCFAQLCHKAQSVSQ
J I			INHKLEAQLVDLKSELTETQAEKVVLEKEVHDQLLQLHSIQLQL
6750	3	428	HAKTGQSADSGTIKAKLSGPSVEELERELKAN
		420	SCESRRPGAKWVWASGALPRDTTGLGSEQPSGDVAQSNRATMGT TAPGPIHLLELCDQKLMEFLCNMDNKDLVWLEEIQEEAERMFTR
1 1			EFSKEPELMPKTPSQKNRRKKRRISYVQDENRDPIRRRLSRRKS
			RSSQLSSRR
6751	152	1417	PTKATEMAGASVKVAVRVRPFNSREMSRDSKCIIQMSGSTTTIV
]		NPKQPKETPKSFSFDYSYWSHTSPEDINYASQKQVYRDIGEEML
i i			QHAFEGYNVCIFAYGQTGAGKSYTMMGKQEKDOOGIIPOLCEDI.
1 1	}		FSRINDTTNDNMSYSVEVSYMEIYCERVRDLLNPKNKGNLRVRE
1			HPLLGPYVEDLSKLAVTSYNDIQDLMDSGNKARTVAATNMNETS
1			SRSHAVFNIIFTQKRHDAETNITTEKVSKISLVDLAGSERADST
1 1		•	GAKGTRLKEGANINKSLTTLGKVISALAEMDSGPNKNKKKKKTD
l }			FIPYRDSVLTWLLRENLGGNSRTAMVAALSPADINYDETLSTLR
l l	j		YADRAKQIRCNAVINEDPNNKLIRELKDEVTRLRDLLYAQGLGD ITDMTNALVGMSPSSSLSALSSRNV
6752	24	1834	RNCVPPLGCYRSRVKFHSDIKMQYSHHCEHLLERLNKQREAGFL
			CDCTIVIGEFQFKAHRNVLASFSEYFGAIYRSTSENNVFLDQSQ
		ĺ	VKADGFQKLLEFIYTGTLNLDSWNVKEIHQAADYLKVEEVVTKC
		ļ	KIKMEDFAFIANPSSTEISSITGNIELNQQTCLLTLRDYNNREK
1			SEVSTDLIQANPKQGALAKKSSQTKKKKKAFNSPKTGQNKTVQY
]	}	}	PSDILENASVELFLDANKLPTPVVEQVAQINDNSELELTSVVEN
į <u> </u>			TFPAQDIVHTVTVKRKRGKSQPNCALKEHSMSNIASVKSPYEAE
' I			NSGEELDQRYSKAKPMCNTCGKVFSEASSLRRHMRIHKGVKPYV
	1	J	CHLCGKAFTQCNQLKTHVRTHTGEKPYKCELCDKGFAOKCOLVF
	1		HSRMHHGEEKPYKCDVCNLQFATSSNLKIHARKHSGEKPYVCDR
	[CGQRFAQASTLTYHVRRHTGEKPYVCDTCGKAFAVSSSLITHSR
·			KHTGEKPFICELCGNSYTDIKNLKKHKTKVHSGADKTLDSSAED
l		1	HTLSEQDSIQKSPLSETMDVKPSDMTLPLALPLGTEDHHMLLPV
6753		1305	TDTQSPTSDTLLRSTVNGYSEPQLIFLQQLY
	~	1305	VPSLPYPPQKVVAHTEFTTSSDSETANGIAKPDPVMPGGEEKAS
			PFGIKLRRTNYSLRFNCDQQAEQKKKKRHSSTGDSADAGPPAAG
	i		SARGEKEMEGVALKHGPSLPQERKQAPSTRRDSAEPSSSRSVPV AHPGPPPASSQTPAPEHDKAANKMPLAQKPALAPKPTSQTPPAS
1			ARPHPPPASS(YFDADEHNKAANKMOLACKBALABKBCCCCCCC

	SEQ	Predicted	Predicted end	I amino
	ID	beginning	nucleotide	Amino acid segment containing signal peptide
	NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
- 1		location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
J		corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
		to first	amino acid	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
ŀ		amino acid	residue of	S=Serine, T=Threonine, V=Valine,
j		residue of	amino acid	W-Truntonhan V Tonochu
		amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
- 1		sequence		\=possible nucleotide deletion,
Ī				PLSKLSRPYLVELLSRRAGRPDPEPSEPSKEDQESSDRRPPSPP
ł				GPEERKGQKRDEEEEATERKPASPPLPATQQEKPSQTPEAGRKE
١				KPMLQSRHSLDGSKLTEKVETAQPLWITLALQKQKGFREQQATR
ł				EERKQAREAKQAEKLSKENVSVSVQPGSSSVSRAGSLHKSTALP
- 1				EEKRPETAVSRLERREQLKKANTLPTSVTVEISYSSPAAPLVKE
L				VSKRFSSPDDAPVSSEPAWLALAKRKAKAWSDCPLIIK
	6754	2	413	FVRRRRRLGGPEVNTMSSLHKSRIADFQDVLKEPSIALEKLRE
٠	·			LSFSGIPCEGGLRCLCWKILLNYLPLERASWTSILAKQRELYAQ
- 1				PLREMIIQPGIAKANMGVSREDVTFEDHPLNPNPDSRWNTYFKD
Ļ				NEVLL
-1	6755	298	1343	PGLQLQVALEADWFLDMPGGRRGPSRQQLSRSALPSLQTLVGGG
				CGNGTGLRNRNGSAIGLPVPPITALITPGPVRHCOTPDLDVDGG
	ŀ			LLFEFLFFIYLLVALFIQYINIYKTVWWYPYNHPASCTGLMENT
	ļ			IDYHLAAFITVMLARRLVWALISEATKAGAASMIHYMVI.TSADI.
				VLLTLCGWVLCWTLVNLFRSHSVLNLLFLGYPFGVYVDLCCPHO (
	1			DSRAHLLLTDYNYVVOHEAVEESASTVGGLAKSKDELGLILEGI
ı				KEQFNNATPIPTHSCPLSPDLIRNEVECLKADFNHRIKEVI.FNG
\vdash	6756	180		LFSAYYVAFLPLCFVKVSGYLTFMCFI.DI.CVNVTNMUETU
	1	. 100	754	IERALGSLPLS PVSWGSLRTLKYQQQPLRPKVLLCQTRVQCHD
	1			LRSLQPQPPGLKQSFCLRVLGLQTGATTPGLRDLTCKELILTE
	.			REAQKRKKRKEKESGMALTQGPLTFRDVAIEFSQEEWKSLDPVQ
1	- 1			KALYWDVMLENYRNLVFLGKDNFALEVKICPRVFLYFLCCLSWE PFHYLTETEALLTHK
Г	6757	2	459	NSRVEAPEAHSRESQGSDAMRKHLSWWWLATVCMLLFSHLSAVQ
1				TRGIKHRIKWNRKALPSTAQITEAQVAENRPGAFIKQGRKLDID
ı		ŀ		FGAEGNRYYEANYWQFPDGIHYNGCSEANVTKEAFVTGCINATQ
L				AANQGEFQKPDNKLHQQVLW
	6758	1	1008	ASGPELPGRRFRDRAPWLPARLLRGVLAVWVSLSALGPGSFCRR
	1			RVPSLAQLGHSEAAPSPDDVRWSRVPDRCPEERDRAWPPPPPPS
ı	1	·		LPPSFRRNMANNSPALTGNSOPOHOAAAAAAOOOOOCCCCC TV
1	,			PAVSGKQGNVLPLWGNEKTMNLNPMILTNILSSPVFKVOLVELV
1	1	1		TYHEVVDEIYFKVTHVEPWEKGSRKTAGOTGMCCGVRCVCTCCT
1			J	VSTAFCLLYKLFTLKLTRKQVMGLITHTDSPYIRALGEMVTDVT
1	1	.	ļ	QPPTDLWDWFESFLDDEEDLDVKAGGGCVMTIGEMIRGETTKI.F
\vdash	6759	<u> </u>		WFSTLFPRIPVPVQKNIDQQIKTRPRKI
1		*	513	RKHNFHSLDGTSTRAFHPQTGLPLLSSPVPQRKTQSGCFDLDSS
1	.]			DLHLKSFSSRSPRPCLNIEDDPDIHEKPFLSSSAPPITSLSLIG
1			ľ	NFEESVLNYRFDPLGIVDGFTAEVGASGAFCPTHLTLDVEVGEV
	6760	239	606	SVSDDNAPSPYMGVITLESLGKRGYRVPPSGTIQVVCVL
	1		000	VLSKKKGLSAEEKRTRMMEIFSETKDVFQLKDLEKIAPKEKGIT
	- 1	1		AMSVKEVLQSLVDDGMVDCERIGTSNYYWAFPSKALHARKHKLE
\vdash	6761	29	1733	VLESQLSEGSQKHASLQKSIEKAKIGRCETEERT
		1	55	ERTLRGLREVAAPSDVADAAVSRRGRCCCCHCTQTQVAQDCPS SSSSVQRCELSLFQSLHTMTSKKLVNSVAGCADDALAGLVACNP
1				NLQLLQGHRVALRSDLDSLKGRVALLSGGGSGHEPAHAGFIGKG
1			1	MITGVIAGAVETEDAVCCII AA IDAVIAGA GEGGGGGGEPAHAGFIGKG
1	- 1		ł	MLTGVIAGAVFTSPAVGSILAAIRAVAQAGTVGTLLIVKNYTGD RLNFGLAREQARAEGIPVEMVVIGDDSAFTVLKKAGRRGLCGTV
l		İ		LIHKVAGALAEAGVGLEEIAKQVNVVTKAMGTLGVSLSSCSVPG
1	1			SKPTFELSADEVELGLGIHGEAGVRRIKMATADEIVKLMLDHMT
1	J		. 1	NTTNASHVPVQPGSSVVMMVNNLGGLSFLELGIIADATVRSLEG
ı	i		· [RGVKIARALVGTFMSALEMPGISLTLLLVDEPLLKLIDAETTAA
	- 1	f	1.	AWPNVAAVSITGRKRSRVAPAEPQEAPDSTAAGGSASKRMALVL
			ľ	ERVCSTLLGLEEHLNALDRAAGDGDCGTTHSRAARATOEWLYEG
	j		1	PPPASPAQLLSKLSVLLLEKMGGSSGALYGLFLTAAAOPI.KAKT
				SLPAWSAAMDAGLEAMQKYGKAAPGDRTMLDSLWAAGQBL

WO 01/53312

PCT/US00/34263

SEQ	1 Dec 32 - E - 3		
ID	Predicted beginning	Predicted end	Amino acid segment containing signal peptide
NO:	nucleotide	nucleotide location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
""	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	HaHistidine, I=Isoleucine, K=Lysine,
}	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
1	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
İ	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	bequence	Codon, /=possible nucleotide deletion,
6762	3	613	\=possible nucleotide insertion)
	-	""	ASTISWRLCVAGAEARRPVPVAGERAGGGAMWFMYLLSWLSLFI
1			QVAFITLAVAAGLYYLAELIEBYTVATSRIIKYMIWFSTAVLIG LYVFERFPTSMIGVGLFTNLVYFGLLQTFPFIMLTSPNFILSCG
	}	Ĭ	LVVVNHYLAFQFFAEEYYPFSEVLAYFTFCLWIIPFAFFVSLSA
1		}	GENVLPSTMQPGDDVVSNYFTKGKRGK
6763	2	760	SGPDFPGRRFRGCCCVRPPAGAGMELGGHWDMNSAPRLVSETAE
l		1	RKQEQKTGTEAEAADSGAVGARRFLLCLYLGGFLDLFGVSMVVP
1			LLSLHVKSLGASPTVAGIVGSSYGILQLFSSTLVGCWSDVVGRR
			SSLLACILLSALGYLLLGAATNVFLFVLARVPAGIFKHTLSISK
1			ALLSDVVPEKERPLVIGHFNTASGVGFILGPVVGGYLTELEDGF
1	1		YLTAFICFLVFILNAGLVWFFPRREAKPGSTE
6764	80	438	LKKMDTMMLSVRNLFEQLVRRVEILSEGNEVQFIQLAKDFEDFR
1			KKWQRTDHELGKYKDLLMKAETERSALDVKLKHARNQVDVEIKR
1			RQRAEADCEKLERQIQLIREMLMCDTSGSIQ
6765	3	550	ARYSRVDHFCRRCCRAVARAPRFLLQFPSGPSRHFLAACVARWL
Į.	}		RGSVLVSEALSGSAMDGIVTEVAVGVKRGSDELLSGSVLSSPNS
			NMSSMVVTANGNDSKKFKGEDKMDGAPSRVLHIRKLPGEVTETE
			VIALGLPFGKVTNILMLKGKNQAFLELATEEAAITNGNYYSAVT
			PHLRNO
6766	1	1287	EGGSFKASLTWLWPLGEMKLHCEVEVISRHLPALGLRNRGKGVR
			AVLSLCQQTSRSQPPVRAFLLISTLKDKRGTRYELRENIEQFFT
			KFVDEGKATVRLKEPPVDICLSKANSSSLKGFLSAMRLAHRGCN
J I			VDTPVSTLTPVKTSEFENFKTKMVITSKKDYPLSKNFPYSLEHI.
1	-		QTSYCGLVRVDMRMLCLKSLRKLDLSHNHIKKLPATIGDLTHLO
		•	ELNLNDNHLESFSVALCHSTLQKSLWSLDLSKNKIKALDVOFCO
i I	[LOBLKNLKLDDNELIOFPCKIGOLINLRFLSAARNKLPFLDSEF
1			RNLSLEYLDLFGNTFEQPKVLPVIKLQAPLTLLESSARTILHNR
1 [i		IPYGSHIIPFHLCQDLDTAKICVCGRFCLNSFIQGTTTMNLHSV
6767	336	0.0	AHTVVLVDNLGGTEAPIISYFCSLGCYVNSSDI
	330	919	APMICLCSSDLQFRYKEAFLRDRGLQIGYCSVDDDPRMKHFLNV
			GRLQSDNEYKKDFAKSRSQFHSSTDQPGLLQAKRSQQLASDVHY
			ROPLPOPTCDPEOLGLRHAQKAHQLQSDVKYKSDLNLTRGVGWT
i	-		PPGSYKVEMARRAAELANARGLGLQGAYRGAEAVEAGDHQSGEV NPDATEILHVKKKKALLL
6768		363	
	_	303	PGSTISCYLLSEGSLPLCMQVACGEEKHRAPTMKTLRARFKKTE
	İ		LRLSPTDLGSCPPCGPCPIPKPAARGRRQSQDWGKSDERLLQAV ENNDAPRVAALIARKGLVPTKLDPEGKSAFHL
6769	284	396	MSTPDFSTAENNQELANEVSCLKAMLTLMLQAMGQAD
6770	1	397	QRNYQVIWSSTMAKLHDYYKDEVVKKLMTEFNYNSVMQVPRVEK
1		·	ITLNMGVGEAIADKKLLDNAAADLAAISGQKPLITKARKSVAGF
1		· i	KIRQGYPIGCKVTLRGERMWEFFERLITIAVPRIRDFRGLSAKS
6771	3	378	APAGTLAMTGKSVKDVDRYQAVLANLLLEEDNKFCADCQSKGPR
			WASWNIGVFICIRCAGIHRNLGVHISRVKSVNLDQWTQEQIQCM
			QEMGNGKANRLYEAYLPETFRRPQIDPYLFWSNLEG
6772	1	1400	AAAFLQCMTVNGFINTVITSL\ERRYDLHSYQSGLIASSYDIAA
1			CLCLTFVSYFGGGG\HKPRWLGWGR\VLMGTGSLVFALPHFTAG
Î		j	P++GWKLDAGVRTCPANPR\PVCAG\HTSGLSRYQLVFMLGQFL
- 1	ľ		HGVGATPLYTLGVTYLDENVKSSCSPIYIAIFYTAAILGPAAGY
	1		LIGGALLNIYTEMGRRTELTTESPLWVGAWWVGFLGSGAAAFFT
1			AVPILGYPRQLPGSQRYAVMRAAEMHQLKDSSRGEASNPDFGKT
1		ļ	IRDLPLSIWLLLKNPTFILLCLAGATEATLITGMSTFSPKFLES
1		Ì	QFSLSASEAATLFGYLVVPAGGGGTFLGGFFVNKLRLRGSAVIK
İ		ļ	FCLFCTVVSLLGILVFSLHCPSVPMAGVTASYGGSLLPEGHLNL
- 1		i i	TAPCNAACSCOPEHYSPVCGSDGLMYFSLCHAGCPAATETNVDG
			QKVYRDCSCIPQNLSSGFGHATAGKCTST
			The state of the s

	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
- 1	ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
		location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
- 1		corresponding	to first	I-Lauging M-Mothismine, K-Lysine,
		to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
- 1		amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
Į		residue of	amino acid	S=Serine, T=Threonine, V=Valine,
i		amino acid	1	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
		sequence	sequence	Codon, /=possible nucleotide deletion,
\vdash	6773			\=possible nucleotide insertion)
- 1	0113] 1	630	PWEAPKEHKYKAEEHTVVLTVTGEPCHFPFQYHRQLYHKCTHKG
		l .	ľ	RPGPQPWCATTPNFDODORWGYCLEPKKVKDHCSYUSDCOVCCT
ŀ			i	CVNMPSGPHCLCPQHLTGNHCOKEKCFEPOLLRFPHKNETWYDT
		!		EQAAVARCQCKGPDAHCORLASOACRTNPC1,HCGPC1,FVFGHP1.
<u> </u>	200			CHCPVGYTGPFCDVGE*GSGASRRPAPRWDGLAR
	6774	146	389	LTELSDQQYFLFFILSS/WVPTFLSMDVDGRVTKADSFSKTTSS
L.				GLRIGFLTGPKPLIERVILHIQVSTLHPSTFNQLMISQ
'	6775	104	614	TCPSQLRVLTARGGRRAPSPQLWTLVLALIEEKWRSHRILRMNS
-				GRPETMENLPALYTIFQGEVAMVTDYGAFIKIPGCRKQGLVHRT
				HMSSCRVDKPSEIVDVGDKVWVKLIGREMKNDRIKVSLSMKVVN
L				QGTGKDLDPNNV\SLSKKRGGGDPSRITLGRRSPLRLS
[•	6776	3	1108	HERHERHEGALSQDALLRISIPLDSNMRPEKCRRFVHPQWQLLH
Į				LNGTFPNTSDADMEPCVDGWVYDRISFSSTIVTEWDLVCDSQSL
ı				TSVAKFVFMAGMMVGGILGGHLSDRFGRRFVLRWCYLQVAIVGT
	į			CAALAPTFLIYCSLRFLSGIAAMSLITHTIMLIAEWATHRFQAM
1				GITLGMCPSGIAFMTLAGLAFAIRDWHILQLVVSVPYFVIFLTS
1	ł			SWILECARM TINNINGER WILDLAND TO THE TOTAL TO THE TOTAL
1				SWLLESARWLIINNKPEEGLKELRKAAHRSGMKNARDTLTLEIL
				KSTMKKELEAAQKKKPFLGERLHMPNICKRISLLPFTKFANFMA
1				YFGLNLHG/LKHLGNNVFLLQTLFGAV/TPPGQLVLHLGHWGSG
1	5777	779	63	RVSSRGRVNCLGLFVLQVW
			63	CFFHGPAWRDCEVRATFAKKQGQSGIISCIAFSPAQPLYACGSY
1	- 1			GRSLGLYAWDDGSPLALLGGHQGGITHLCFHPDGNRFFSGARKD
1			'	ABLLCWDLRQSGYPLWSLGREVTTNQRIYFDLDPTGQFLVSGST
	1			SGAVSVWDTDGPGNDGKPEPVLSFLPQKDCTNGVSLHPSLPLLG
1 .	i			HCLPVSVCFLSPTESGGRRRGAGPSLGSPRRHVHLECRLQLWWC
-6	778	311	005	GGGARLQHP**SPRARKGR
`		7.1	805	IQSITDESRGSIRRKNPANTRLRLNVP\EBTAGDSE/ERSPEEE
	ĺ	i	i	VQADPRIRSASPKCPTSSPFPKGRSPEGEGET\DPEKVHFHPGP
]	!			KDKSVAEKN\KGP\SPVSSEGIKDFFSMKPEWENLNQSNVRRMH
1 - 6	779	2		T\AVRLNEVIVKKSRDAKLVLLNMPGPPRNRNGDENY
*	'''	-	535	RALRROPRLLAANGIEPESMAISEPIKGSRKPCVNKEELALKKP
	- 1	í		MAKCAWKGPREPPQDARAEAESPGGASESDQDGGHESPPKKKAV
1	- 1	i		AWVSAKNPAPMRKKKKVSLGPVSYVLVDSEDGRKKPVMPKKGPG
1	- 1	į	j	SRREASDQKAPRGQQPAEATASTSRGPKAKPEGSPRRATNESRK
 -	780			V
۱ °	, 90	3	403	HEVNDNKPEININLMSPGKEEISYIFEGDPIDTFVALVRVQDKD
1	ľ	į	1	SGLNGEIVCKLHGHGHFKLQKTYENNYLILTNATLDREKRSEVS
l	- 1	.]		LTVIAEDRGTPSLSTVKHFTVQINDINDNPPHFQRSRYEFVISE
	781			K
"	ADT [1	1269	APTRPVFPTLQDLSSSKEPSNSLNLPHSNELCSSLVHPBLSEVS
l		- 1	1200	THE TELEPHONOMIC ON SHARP STANDED COSTANDE COSTANDED COSTANDED COSTANDED COSTANDED COSTANDED COSTANDED COS
	1	_		SNVAPSIPPVMSRPVSSSSISTPLPPNOITVFVTSNPTTTSANT
l		_		SNVAPSIPPVMSRPVSSSSISTPLPPNQITVFVTSNPITTSANT SAALPTHLQSALMSTVVTMPNAGSKVMVSRGOSAAOSNAPDORT
				SNVAPSIPPVMSRPVSSSSISTPLPPNQITVFVTSNPITTSANT SAALPTHLQSALMSTVVTMPNAGSKVMVSEGQSAAQSNARPQFI TPVFINSSSIIQVMKGSQPSTIPAAPLTTNSGLMPPSVAVVGDI
				SNVAPSIPPVMSRPVSSSSISTPLPPNQITVFVTSNPITTSANT SAALPTHLQSALMSTVVTMPNAGSKVMVSEGQSAAQSNARPQFI TPVFINSSIIQVMKGSQPSTIPAAPLTTNSGLMPPSVAVVGPL HIPQNIKFSSAPVPPNALSSPAPNIOTGRPLVLSSRATPVOLD
				SNVAPSIPPVMSRPVSSSSISTPLPPNQITVFVTSNPITTSANT SAALPTHLQSALMSTVVTMPNAGSKVMVSEQQSAAQSNARPQFI TPVFINSSSIIQVMKGSQPSTIPAAPLITINSGLMPPSVAVVGPL HIPQNIKFSSAPVPPNALSSSPAPNIQTGRPLVLSSRATPVQLP SPPCTSSPVVPSHPPVQQVKELNPDEASPOWNTSADONTLPSSO
				SNVAPSIPPVMSRPVSSSSISTPLPPNQITVFVTSNPITTSANT SAALPTHLQSALMSTVVTMPNAGSKVMVSEGQSAAQSNARPQFI TPVFINSSSIIQVMKGSQPSTIPAAPLTTNSGLMPPSVAVVGPL HIPQNIKFSSAPVPPNALSSPAPNIQTGRPLVLSSRATPVQLP SPPCTSSPVVBSHPPVQQVKELNPDEASPQVNTSADQNTLPSSQ STTMVSPLLTNSPGSSGNRRSPVSSSKGKGKVDKIGOILLTKAC
				SNVAPSIPPVMSRPVSSSSISTPLPPNQITVFVTSNPITTSANT SAALPTHLQSALMSTVVTMPNAGSKVMVSEGQSAAQSNARPQFI TPVFINSSSIIQVMKGSQPSTIPAAPLTTNSGLMPPSVAVVGPL HIPQNIKFSSAPVPPNALSSSPAPNIQTGRPLVLSSRATPVQLP SPPCTSSPVVPSHPPVQQVKELNPDEASPQVNTSADQNTLPSSQ STTMVSPLLTMSPGSGMRRSPVSSSKGKGKVDKIGQILLTKAC KKVTGSLEKGEEQYGADGETEGQGLDTTAPGLMGTEOLSTFLDS
				SNVAPSIPPVMSRPVSSSSISTPLPPNQITVFVTSNPITTSANT SAALPTHLQSALMSTVVTMPNAGSKVMVSEGQSAAQSNARPQFI TPVFINSSSIIQVMKGSQPSTIPAAPLTTNSGLMPPSVAVVGPL HIPQNIKFSSAPVPPNALSSSPAPNIQTGRPLVLSSRATPVQLP SPPCTSSPVVPSHPPVQQVKELNPDEASPQVNTSADQNTLPSSQ STTMVSPLLTMSPGSGMRRSPVSSSKGKGKVDKIGQILLTKAC KKVTGSLEKGEEQYGADGETEGQGLDTTAPGLMGTEOLSTFLDS
				SNVAPSIPPVMSRPVSSSSISTPLPPNQITVFVTSNPITTSANT SAALPTHLQSALMSTVVTMPNAGSKVMVSEGQSAAQSNARPQFI TPVFINSSSIIQVMKGSQPSTIPAAPLTTINSGLMPPSVAVVGPL HIPQNIKFSSAPVPPNALSSSPAPNIQTGRPLVLSSRATFVQLP SPPCTSSPVVPSHPPVQQVKELNPDEASPQVNTSADQNTLPSSQ STTMVSPLLTMSPGSGNRRSPVSSSKGKGKVDKIGQILLTKAC KKVTGSLEKGEEQYGADGETEGQGLDTTAPGLMGTEQLSTELDS KTPTPPAPTLLKMTSSPVGPGTASAGPSLPGGALPTSVRSIVTT
67	782	3		SNVAPSIPPVMSRPVSSSSISTPLPPNQITVFVTSNPITTSANT SAALPTHLQSALMSTVVTMPNAGSKVMVSEGQSAAQSNARPQFI TPVFINSSSIIQVMKGSQPSTIPAAPLITINSGLMPPSVAVVGPL HIPQNIKFSSAPVPPNALSSPAPNIQTGRPLVLSSRATPVQLP SPPCTSSPVVPSHPPVQQVKELNPPDEASPQVNTSADQNTLPSSQ STTMVSPLLTNSPGSSGNRRSPVSSSKGKVDKIGQILLTKAC KKVTGSLEKGEQYGADGETEGQGLDTTAPGLMGTEQLSTELDS KTPTPPAPTLLKMTSSPVGPGTASAGPSLPGGALPTSVRSIVTT LVPSELISAVPTTKSNHGGIASESLAG
67	782		1327	SNVAPSIPPVMSRPVSSSSISTPLPPNQITVFVTSNPITTSANT SAALPTHLQSALMSTVVTMPNAGSKVMVSEGQSAAQSNARPQFI TPVFINSSIIQVMKGSQPSTIPAAPLTTNSGLMPPSVAVVGPL HIPONIKFSSAPVPPNALSSPAPNIQTGRPLVLSSRATPVQLP SPPCTSSPVVPSHPPVQQVKELNPDEASPQVMTSADQNTLPSSQ STTMVSPLLTNSPGSSGNRRSPVSSSKGKGKVDKIGQILLTKAC KKVTGSLEKGEEQYGADGETEGQGLDTTAPGLMGTEQLSTELDS KKPTGSLEKGEEQYGADGETEGGGBDTTAPGLMGTEQLSTELDS LVPSELISAVPTTKSNHGGIASESLAG RKPTVIRIPAKPGKCLHEDPOSPPPLPAEKPIGNTPSTVSGKLG
67	782		1327	SNVAPSIPPVMSRPVSSSSISTPLPPNQITVFVTSNPITTSANT SAALPTHLQSALMSTVVIMPNAGSKVMVSEQQSAAQSNARPQFI TPVFINSSIIQVMKGSQPSTIPAAPLITINSGLMPPSVAVVGPL HIPQNIKFSSAPVPPNALSSSPAPNIQTGRPLVLSSRATPVQLP SPPCTSSPVVPSHPPVQQVKELNPDEASPQVNTSADQNTLPSSQ STTMVSPLLTNSPGSSGNRRSPVSSSKGKGKVDKIGQILLTKAC KKVTGSLEKGEEQYGADGETEGQGLDTTAPGLMGTEQLSTELDS KTPTPPAPTLLKMTSSPVGPGTASAGPSLPGGALPTSVRSIVTT LVPSELISAVPTTKSNHGGIASESLAG RKPTVIRIPAKPGKCLHEDPQSPPPLPAEKPIGNTFSTVSGKLS NVERTRNLESNHPGOTGGFVRVPPRLPPRPVMGKTIPTOOPPTK
67	782		1327	SNVAPSIPPVMSRPVSSSSISTPLPPNQITVFVTSNPITTSANT SAALPTHLQSALMSTVVTMPNAGSKVMVSEQQSAAQSNARPQFI TPVFINSSIIQVMKGSQPSTIPAAPLITINSGLMPPSVAVVGPL HIPQNIKFSSAPVPPNALSSSPAPNIQTGRPLVLSSRATPVQLP SPPCTSSPVVPSHPPVQQVKELNPDEASPQVMTSADQNTLPSSQ STTMVSPLLTNSPGSSGNRRSPVSSSKGKGKVDKIGQILLTKAC KKVTGSLEKGEEQYGADGETEGQGLDTTAPGLMGTEQLSTELDS KTPTPPAPTLLKMTSSPVGPGTASAGPSLPGGALPTSVRSIVTT LVPSELISAVPTTKSNHGGIASESLAG RKPTVIRIPAKPGKCLHEDPQSPPPLPAEKPIGNTFSTVSGKLS NVERTRNLESNHPGQTGGFVRVPPRLPPRPVNGKTIPTQQPPTK VPPERPPPPPKLSATRSNKKLPFTRSSSDMDLOKKOSNIATGLS
67	782		1327	SNVAPSIPPVMSRPVSSSSISTPLPPNQITVFVTSNPITTSANT SAALPTHLQSALMSTVVTMPNAGSKVMVSEQQSAAQSNARPQFI TPVFINSSSIIQVMKGSQPSTIPAAPLITINSGLMPPSVAVVGPL HIPONIKFSSAPVPPNALSSSPAPNIQTGRPLVLSSRATPVQLP SPPCTSSPVVBSHPPVQQVKELNPDEASPQVNTSADQNTLPSSQ STTMVSPLLTNSPGSSGNRRSPVSSKGKGKVDKIGQILLTKAC KKVTGSLEKGEEQYGADGETEGQGLDTTAPGLMGTEQLSTELDS KTPTPPAPTLLKMTSSPVGPGTASAGPSLPGGALPTSVRSIVTT LVPSELISAVPTTKSNHGGIASESLAG RKPTVIRIPAKPGKCLHEDPQSPPPLPAEKPIGNTFSTVSGKLS NVERTRNLESNHPGQTGGFVZVPPRLPRPVNGKTIPTQQPPTK VPPERPPPPKLSATRRSNKKLPFNRSSSDMDLQKKQSNLATGLS KAKSQVFKNQDPVLPPRPKPGHPLYSKYMLSVPHGTAMRDIVSO
67	782		1327	SNVAPSIPPVMSRPVSSSSISTPLPPNQITVFVTSNPITTSANT SAALPTHLQSALMSTVVTMPNAGSKVMVSEQQSAAQSNARPQFI TPVFINSSIIQVMKGSQPSTIPAAPLTTNSGLMPPSVAVVGPL HIPQNIKFSSAPVPPNALSSSPAPNIQTGRPLVLSSRATPVQLP SPPCTSSPVVPSHPPVQQVKELNPDEASPQVNTSADQNTLPSSQ STTMVSPLLTNSPGSSGNRRSPVSSSKGKGKVDKIGQILLTKAC KKVTGSLEKGEEQYGADGETEGQGLDTTAPGLMGTEQLSTELDS KTPTPPAPTLLKMTSSPVGPGTASAGPSLPGGALPTSVRSIVTT LVPSELISAVPTTKSNHGGIASESLAG RKPTVIRIPAKPGKCLHEDPQSPPPLPAEKPIGNTFSTVSGKLS NVERTRNLESNHPGQTGGFVRVPPRLPPRPVNGKTIPTQQPPTK VPPERPPPPKLSATRRSNKKLPFRRSSSDMDLOKKOSNLATGLS

SEQ	Predicted	Predicted end	Amino soid compat
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
i i	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ŀ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
j	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
}	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
		 	DDLNLTSGEIVYLLEKIDTDWYRGNCRNQIGIFPANYVKVIIDI
j	1	1	PEGGNGKRECVSSHCVKGSRCVARFEYIGEQKDELSFSEGEIII
	1		LKEYVNEEWARGEVRGRTGIFPLNFVEPVEDYPTSGANVLSTKV
1.		ł	DI.KTKKEDGGENGOINGI DA BUGERA MODERA DE COMO
			PLKTKKEDSGSNSQVNSLPAEWCEALHSFTAETSDDLSFKRGDR
6783	3	1750	
	-	1/30	SYHHHAQQSAASPNLTASQKTVTTTSMITTKTLPLVLKAATA
1	1		TMPASVVGQRPTIAMVTAINSQKAVLSTDVQNTPVNLQTSSKVT
J		ĺ	GPGAEAVQIVAKNTVTLQVQATPPQPIKVPQFIPPPRLTPRPNF
1			LPQVRPKPVAQNNIPIAPAPPPMLAAPQLIQRPVMLTKFTPTTL
			PTSQNSIHPVRVVNGQTATIAKTFPMAQLTSIVIATPGTRLAGP
ľ			QTVQLSKPSLBKQTVKSHTETDEKQTESRTITPPAAPKPKREEN
			PQKLAFMVSLGLVTHDHLEEIQSKRQERKRRTTANPVYSGAVFE
1	1		PERKKSAVTYLNSTMHPGTRKRGRPPKYNAVLGFGALTPTSPQS
i			SHPDSPENEKTETTFTFPAPVQPVSLPSPTSTDGDIHEDFCSVC
			RKSGQLLMCDTCSRVYHLDCLDPPLKTIPKGMWICPRCQDQMLK
	i		KEEAIPWPGTLAIVHSYIAYKAAKEEEKQKLLKWSSDLKQEREQ
1	}		LEQKVKQLSNSISKCMEMKNTILARQKEMHSSLEKVKQLIRLIH
	i .	•	GIDLSKPVDSEATVGAISNGPDCTPPANAATSTPAPSPSSQSCT
6774			ANCNOGEETK
6784	3	1750	SYHHHHAQQSAAASPNLTASQKTVTTTSMLTTKTLPLVLKAATA
1	1		TMPASVVGQRPTIAMVTAINSQKAVLSTDVONTPVNLOTSSKVT
ł			GPGAEAVQIVAKNTVTLQVQATPPQPIKVPOFIPPPRLTPRPNF
}	1		LPQVRPKPVAQNNIPIAPAPPPMLAAPQLIQRPVMLTKFTPTTI.
Ì	1		PTSQNSIHPVRVVNGQTATIAKTFPMAQLTSIVIATPGTRLAGP
	1		QTVQLSKPSLEKQTVKSHTETDEKOTESRTITPPAAPKPKREEN
	l		PQKLAFMVSLGLVTHDHLBEIQSKRQERKRRTTANPVYSGAVPE
1	j j		PERKKSAVTYLNSTMHPGTRKRGRPPKYNAVLGFGALTPTSPQS
			SHPDSPENEKTETTFTFPAPVQPVSLPSPTSTDGDIHEDFCSVC
}	l i		RKSGQLLMCDTCSRVYHLDCLDPPLKTIPKGMWICPRCODOMLK
1			KEEAIPWPGTLAIVHSYIAYKAAKEEEKOKLLKWSSDLKORREO
1	ļ		LEQKVKQLSNSISKCMEMKNTILARQKEMHSSLEKVKQLIRLIH
1 .		•	GIDLSKPVDSEATVGAISNGPDCTPPANAATSTPAPSPSSQSCT
	<u> </u>		ANCNOGEETK
6785	1	528	LGNTVLHYCSMYSKPECLKLLLRSKPTVDIVNQAGETALDIAKR
	1		LKATQCEDLLSQAKSGKFNPHVHVEYEWNLRQEEIDESDDDLDD
1			KPSPVKKERSPRPQSFCHSSSISPQDKLALPGFSTPRDKQRLSY
			GAFTNQIFVSTSTDSPTSPTTEAPPLPPRNAGKGPTGPPITPHR
6786	1820	1397	RSPKVLVLAPTRELANHVSRDFKDI\TRKLTVARFYGGTSYQSQ
<u> </u>	1		INHIRNGIDILVGTPGRIKDHLQSGRLDLSKLRHVVLDEVDQML
	}	j	DLGFAEQVEDIIHESYKTDSEDNPQTLLFSATCPQWVYTVA\KK
i i]		YMKSRYEQVDLDGKMTQKAATTVEHLAIQCHWSQRPAVIGDVLQ
, ,	1	ł	VYSGSEGRAIIFCETKKNVTEMAMNPHIKQNAQCLHGDIAQSQR
1 1			EITLKGFREGSPKVLVATNVAARGLDIPEVDLVIQSSPPQDVES
-	ļ		YIHRSGRTGRAGRTGICICFYQPRERGQLRYVEQKAGITFKRVG
			VPSTMDLVKSKSMDAIRSLASVSYAAVDFFRPSAQRLIEEKGAV
1 1			DALAAALAHISGASSFEPRSLITSDKGFVTMTLESLEEIQDVSC
; !		ļ	AWKELNRKLSSNAVSQITRMCLLKGNMGVCFDVPTTESERLQAE
1 (WHDSDWILSVPAKLPEIEEYYDGNTSSNSRQRSGWSSGRSGRSG
<u> </u>			PSGGPSGGPSGGPSGGPSGGSGGSGGSGGSGGSGGSGGSG
Į l			RSGGRSGGRSGRQSRQGSRSGSRQDGRRRSGNRNRSRSGGHKRS
Į			FD+VFYHLVDFLSDFLVDSVYLTGRQIDHLTGLTGLIDHLTSHS
6787	2646		SVWN
***	2020	2270	PSSFPKNVPLEELEEPPK*KRSGLGSLTPKSQIQNGP*PQTFFF
	ļ		FELGSPSGVISAHCNLRLLGSSDSPAPASRVAGIIGTCHHAWLI
6788	16		LVFLVBMGFHHVGQAGLKLLTL\VIHPPWPPKVLGLQT
"'""	70	936	GGTVDLR\DMLAVSVLAAVRGGR/ATVRRVRESNVLHEKSKGKT
<u> </u>			REGAEDKMTSGDVLSNRKMFYLLKTAFPSVQINTEEHVD\ELDQ

SEQ	Predicted	Predicted end	l hmine and d
DI	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
J	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
l	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ł	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
i	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence	1	\=possible nucleotide insertion)
- 1			EVILWGS*DS*GYPKGK*LLPKEVPSR/RVLLSGLTPLDATORY
			FTEDLSK\YVTTMVCVAVNGKPMLGVIHKPFSEYTAWAMUDGGG
1			NVKARSSYNEKTPRIVVSRSHSGMVKOVALOTEGNOTTITPAGG
	1		AGYKVLALLDVPDKSQEKADLYIHVTYIKKWDTCAGNATLYALG
	i	1	GHMTTLSGEEISYTGSDGIEGGLLASIRMNHOALVRKLPDLRKT
6789	 2		I GHK
0,03	'	678	GNGINVLKIAPESAIKFMAYEQIKRLVW**PGDS*GF/YERLVA
		i	GSLAGAIAQSSIYPMEVLKTRMALRKTGOYSGMIDCADDIIADD
1		j	GVAAFYKGYVPNMLGIIPYAGIDLAVYETLKNAWLQHYAVNSAD
ı			PGVFVLLACGTMSSTCGQLASYPLALVRTRMQAQASIEGAPEVT
1	İ		MSSLFKHILRTEGAFGLYRGLAPNFMKVIPAVSISYVVYENLKI
6790	2	4068	TLGVQSR
1	1 ~	1000	APPAGRRRMQAAPRAGCGAALLLWIVSSCLCRAWTAPSTSQKCD
1			EPLVSGLPHVAFSSSSSISGSYSPGYAKINKRGGAGGWSPSDSD
ŀ			HYOWLQVDFGNRKQISALATQGRYSSSDWVTQYRMLYSDTGRNW
	ļ		KPYHQDGNIWAFPGNINSDGVVRHELQHPIIARYVRIVPLDWNG EGRIGLRIEVYGCSYWADVINFDGHVVLPYRFRNKKMKTLKDVI
1			ALNFKTSESEGVILHGEGQQGDYITLBLKKAKLVLSLNLGSNQL
			GPIYGHTSVMTGSLLDDHHWHSVVIERQGRSINLTLDRSMQHFR
			TNGEPDYLDLDYEITFGGIPFSGKPSSSSRKNFKGCMESINYNG
ľ			VNITDLARRKKLEPSNVGNLSFSCVFPYTVPVFFNATSVLEVDC
			RLNQDLFSVSFQFRTWNPNGLLVFSHFADNLGNVEIDLTESKUG
1			VHINTIQIKMSQIDISSGSGLNDGOWHEVRFLAKENFATITIDG
]			DEASAVRTNSPLQVKTGEKYFFGGFLNOMNNSSHSVI.OPSFOCC
			MQLIQVDDQLVNLYEVAORKPGSFANVSIDMCATIDECUPATION
			HGGKCSQTWDSPKCTCDETGYSGATCHNSTYEDSCEAVKULCOT
			SNYYWIDPDGSGPLGPLKVYCNMTEDKVWTIVSHDLQMQTPVVG
i 1			YNPEKYSVTQLVYSASMDQISAITDSABYCEQYVSYFCKMSRLL
] [1		NTPDGSPYTWWVGKANEKHYYWGGSGPGIQKCACGIERNCTDPK
1 1	ì		YYCNCDADYKQWRKDAGFLSYKDHLPVSQVVVGDTDRQGSEAKL
1 1			SVGPLRCQGDRNYWNAASFPNPSSYLHFSTFQGETSADISFYFK TLTPWGVFLENMGKEDFIKLBLKSATEVSFSFDVGNGPVEIVVR
1 1	į		SPTPLNDDQWHRVTAERNVKQASLQVDRLPQQIRKAPTEGHTRL
1 1	İ		ELYSQLFVGGAGGQQGFLGCIRSLRMNGVTLDLEERAKVTSGFI
1 1			SGCSGHCTSYGTNCENGGKCLERYHGYSCDCSNTAYDGTFCNKD
]	İ		VGAFFEEGMWLRYNFQAPATNARDSSSRVDNAPDOONSHDDLAG
1.	i		EEIRFSFSTTKAPCILLYISSFTTDFLAVLVKPTGSIOIDVNIG
1 1	1		GTREPYNIDVDHRNMANGQPHSVNITRHEKTIFI.KI.DHYDSVSV
1 1			HLPSSSDTLFNSPKSLFLGKVIETGKIDOEIHKYNTPGFTGCLG
1 1		1	RVQFNQIAPLKAALRQTNASAHVHIOGELVESNCGASDI.TI.SDM
] !	1	1	SSATOPWHLDHLDSASADFPYNPGOGOATRNGVNDNGATTGGVT
]]	1		A\VVIFTPSLCTP\VLP*SR*HVSPHKGTLPIPNEAKGAGSPOK
6791	1801	1103	RPGRRPSMNNDPPTSQRPIDESKKEWPHLRGGYLAMG
		1193	TGHEGAKGEKGDKGDLGPRGERGQHGPKGBKGYPGIPPEL/PGW
1	ĺ	1	SAVV*SWLTAASTKVQAILLPQPLE*LGLQIAFMASLATHFSNQ
1 1	ł]	NSGIIFSSVETNIGNFFDVMTGRFGAPVSGVYFFTFSMMKHEDV
L I	ļ		EEVYVYLMHNGNTVFSMYSYEMKGKSDTSSNHAVLKLAKGDEVW
6792	33	1073	LRMGNGALHGDHQRFSTFAGFLLFETK
, ,			VRHTNWGVDMYLFSLGSESPKGAIGHIVSTEKTILAVERNKVLL
		1	PPLWNRTFSWGFDDFSCCLGSYGSDKVLMTFENLAAWGRCLCAV CPSPTTIVTSGTSTAVCUMBI CAMPAGEDDOX
1			CPSPTTIVTSGTSTVVCVWELSMTKGRPRGLRLRQALYGHTQAV
 	į		TCLAASVTFSLLVSGSQDCTCILWDLDHLTHVTRLPAHREGISA ITISDVSGTIVSCAGAHLSLWNVNGQPLASITTAWGPEGAITCC
1	1	1.	CLMEGPAWDTSQIIITGSQDGMVRVWKT/VGCEDVCSWTASRRG
]		APGSASKPKRPQVGEEPGLESRAGR*HCFDREAQQNQP\PVTAL
			AVSRNHTKLLVGDERGRIFCWSADG*EERGSRGSGTTVPG
			THE STATE OF THE S

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	
]	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid		P=Proline, Q=Glutamine, R=Arginine,
	residue of	residue of	S=Serine, T=Threonine, V=Valine,
		amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ļ	amino acid	sedneuce	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
6793	2340	805	GRKEANY\YGSLTQAGTVSLGLDAEGQEVFVPFSAVLPMVAPND
1	ŀ		LVFDGWDISSLNLAEAMRRAKVLDWGLQEQLWPHMEALRPRPSV
1	1		YIPEFIAANQSARADNLIPGSRAQQLEQIRRDIRDFRSSAGLDK
1			VIVLWTANTERFCEVIPGLNDTAENLLRTIBLGLEVSPSTLFAV
1			ASILEGCAFLNGSPQNTLVPGALELAWQHRVFVGGDDFKSGQTK
			VKSVLVDFLIGSGLKTMSIVSYNHLGNNDGENLSAPLQFRSKEV
1		•	SKSNVVDDMVQSNPVLYTPGEEPDHCVVIKYVPYVGDSKRALDE
1			YTSELMLGGTNTLVLHNTCEDSLLAAPIMLDLALLTELCQRVSF
1	1		CTDMDPEPQTFHPVLSLLSFLFKAPLVPPGSPVVNALFRQRSCI
ŀ			ENILRACVGLPPQNHMLLEHKMERPGPSLKRVGPVAATYPMLNK
			KGPVPAATNGCTGDANGHLQEEPPMPTT*GPGHTVSRLFLPAAP
			HDPTLKAPTNKGRCHFSPPSTWGSWGL
6794	169	1349	DDVKRKPEASAH*EKPGPPSRPGVRGGRERAGGRGSHGARSCR\
1	1		EPAPPAPAPPEDHPDEEMGFTIDIKSFLKPGEKTYTQRCRLFVG
1	<u> </u>		NLPTDITEEDFKRLFERYGEPSEVFINRDRGFGFIRLESRTLAE
1			IAKAELDGTILKSRPLRIRFATHGAALTVKNLSPVVSNELLEQA
<i>!</i>		•	FSQFGPVEKAVVVVDDRGRATGKGFVEFAAKPPARKALERCGDG
1			AFLLTTTPRPVIVEPMEQFDDEDGLPEKLMQKTQQYHKEREQPP
			RFAQPGTFEFEYASRWKALDEMEKQQREQVDRNIREAKEKLEAE
ŀ			MEAARHEHQLMLMRQDLMRRQEELRRLEELRNQELQKRKQIQLR
	·		HEBEHRRREEEMIRHREQEELRRQQEGFKPNYMENYVCHFLR
6795	1740	1010	GPRRQTQVRDHELDSF*DWAAQETDCAQNSGERL*KGV/LENFS
			TMSKSAVKISLDLLSNPLCEQDQDLLNMVTALDTAMKRMDAFNQ
			EKVNQIQKTVIEPLKKFGSVFPSLNMAVKRREQALQDYRRLQAK
1			VEKYEEKEKTGPVLAKLHQAREELRPVREDFBAKNRQLLEEMPR
ì			FYGSRLDYFQPSFESLTRAQVVYYSEMHKIFGDLSHQLDQPGHS
6796	40		DEQRERENEAKLSELRALSIVADD
0/96	48	683	GKEIQIPTIKLAWLLFGLE*PVGALGKGVVSF**SHVALGQLGW
i			LTRAVRSSWRWELCVSAQEVVSQRSA*SSPSPVGACPSLNPPET
			SVQEGRDCWQR*LPRLFSALVGQPGCWPQGAPPERCV*PGRCKW
	. 1		HLQSQVLR*ERRRCCRCLPRFA*GWRRRHQRLGLGIHPAPLGST
6797	1620	211	SPPHPEGNSQQCRR*GWAAELRLPSSVVL*GKLGC*
1 3.3.	1020	211	TERMTPSQPTRGSSCTRPSSMLWTSTWRCLTCHWAGMRMSVVGV
			TLGPMAQGLLSASGTTTEATWTRPTTHLTLIRWWLLTASRVDPP
			ERPPPPPSDDLTLLESSSSYKNL/DAQIPQ/DWSMSPSTSG*RP LTSRASSIMRSRTAIPSAS*SRLTTKHTVGGSPSAWRPRPTSRS
			VSTPVSSSTETTASGSCLTWWSSSPAPCPSSSAPAHSFEASCCK
1			TSLWGSCGGSGDGSSACGSGWNLSMAGTSCSSPAMCSPSRAPS*
			RSASRPRTWRATTSAASSWAPRRCWCGWA*SAT*PSSTTTISSS
1			PHCGWPCPASCASAAAWLSSTWATASVAGSCWGPIM*SSAHSPW
1			CLSACSRSSMGTTCL+RSPP\SGASRAAAAWCGSSPSSTFTPSS
			ASSSTWCSASSSRSSPAPTTPSSIPAAQAQRRASCRPTSHSART
			APPPASSAAGAARPAAFSAAAEGTPRRSIRCW
6798	3894	1696	STISWESLESWLNKATNPSNRQEDWEYIIGFCDQINKELEG*VS
	· • • • • • • • • • • • • • • • • • • •	-	ALWGQLRGSGLGRGTTMAKEGQPGSPRLSALECVLLVPQ\POIA
	<u> </u>		VRLLAHKIQSPQEWEALQALTYLGDRVSEKVKTKVIELLYSWTM
.	ŀ		ALPEEAKIKDAYHMLKRQGIVQSDPPIPVDRTLIPSPPPRPKNP
1 1	ľ		VFDDEEKSKLLAKLLKSKNPDDLQEANKLIKSMVREDEARIOKV
	į		TKRLHTLEEVNNNVRLLSEMLLHYSQEDSSDGDRELMKELFDQC
]	İ		ENKRRTLFKLASETEDNDNSLGDILQASDNLSRVINSYKTIIEG
	į		QVINGEVATLTLPDSEGNSQCSNQGTLIDLAELDTTNSLSSVLA
	ĺ		PAPTPPSSGIPILPPPPQASGPPRSRSSSQAEATLGPSSTSNAL
	1		SWLDEELLCLGLADPAPNVPPKESAGNSQWHLLQREQSDLDFFS
	l	ļ	PRPGTAACGASDAPLLQPSAPSSSSSQAPLPPPFPAPVVPASVP
		l	APSAGSSLFSTGVAPALAPKVEPAVPGHHGLALGNSALHHLDAL
[1			DQLLEEAKVTSGLVKPTTSPLIPTTTPARPLLPFSTGPGSPLFO
			

WO 01/53312

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
J	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ŀ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	F-Florine, Q=Glucamine, K=Arginine,
1	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
l	amino acid	1	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
İ			PLSFQSQGSPPKGPELSLASIHVPLESIKPSSALPVTAYDKNGF
			RILFHFAKECPPGRPDVLVVVVSMLNTAPLPVKSIVLQAAVPKS
1	1		MKVKLQPPSGTELSPFSPIQPPAAITQVMLLANPLKEKVRLRYK
			LTFALGEQLSTEVGEVDQFPPVEQWGNL
6799	3894	1696	STISWESLESWLNKATNPSNRQEDWEYIIGFCDQINKELEG*VS
1			ALWGQLRGSGLGRGTTMAKEGQPGSPRLSALECVLLVPQ\PQIA
}	ł		VRLLAHKIQSPQEWEALQALTYLGDRVSEKVKTKVIELLYSWTM
1			ALPEEAKIKDAYHMLKRQGIVQSDPPIPVDRTLIPSPPPRPKNP
-			VFDDEEKSKLLAKLLKSKNPDDLQEANKLIKSMVREDEARIQKV
	1		TKRLHTLEEVNNNVRLLSEMLLHYSQEDSSDGDRELMKELFDQC
	Ì		ENKRRTLFKLASETEDNDNSLGDILQASDNLSRVINSYKTIIEG
1		·	QVINGEVATLTLPDSEGNSQCSNQGTLIDLAELDTTNSLSSVLA
			PAPTPPSSGIPILPPPPQASGPPRSRSSQAEATLGPSSTSNAL
			SWLDEELLCLGLADPAPNVPPKESAGNSQWHLLQREQSDLDFFS
]		DEBCTA COLORADIA ODGA DEGGGGGGGA DI DEBCTA COLORADIA ODGA DEGGGGGGGGA DI DEBCTA COLORADIA ODGA DEGGGGGGGA DI DEBCTA DEGGGGGGGA DE DEGGGGGGGGA DEGGGGGGGGA DE DEGGGGGGGA DE DEGGGGGGGGA DE DEGGGGGGGGA DE DEGGGGGGGGA DE DEGGGGGGGA DE DEGGGGGGGA DE DEGGGGGGGA DE DEGGGGGGGA DE DEGGGGGGGA DE DEGGGGGGA DE DEGGGGGGGA DE DEGGGGGGGA DE DEGGGGGGGA DE DEGGGGGGGA DE DEGGGGGGGA DE DEGGGGGGGA DE DEGGGGGGGGA DE DEGGGGGGGGA DE DEGGGGGGGA DE DEGGGGGGGGA
			PRPGTAACGASDAPLLQPSAPSSSSSQAPLPPPPPPAPVVPASVP
1			APSAGSSLFSTGVAPALAPKVEPAVPGHHGLALGNSALHHLDAL
į			DOLLERAKVTSGLVKPTTSPLIPTTTPARPLLPFSTGPGSPLFQ
1			PLSFQSQGSPPKGPELSLASIHVPLESIKPSSALPVTAYDKNGF
			RILFHFAKECPPGRPDVLVVVVSMLNTAPLPVKSIVLQAAVPKS
Ī	į		MKVKLQPPSGTELSPFSPIQPPAAITQVMLLANPLKEKVRLRYK
6800			LTFALGEQLSTEVGEVDQFPPVEQWGNL
6800	404	1646	RRSPSTGLSPVPQPSSPSLSDYSIPWSLLLSGTIAWATPGK*AG
1			*PQAW*LGLAPAIAFI/GLTRGRKQNKEKMAEGGSGDVDDAGDC
1			SGARYNDWSDDDDDSNESKSIVWYPPWARIGTEAGTRARARA
			RATRARRAVOKRASPNSDDTVLSPQELQKVLCLVEMSEKPYILE
1			AALIALGNNAAYAFNRDIIRDLGGLPIVAKILNTRDPIVKEKAL
1			IVLNNLSVNAENQRRLKVYMNQVCDDTITSRLNSSVQLAGLRLL
1 1			TNMTVTNEYQHMLANSISDFFRLFSAGNEETKLQVLKLLLNLAE
			NPAMTRELLRAQVPSSLG\SLFNKKENKEVILKLLVIFENINDN
1			FKWEENEPTONOFGEGSLFFFLKEFQVCADKVLGIESHHDFLVK
Ł i			VKVGKFMAKLAEHMFPKSQE
6801	2	1755	SABEFESQQASVTMHDVDAESFEVLVDYCYTGRVSLSEANVERL
1 1			YAASDMLQLEYVREACASFLARRLDLINCTAILKFADAFGHRKL
ł I			RSQAQSYIAQNFKQLSHMGSIREETLADLTLAQLLAVLRLDSLD
1 1	1		VESEQTVCHVAVQWLEAAPKERGPSAAEVFKCVRWMHFTEEDQD
i :	j		VIEGITARDIARANCE DALECT ONDAODI I AND INDIANA
			YLEGLLTKPIVKKYCLDVIEGALQMRYGDLLYKSLVPVPNSSSS
1 1	ı		/R*QQQLSCICSRKSTPETGYVCQGDGDLLWTPQRSLS\RYDPY
]]	J		SGDIYTMPSPLTSFAHTKTVTSSAVCVSPDHDIYLAAQPRKDLW
ļ !	•		VYKPAQNSWQQLADRLLCREGMDVAYLNGYIYILGGRDPITGVK
] 1	- 1		LKEVECYSVQRNQWALVAPVPHSFYSFELIVVQNYLYAVNSKRM
]		•	LCYDPSHNMWLNCASLKRSDFQEACVFNDEIYCICDIPVMKVYN
j. j	ļ		PARGEWRRISNIPLDSETHNYQIVNHDQKLLLITSTTPQWKKNR
1 1		i	VTVYEYDTREDQWINIGTMLGLLQFDSGFICLCARVYPSCLEPG
			QSFITEEDDARSESSTEWDLDGFSELDSESGSSSSFSDDEVWVQ
6802			VAPQRNAQDQQGSL
0002	157	1341	ETFPLFFFLLSKTPGKTASMAHFVQGTSRMIAAESSTEHKECAE
]			PSTRKNLMNSLEQKIRCLEKQRKELLEVNQQWDQQFRSMKELYE
			RKVAELKTKLDAAERFLSTREKDPHQRQRKDDRQREDDRQRDLT
[]		ļ	RDRLQREEKEKERLNEELHELKEENKLLKGKNTLANKEKEHYEC
[]		ļ	EIKRLNKALQDALNIKCSFSEDCLRKSRVEFCHEEMRTEMEVLK
	İ		QQVQIYEEDFKKERSDRERLNQEKEELQQINETSQSQLNRLNSQ
J J		1	IKACQMEKEKLEKQLKQMYCPPCNCGLVFHLQDPWVPTGPGAVQ
	1	İ	KQREHPPDYQWYALDQLPPDVQHKAN/DWCLAPPPPVCCQAG/PR
 	Ĺ	ļ	TPGLK+SSCLWLPKC+NFRFILSKESPSVEVHTNRERQQATRER
ļ	1	i	G G
6803	1	2203	KLSGRPYRHMGVLGTSKLYDIRKTIFTFTPQFIDQQGFYLALDN
			TYTHE A TOTAL TATE TATE TO THE TATE TO THE TOTAL TYTHE A TOTAL TYTHE A TOTAL TYTHE TATE TO THE TATE TO

SEO	Predicted	Predicted end	Dining and compat containing along
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	b=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
İ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ı	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	-	\=possible nucleotide insertion)
		· · · · · · · · · · · · · · · · · · ·	KMIVEMLRTDLSYLCSRWRMTGOPTITFPISHSMLDEDGTSLNS
i			SILAALRKMQDGYFGGARVQTGKLSEFLTTSCCTHLSFMDPGPE
i			GKLYSEDYDDNYDYLESGNWMNDYDSTSHARCGDEVARYLDHLL
1			AHTAPHPKLAPTSQKGGLDRFQAAVQTTCDLMSLVTKAKELHVQ
1	1		NVHMYLPTKLFQASRPSFNLLDSPHPRQENQVPSVRVEIHLPRD
			QSGEVDFKALVLQLKETSSLQEQADILYMLYTMKGPDWNTELYN
			ERSATVRELLTELYGKVGEIRHWGLIRYISGILRKKVEALDEAC
l			TDLLSHOKHLTVGLPPEPREKTISAPLPYEALTQLIDEASEGDM
	ļ		SISILTQEIMVYLAMYMRTQPGLFAEMPRLRIGLIIQVMATELA
			HSLRCSAEEATEGLMNLSPSAMKNLLHHILSGKEFGVERK/SVR
1			PTDSNVSPAISIHEIGAVGATKTERTGIMQLKSEIKQVEFRRLS
ł	}		ISAESQSPGTSMTPSSGSFPSAYDQQSSKDSRQGQWQRRRRLDG
1			ALNRVPVGFYQKVWKVLQKCHGLSVEGFVLPSSTTREMTPGEIK
i			FSVHVES\VLNVLLRPEYRQLLVEAILVLTMLADIEIHSIGSII
j			AVEKIVHIANDLFLQEQKTLGP\DDTMLAKDPASG\ICTLR\YD
6804	ļ	0.53	SAPSGRFGTMTYLS\RAA\ATYVQEFLP\HSICAMQ
0004	1	951	GSPGKKEEKAKNKESLCMENSSNSSSDEDEBETKAKMTPTKKYN
			GLEEKRKSLRTTGFYSGFSEVAEKRIKLLNNSDERLQNSRAKDR
			KDVWSSIQGQWPKKTLKELFSDSDTEAAASPPHPAPEEGVAEES
1			LQTVAEEESCSPSVELEKPPPVNVDSKPIEEKTVEVNDRKAEFP
			SSGSNFSA*IPLPYLHLNRLHQSL*QKGSRQQSSVTVSEPLAPN QEEVRSIKSETDSTIEVDSVAGELQDLQSERE*LASRF*COCEL
}			KQ**SARTRTS*KSLYRSEKSERCSGRRKFIKKAEKKP*SNSGK
1			OOKEGKRHK
6805	1539	206	RQPDLKYFGKSFDVSVSESSSLLSNDLPKFADGIKARNRNONYL
	1		VPSPVLRILDHTAFSTEKSADIVICDEECDSPESVNQOTOEESP
			IEVHTAEDVPIAVEVHAISEDYDIETENNSSESLODOTDEEPPA
			KLCKILDKSQALNVTAQQKWPLLRANSSGLYKCELCEFNSKYFS
	1		DLKQHMILKHKRTDSNVCRVCKESFSTNMLLIEHAKLHEEDPYI
1	1		CKYCDYKTVIFENLSQHIADTHFSDHLYWCEQCDVQFSSSSELY
ł	1		LHFQEHSCDEQYLCQFCEHETNDPEDLHSHVVNEHACKLIELSD
	1		KYNNGEHGQYSLLSKITFDKCKNFFVCQVCGFRSRLHTNVNRHV
]		AIEHTKIPPHVCDDCGKGFSSMLE\IAKHLNSHLSEGIYLCQYW
1 .			EYSTGQIEDLKIHLDFKHSADLPHKCSDCLMRFGNERBLISHLP
			VHETT
6806	272	3794	VALCFPNSDPVMFMDAFYGCLLAELGPVPIEVPLTRKDAGSQQV
Ì	ļ i		GFLLGSCGVFLALTTDACQKGLPKAQTGEVAAFKGWPPLSWLVI
			DGKHLAKPPKDWHPLAQDTGTGTAYIEYKTSKEGSTVGVTVSHA
1			SLLAQCRALTQACGYSEAETLTNVLDFKRDAGLWHGVLTSVMNR
1			MHVVSVPYALMKANPLSWIQKVCFYKARAALVKSRDMHWSLLAQ
			RGQRDVSLSSLRMLIVADGANPWSISSCDAFLNVFQSRGLRPEV
•			ICPCASSPEALTVAIRRPPDLGGPPPRKAVLSMNGLSYGVIRVD
			TREKLSVLTVQDVGQVMPGANVCVVKLEGTPYLCKTDEVGEICV SSSATGTAYYGLLGITKNVFEAVPVTTGGAPIFDRPFTRTGLLG
1			FIGPDHLVFIVGKLDGLMVTGVRRHNADDVVATALAVEPMKFVY
I	i .		RGRIAVFSVTVLHDDRIVLVAEQRPDASEEDSFQWMSRVLQAID
			SIHQVGVYCLALVPANTLPKAPLGGIHISETKQRFLEGTLHPCN
			SIHQVGVYCLALVPANTLPKAPLGGIHISETKQRFLEGTLHPCN VLMCPHTCVTNLPKPRQKQPEVGPASMIVGNLVAGKRIAQASGR
			SIHQVGVYCLALVPANTLPKAPLGGIHISETKQRFLEGTLHPCN VLMCPHTCVTNLPKPRQKQPEVGPASMIVGNLVAGKRIAQASGR ELAHLEDSDQARKFLFLADVLQWRAHTTPDHPLFLLLNAKGTVT
			SIHQVGVYCLALVPANTLPKAPLGGIHISETKQRFLEGTLHPCN VLMCPHTCVTNLPKPRQKQPEVGPASMIVGNLVAGKRIAQASGR ELAHLEDSDQARKFLFLADVLQWRAHTTPDHPLFLLLNAKGTVT STATCVQLHKRAERVAAALMEKGRLSVGDHVALVYPPGVDLIAA
			SIHQVGVYCLALVPANTLPKAPLGGIHISETKQRFLEGTLHPCN VLMCPHTCVTNLPKPRQKQPEVGPASMIVGNLVAGKRIAQASGR ELAHLEDSDQARKFLFLADVLQWRAHTTPDHPLFLLLNAKGTVT STATCVQLHKRAERVAAALMEKGRLSVGDHVALVYPPGVDLIAA FYGCLYCGCVPVTVRPPHPQNLGTTLPTVKMIVEVSKSACVLTT
			SIHQVGVYCLALVPANTLPKAPLGGIHISETKQRFLEGTLHPCN VLMCPHTCVTNLPKPRQKQPEVGPASMIVGNLVAGKRIAQASGR ELAHLEDSDQARKFLFLADVLQWRAHTTPDHPLFLLLNAKGTVT STATCVQLHKRAERVAAALMEKGRLSVGDHVALVYPPGVDLIAA FYGCLYCGCVPVTVRPPHPQNLGTTLPTVKMIVEVSKSACVLTT QAVTRLLRSKEAAAAVDIRTWPTILDTDDIPKKKIASVFRPPSP
			SIHQVGVYCLALVPANTLPKAPLGGIHISETKQRFLEGTLHPCN VLMCPHTCVTNLPKPRQKQPEVGPASMIVGNLVAGKRIAQASGR ELAHLEDSDQARKFLFLADVLQWRAHTTPDHPLFLLLNAKGTVT STATCVQLHKRAERVAAALMEKGRLSVGDHVALVYPPGVDLIAA FYGCLYCGCVPVTVRPPHPQNLGTTLPTVKMIVEVSKSACVLTT
			SIHQVGVYCLALVPANTLPKAPLGGIHISETKQRFLEGTLHPCN VLMCPHTCVTNLPKPRQKQPEVGPASMIVCNLVAGKRIAQASGR ELAHLEDSDQARKFLFLADVLQMRAHTTPDHPLFLLLMAKGTVT STATCVQLHKRAERVAAALMEKGRLSVGDHVALVYPPGVDLIAA FYGCLYCGCVPVTVRPPHPQNLGTTLPTVKMIVEVSKSACVLTT QAVTRLLRSKEAAAAVDIRTWPTILDTDDIPKKKIASVFRPPSP DVLAYLDFSVSTTGILAGVKMSHAATSALCRSIKLQCELYPSRQ
			SIHQVGVYCLALVPANTLPKAPLGGIHISETKQRFLEGTLHPCN VLMCPHTCVTNLPKPRQKQPEVGPASMIVGNLVAGKRIAQASGR ELAHLEDSDQARKFLFLADVLQWRAHTTPDHPLFLLLNAKGTVT STATCVQLHKRAERVAAALMEKGRLSVGDHVALVYPPGVDLIAA FYGGLYCGCVPVTVRPPHPQNLGTTLPTVKMIVEVSKSACVLTT QAVTRLLRSKEAAAAVDIRTWPTILDTDDIPKKKIASVFRPPSP DVLAYLDFSVSTTGILAGVKMSHAATSALCRSIKLQCELYPSRQ IAICLDPYCGLGFALWCLCSVYSGHQSVLVPPLELESNVSLWLS

WO 01/53312

PCT/US00/34263

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ì	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
			LOGTAGPDPTTVYVDMRALRHDRVRLVERGSPHSLPLMESGKIL
			PGVKVIIAHTETKGPLGDSHLGEIWVSSPHNATGYYTVYGEEAL
			HADHFSARLSFGDTQTIWARTGYLGFLRRTELTDASGGRHDALY
ł			VVGSLDETLELRGMRYHPIDIETSVIRAHRSIAECAVFTWTNLL
1			VVVVELDGLEQDALDLVALVTNVVLEEHYLVVGVVVIVDPGVIP
Ĺ			INSRGEKQRMHLRDGFLADQLDPIYVAYNM
6807	1444	606	VGHDTVHAMFTCFPKCLGFSPPVNVTVSPRSEESHTTTVSGGNG
ļ			.SVFQAGPQLQALANLEARRGSIGAALSSRDVSGLPVYAQSGEPR
	1		RLTQAQVAAFPGENALEHSSDQDTWDSLRSPGFCSPLSSGGGAE
			SLPPGGPGHAEAGHLGKVCDFHLNHQQPSPTSVLPTEVAAPPLE
			KILSVDSVAVDCAYRTVPKPGPQPGPHGSLLTEGCLRSLSGDLN
			RFPCGMEVHSGQRELESVVAVGEAMA\LKFPMGAMSYCLRDRSR
	[1	FLFRLPMGLSCPLQVQ
6808	2063	737	GVGSGAASALARSRPLASRLSSRRRTRAPRSGAMORLAMDLRML
ł			SRELSLYLEHQVRVGFFGSGVGLSLILGFSVAYAFYYLSSIAKK
1			PQLVTGGESFSRFLQDHCPVVTETYYPTVWCWEGRGQTLLRPF\
}			ITSKPPVQYRNELIKTADGGQISLDWFDNDNSTCYMDASTRPTI
			LLLPGLTGTSKESYILHMIHLSEELGYRCVVFNNRGVAGENLLT
1	,		PRTYCCANTEDLETVIHHVHSLYPSAPFLAAGVSMGGMLLLNYL
	ł		GKIGSKTPLMAAATFSVGWNTFACSESLEKPLNWLLFNYYLTTC
1			LQSSVNKHRHMFVKQVDMDHVMKAKSIREFDKRFTSVMFGYOTT
[.			DDYYTDASPSPRLKSVGIPVLCLNSVDDVFSPSHAIPIETAKON
	•		PNVALVLTSYGGHIGFLEGIWPRQSTYMDRVFKQFVQAMVEHGH
6809		·	RLS
6009	939	65	DYSGQTPVPTEHGMTLYTPAQTHPEQPGSEASTQPIAGTQTVPQ
1 1			TDEAAQTDSQPLHPSDPTEKQQPKRLHVSNIPFRFRDPDLROMF
}			GQFGKILDVEIIFNERGSKGFGFVTFETSSDADRAREKLNGTIV
1.			EGRKIEVNNATARVMTNKKTGNPYTNGWKLNPVVGAVYGPEFYA
1			VTGFPYPTTGTAVAYRGAHLRGRGRAVYNTFRAAPPPPPIPTYG
			AVVYQDGFYGAEI\LEATQPTDTLSPLQRRQPTATVTAESTQLP
6810	939		TRTITPSGPRRPTALEPCETFHRFLLGP
1 222	333	65	DYSGQTPVPTEHGMTLYTPAQTHPEQPGSEASTQPIAGTQTVPQ
i i			TDEAAQTDSQPLHPSDPTEKQQPKRLHVSNIPFRFRDPDLRQMF
1			GOFGKILDVEIIFNERGSKGFGFVTFETSSDADRAREKLNGTIV
l [EGRKIEVNNATARVMTNKKTGNPYTNGWKLNPVVGAVYGPEFYA
	İ		VTGFPYPTTGTAVAYRGAHLRGRGRAVYNTFRAAPPPPPIPTYG
			AVVYQDGFYGAEI\LEATQPTDTLSPLQRRQPTATVTAESTQLP TRTITPSGPRRPTALEPCETFHRFLLGP
6811	1522	658	DLVTVWSFVDCRVIASTHGH\KSWVSVVAFDPYTTSVEEGDPME
			FSGSDEDFQDLLHFGRDRADSTQCRLSRRNSTDSRPVSVTYRFG
	ľ		SVGQDTQLCLWDLTEDILFPHQPLSRARTHTNVMNATSPPAGSN
l			GNSVTTPGNSVPPPLPRSNSLPHSAVSNAGSKSSVMDGAIASGV
İ			SKFATLSLHDRKERHHEKDHKRNHSMGHISSKSSDKLNLVTKTK
}			TDPAKTLGTPLCPRMBDVPLLEPLICKKIAHERLTVLIFLEDCI
		-	VTACQEGFICTWGRPGKVVSFNP
6812	4001	1682	EDAVFSLDLSTI1QGTWFLNGEELKSNEPEGQVEPGALRYRIEQ
1			KGLQHRLILHAVKHQDSGALVGFSCPGVQDSAALTIQESPVHIL
ľ			SPQDKVSLTFTTSERVVLTCELSRVDFPATWYKDGQKVEESELL
	İ		VVKMDGRKHRLILPEAKVQDSGEFECRTEGVSAFFGVTVQDPPV
1			HIVDPREHVFVHAITSECVMLACEV\DR\EDAPVRWYKDGQEVE
	ļ		ESDFVVLENEGPHRRLVLPATQPSDGGEFQCVAGDECAYFTVTI
ŀ			TDVSSWIVYPSGKVYVAAVRLERVVLTCELCRPWAEVRWTKDGE
		,	EVVESPALLLQKEDTVRRLVLPAVQLEDSGEYLCEIDDESASFT
		.	VIVIEPPVRIIYPRDEVTLIAVILECVVLMCELSREDAPVRWYK
		ľ	DGLEVEESEALVLERDGPRCRLVLPAAQPEDGGEFVCDAGDDSA
<u> </u>		1	FFTVTVTEPPVQFLALETTPSPLCVAPGEPVVLSCELSRAGAPV

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
Ì	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
Į.	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	•	\=possible nucleotide insertion)
	 		VWSHNGRPVQEGEGLELHAEGPRRVLCIQAAGPAHAGLYTCQSG
1			AAPGAPSLSFTVQVAEPPVRVVAPEAAQTRVRSTPGGDLELVVH
1			LSGPGGPVRWYKDGERLASQGRVQLEQAGARQVLRVQGARSGDA
1			GEYLCDAPQDSRIFLVSVEEPLLVKLVSDLTPLTVHEGDDATFR
ı		l	CEVSPPDADVTWLRNGAVVTPGPQRQSCCSYGGCRMCGQRKART
Į.			CVSKWRQAEWVQRGPCAGCEVGSPCPTTLACPWPRMGTSTASSS
!	İ		MVSYWPTRAPTAARATTIAPWPGSA
6813	و	836	SSTQQRPGVPAGPRPLDGYLGVADHKPLKMHCRDCALVTSSGHL
1	ł.	,	LHSRQGSQIDQTECVIRMNDAPTRGYGRDVGNRTSLRVIAHSSI
1	Į.		QRILRNRHDLLNVSQGTVFIFWGPSSYMRRDGKGQVYNNLHLLS
			QVLPRLKAFMITRHKMLQFDELFKQETGQ\NRKISNTWLSTGWF
1			TMTIALELCDRINVYGMGPPDFCRDPNHPSVPYHYYEPFGPDEC
ì			TMYLSHERGRKGSHHRFITEKRVFKNWARTFNIHFFQPDWKPES
			LAINHPENKPVF
6814	3	737	KFRRQEAN/ARERNRMHGLNDALDNLRKVVPCYSKTQKLSKIET
			LRLAKNYIWALSEILRIGKRPDLLTFVQNLCKGLSQPTTNLVAG
}			CLQLNARSFLMGQGGEAAHHTRSPYSTFYPPYHSPELTTPPGHG
			TLDNSKSMKPYNYCSAYESFYESTSPECASPQFEGPLSPPPINY
1			NGIFSLKQEBTLDYGKNYNYGMHYCAVPPRGPLGQGAMFRLPTD
			SHFPYDLHLRSQSLTMQDELNAVFHN
6815	906	553	QGLDPASQTKVVELLKDGSGRRGDRRSSRDMAGGAGPRSESDLE
			DVGPTAEWNGDGSGSLRRSGSFGKLRDALRRSSEMLVKKLQGGT
<u> </u>			PQBPPNPRMKRASSLNFLNKSVEEPTQPGG
6816	1	803	NLLKTHKF\LLGQDEDSLHSVPVAQMGNYQEYLKTLASPLREID
1		*	PDQPKRLHTFGNPFKQDKKGMMIDEADEFVAGPQNKVKRPGEPN
1			SPMSSKRRRSMSLLLRKPQTPPTVTNHVGGKGPPSASWFPSYPN
			LIKPTLVHTDATIIHDGHEEKMENGQITPDGFLSKSAPSELINM
			TGDLMPPNQVDSLSDDFTSLSKDGLIQKPGSNAFVGGAKNCSLS
			VDDQKDPVASTLGAMPNTLQITPAMAQGINADIKHQLMKEVRKF
			GRSK
6817	172	3457	LGMMDSPKIGNGLPVIGPGTDIGISSLHMVGYLGKNFDSAKVPS
			DEYCPACKEKGKLKALKTYRISFQESIFLCEDLQCIYPLGSKSL
			NNLISPDLEECHTPHKPQKRKSLESSYKDSLLLANSKKTRNYIA
			IDGGKVLNSKHNGEVYDETSSNLPDSSGQQNPIRTADSLERNEI
1 1	ļ.		LEADTVDMATTKDPATVDVSGTGRPSPQNEGCTSKLEMPLESKC
1			TSFPOALCVOWKNAYALCWLDCILSALVHSEELKNTVTGLCSKE
			ESIFWRLLTKYNQANTLLYTSQLSGVKDGDCKKLTSEIFAEIET
			CLNEVRDEIFISLQPQLRCTLGDMESPVFAFPLLLKLETHIEKL
j i			FLYSFSWDFECSQCGHQYQNRHMKSLVTFTNVIPEWHPLNAAHP
			GPCNNCNSKSQIRKMVLEKVSPIFMLHFVEGLPQNDLQHYAFHF
į l			EGCLYQITSVIQYRANNHFITWILDADGSWLECDDLKGPCSERH
			KKFEVPASEIHIVIWERKISQVTDKEAACLPLKKTNDQHALSNE
1 1			KPVSLTSCSVGDAASAETASVTHPKDISVAPRTLSQDTAVTHGD
]		HLLSGPKGLVDNILPLTLEETIQKTASVSQLNSEAFL\LENKPV
1	İ		AENTGILKTNTLLSQESLMASSVSAPCNEKLIQDQFVDISFPSQ
		•	VVNTNMQSVQLNTEDTVNTKSVNNTDATGLIQGVKSVEIEKDAQ
[LKQFLTPKTEQLKPERVTSQVSNLKKKETTADSQTTTSKSLQNQ SLKENQKKPFVGSWVKGLISRGASFMPLCVSAHNRNTITDLOPS
	İ		
			VKGVNNFGGFKTKGINQKASHVSKKARKSASKPPPISKPPAGPP
			SSNGTAAHPHAHAASEVLEKSGSTSCGAQLNHSSYGNGISSANH
]	1	j	EDLVEGQIHKLRLKLRKKLKAEKKKLAALMSSPQSRTVRSENLE
	ļ	ļ	QVPQDGSPNDCESIEDLLNELPYPIDIANESACTTVPGVSLYSS
]	QTHEBILAELLSPTPVSTELSENGEGDFRYLGMGDSHIPPPVPS
l i	j		EFNDVSQNTHLRQDHNYCSPTKKNPCEVQPDSLTNNACVRTLNL
6818	2	240	ESPMKTDIFDEFFSSSALNALANDTLDLPHFDEYLFENY RGFDKVLWT/LSGAVK\CVOFSRISPDGEEGYPGELKVWVTYTL
للتنسب			NO. 2017 HOOMYK (CVQFORISPUGEEGIPGEDKVWVTITE

Deginning	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
No: nucleotide	_			(A-Alanina C-Combains B Asserbia 2012
location corresponding to first to f			1	Glutamic Acid Fabbandalanian C Classics
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FFAFSLIEGYI\SIVMDAETQKKFPSDLLLITSSSGELWRMVRIG GQPLGFDECGIVAQIAGPLAAADISAYYISTFNPDHALVPEDGI GSVIEVLQRRQEGLAS FEDIYR/EVGGEPVPVTRDDSSNGFPRTQHGPSPTVHPIQSPQN RRCVLTLDPETLPAIATTLIDULFSHESTFKEAASSSPEPSSIT FFAFSLIEGYI\SIVMDAETQKKPPSDLLITSSSGELWRMVRIG GQPLGFDECGIVAQIAGPLAAADISAYYISTFNPDHALVPEDGI GSVIEVLQRRQEGLAS 6823 654 221 PPKLLSRWARMGHGBEIV\LSDLNFPGLLHLPVVGPWRSVQTAC GIPQLLEAVLKLLPLDTYVESPAAVMELVPSDKERGLQTPVWTE YESILRRAGCVRALAKIERFEFYPRAKKAFAVVATGETALYGNL ILRKGVLALNPLL 6824 858 104 LLLAGRWGWG\CCFFSLAVSVKMNVLLFAFGLLFLLTQFGFRG ALPKLGICAGLQVVLGLPFLLENPSGYLSRFPDLGRQFLFHWTV NWRFLPEALFLHRAFHLALLTLLLLEALCRWHRTGESILS LLRPSKRKVPPQPLTPMQIVSTLFTENFIGICFSSLHYQFYV WYPHTLPYLLWAMPARWLTHLLRLLVLGLIELSWNTYPSTSCSS AALHICHAVILLQLWLGPQFFPKSTQHSKKAH 6825 3 1173 SSGPFGLOADIMWTISDTGWHILITLCSLMEPWALGACTFVHLL PKFDPLVILKTLSSYPIKSMMGAPIVYRMLLQQDLSSYKFPHLQ NCLAGGESLLPBTLENWRAQTGLDIREFYGQTBTGLTCMVSKTM KIKPGYMGTAASCYDVQIIDDKGNVLPPGTEGDIGIRVKPIRPI GIFSGYVDNPDKTAANIRGDFWLLGDRGIKDEDGYFQFMGRADD IINSSGYRIGPBSVENALMEHPAVVETAVISSPDPVRGEVVKAF VILALQFLSHDPBQLTKELQQVKSVTAPYKYPRKIEFVLINLPK TVTCKIQRA\KIRDKEWKNSGKAPCAVRHLRDIHLDSPLLSLSF PFGPLALPMDGYGDSLWBEHEYKFCLALVISTKLYHVRC 6826 2304 954 LKTESFKPW/VNIALAFHLLGERASPNSFWQPYIQTLPREYDTF LYFEBDEVRYLQSTQAIHDVFSQYKNTARQYAYFYKYIQTHPHA NKLPLKDSFTYEDYRWAVSSVMTRQNQIPTEDGSRVTLALIPLW MKLPLKDSFTYEDYRWAVSSVMTRQNQIPTEDGSRVTLALIPLW NKLPLKDSFTYEDYRWAVSSVMTRQNQIPTEDGSRVTLALIPLW DMCNHTNGLITTGYWLEDDRCECVALQDFRAGEGIYIFYGTRSN AEPVIHSGFFFDNNSHDRVKIKLGVSKSDRLYAMKABVLARAGI PTSSVFALHFTEPPISAQLLAFLRVFCWTEEELKEHLLGDSAII PTSSVFALHFTEPPISAQLLAFLRVFCWTEEELKEHLLGDSAID	[RFCVLTLDPETLPAIATTLIDVLFYSHSTPKEAASSSPEPSSIT
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REVLITIDPETLPATATILIDVLEYSHATPKEAASSSPEPSSIT FFAFSLIEGYI\SIVMDAETOKKPPSDLLITSSSGELWRWVRIG GQPLGFDECGIVAQIAGPLAAADISAYYISTFNFDHALVPEDGI GSVIEVLQRRQEGLAS 6823 654 221 PPKLLSRWARWGHGDEIV\LSDLNFPGLLHLPVVGFWRSVQTAC GIPQLLEAVLKLLPLDTYVESPAAVMELVPSDKERGLQTPVWTE YESILRRAGCVRALAKIERFEFYERAKKAFAVVATGETALYGNL ILRKGVLALNPLL 6824 858 104 LLLAQRWGWG\CCFFSLAVSVKMNVLLFAPGLLFLLLTQFGFRG ALPKLGICAGLQVVJGLPFILEBPSGYLSRSFDLGRQPFLFHWTV NWRFLPEALPLHRAFHLALLTAHLTLLLFALCRHHRTGESILS LLRPSKRKVPPQPLTPNGIVSTLFTENFIGICFSRSLHVQFYV WYYPHTLPYLLWAMPARWLTHLLRLLVLGLIELSWNTYPSTSCSS AALHICHAVILLQLWLGPQPFPKSTQHSKKAH PKFDPLVILKTLSSYPIKSMMGAPIVYRMLQQDLSSYKFPHLQ NCLAGGESLLPETLENWRAQTGLDIREFYGQTETGLTCMVSKTM KIKPGYMGTAASCYDVQIIDDKGNVLPPGTSGDIGIRVRPIRPI GIFSGYVDNPDKTAANIRGDFWLLGDRGIKDEDGYFOFMGRADD IINSSGYRIGPSEVENALMHEPAVVETAVISSPDPVRGEVVKAR VILALQFLSHDPBQLTKBLQQNVKSVTAPKYPRRIEFVLNLPK TVTGKIQRA\KLRDKEWKMSGKAPCAVRHLRDIHLDSPLLSLSF PFGPLALPMDGYGDSLWEHEYKFCLALVISTKLYHVRC 6826 2304 954 LKTESFKPW/VNIALAFHLLGERASPNSFWQPYIQTLPREYDTP LYFEEDEVRYLQSTQAHDVFSGYKNTARQYAYFYKVIQTHPHA NKLPLKDSFTYEDYRWAVSSVMTRQNQIPTEDGSRVTLALIPLW DMCNHTNGLITTGYNLEDDGCCVALQDFRAGEGIYIFYGTRSN AEFVHINGSFFYNNSHDRVKIKLGVSKSDRLYAMKAEVLARAGI PTSSVFALHFTEPPISAQLLAFLRVFCMTEEELKEHLLGDSAID	6822	1088	518	EFDIYR/EVGGEFVPVTRDDSSNGFPRTQHGPSPTVHPIOSPON
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GSSSDSTAGVKE	<u> </u>		<u></u>	GSSSDSTAGVKE

SEQ Predicted Predicted end Amino acid segment containing sign	
ID beginning nucleotide (A=Alanine, C=Cysteine, D=Aspartic	nal peptide
NO: nucleotide location Glutamic Acid, FaPhenylalanine, G	CACIO, E=
location corresponding Halistidine, IaIsoleucine, Kalysin	egraciue,
corresponding to first L=Leucine, M=Methionine, N=Asparac	ne,
to first amino acid P=Proline, Q=Glutamine, R=Arginine	ane,
amino acid residue of S=Serine, T=Threonine, V=Valine,	Ξ,
residue of amino acid W=Tryptophan, Y=Tyrosine, X=Unknow	- + 05
amino acid sequence Codon, /=possible nucleotide delet	wii, -=scop
sequence \=possible nucleotide insertion)	.1011,
6827 1 779 SSVVEFGLSVLGGLFLLFVLENMLGLLRHRGLRI	DCCDDWDDNT.
ETRNLDPENGSGMALQPLQAAPEPGAQGQREKNS	COUNTY AND THE
HQGHSHGHQGGTDITWMVLLGDGLHNLTDGLAIO	SPERMINERSE
LSTTLAVFCHELPHELGDFAMLLQSGLSFRRLLI	J.ST.VSGALGI.
GGAVLGVGLSLGPVPLTPWVFGVTAGVFLYVALV	/DMI.PAI.FPSS
GAPAYA\HVLLQGLGLLLGGCLMLAITLLEERLI	PVTTEG
6828 3 1654 KSQHG/WILQLMHSCKEGYVKDLKGNPGLHRAMI	DIDNGTRESE
LGHLSQTASLKRGSSFQSGRDDTWRYKTPHRVA	VEKLTKLVIS
QLPNFWKLWISYVNGSLFSETAEKSGQIERSKN	RORONDEKKM
IQEVMHSLVKLTRGALLPLSIRDGEAKQYGGWEV	/KCELSGOWLA
HAIQTVRLTHESLTALEIPNDLLQTIQDLILDLE	RVRCVMATLOH
TAEEIKRLAEKEDWIVDNEGLTSLPCQFEQCIVC	SLOSLKGVLE
CKPGEASVFQQPKTQEEVCQLSINIMQVF1YCLE	QLSTKPDADI
DTTKLSVDVSSPDLFGSIHEDFSLTSEQRLLIVI	SNCCYLERHT
FLNIAEHFEKHNFQGIEKITQVSMASLKELDORI	FENYIELKAD
PIVGSLEPGIYAGYFDWKDCLPPTGVRNYLKEAL	VNIIAVHAEV
FTISKELVPRVLSKVIEAVSEELSRLMQCVSSFS	KNGALQARLE
ICALRDTVAVYLTPESKSSFKQALEALPQLSSGA	DKKLLEELLN
KFKSSMHLQLTCFQAASSTMMKT	
1 INDIEAGEAAPPAGAGGRAAGGWGRWVRLNVGGTV	FLTTRQTLCR
EQKSFLSRLCQGEELQSDRDETGAYLIDRDPTYF	GPILNFLRHG
KLVLOKDMAEEGVLEEAEFYNIGPLIRIIKDRME	EKDYTVTQVP
PKHVYRVLQCQEEELTQMVSTMSDGWRFEQLVNI	GSSYNYGSED
QAEFLCVVSKELHSTPNGLSSESSRKTKSTEEQL	EEQQQQEEEV
EEVEVEQVQVEADAQEK/CCYKPEAPGCEAPDHL	QGLGVPI
- INDEAGACHUSIVIKSKDEUVANKHWDAKIDSKAW	RETLTLQKQL
RYRFPELADPDTCYGFRFCHQLDFSTSGALCVAL	NKAAAGSAYR
CFKERRVTKAYLALLRGHIQESRVTISHAIGRNS EGSQGCENPKPSLTDLVVLEHGLYAGDPVSKVLL	TEGRAHTMCI
RV\HCSALGHPVVGDLTYGEVSGREDRPFRMMLH	KPLTGRTHQL
ECVEVCTPDPFLPSLDACWSPHTLLQSLDQLVQA	AFILKIPIDI
DRGPRPGSPSALLPGPGRPPPPPTKPPETEAQRG	DCT OWT ORWER
LEPDS	ECTIONTISEMI.
6831 3 1087 SLFFGSSTPDNKVAEQEDLETQPSPSVEKAVTVI	DDFCT7 DTMF
NVAEKPADHSLSEVKLKTADEPRGTLVKSGDGQN	UKEKSMIT.CM
VEDLQQPKFISEVSREDYGKKEISGDSEEMNINS	WITSANGENT.
EIQSYSLIGEKLVMEEAKTIVPPHVTDSKRVQKP	ATAPPSKWNT
SIFKEEPRSDQKQKSLLSFDVVDKVPQQPKSASSI	NEASKNITKE
SEKPESIILPVEESKGSLIDFSEDRLKKEMONPT	SLKISEERTK
LRSVSPTEKKDNLENR\SYTL\AEKKVLAEKQNS	V\APLELRDS
NEIGKTQITLGSRSTELKESKADAMPQHFYQNED	YNERPKIIVG
SEKEKDEKKKK	
6832 1809 412 MGSGLISGPPQDNSGEALKEPERAQEHSLPNFAGG	GHFFEYLLV
VSLKKKRSEDDYEPIITYQFPKRENLLRGQQEEE	ERLLKAIPLF
CFPDGNEWASLTEYPRETFSFVLTNVDGSRKIGYC	TRRLLPAGPG
PRLPKVYCIISCIGCFGLFSKILDEVEKRHOISM	VIYPFMOGL
REAAFPAPGKTVTLKSFIPDSGTEFISLTRPLDSF	LEHVDFSSL
LHCLSFEQILQIFASAVLERKIIFLAEGLSTLSQC	CIHAAAALLY
PFSWAHTYIPVVPESLLATVCCPTPFMVGVOMRFC	OCEVMDSPME
EVLLVNLCEGTFLMSVGDEKDILPPKLQDDILDSI	GQGINELKT
AEQINEHVSGPFVQFFVKIVGHYASYIKREANGQG	HFOERSFCK
ALTSKTNRRFVKKFVKTQLFSLFIQEAEKSKNPPA	GYFQQKILE
YEEQKKQ/TETKGKNCEIRAVVNKND	1
TIPS PROTESTED	TRPGSSDIN
VAPGEQGPDQEETNTLVANTSNSNGLKLDPADPEN	PRSCOTVEV
QVNGNLVREPDHMELEEDRAGQLNMRGVFLHVLGD	

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ł	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
ļ	sequence	1	\=possible nucleotide insertion)
			NALVFYFSWKGCSEGDFCVNPCFPDPCKAFVEIINSTHASVYFA
			GPCWVLYLDPTLCVVMVCILLYTTYPLLKESALILLOTVPKOID
İ			IRNLIKELRNVEGVEEVHELHVWQLAGSRIIATAHIKCEDDTSY
1			MEVAKTIKDVFHNHGIHATTIQPEFASVGSKSSVVPCELACRTO
J	j ·	•	CALKQCCGTLPQAPSGKDAEKTPAVSISCLELSNNLRKKPRRTK
6834			AENIPA\VVIEIKN\IPNK\QPESSL
6634	78	1151	AGQERPAPIWRLLWLPTPSVSRKAEPAHIPINR*GA*E*RGGLP
i		1	LCGSSASAYGWH*RLTPWSPGGS*HM*SSKAPVTQAREVLVAGP
<u> </u>			CSKLVLSGARGIVGTTVQVLVEAQQPLLLLFTGVWGLNLRAGEE
	1		SRAL+LIBEVTQVRDAHLGNAVVGCAQCLSQGQVGSALAKALLE
j			AAAAVRDCKEVLTVSGDKQQAEVSVRL+VRDVCVEEAGCVEFGQ
	Ì		AHGRPGLALAKGRGGTNEVEEQVQVDGVQKLVLSAHECHELVAG
1		1	QQDGEDQAARTRLLQAGAHSVAHGRRQGQAPCRPHQEAGVSCHE
	1		LQQVVGDAL*ARE*APQIIVLLLLEDVAQLRTGKKA*DLVVDVE
6835	1	834	GIPAADR\EASLELIKLDISRTFPNLCIFQQGGPYHDMLHSILG
•			AYTCYRPDVGYVQGMSFIAAVLILNLDTADAFIAFSNLLNKPCQ
1			MAPFRVDHGLMLTYFAAFEVPFEENLPKLPAHFKKNNLTPDIYL
1			IDWIFTLYSKSLPLDLACRIWDVFCRDGEBFLFRTALGILKLFE
		·	DILTKMDFIHMAQFLTRLPEDLPAEELFASIATIQMQSRNKKWA
1		Ĭ	QVLTALQKDSREMREGKSVPPTLRLQREFALGTNQSPMPRPLCC
			FRLTPGQPRRTDAL
6836	1	850	MSCGRPPPDVDGMITLKV\DNLTYRTSPDSLRRVFEKYGRVGDV
<u>]</u> .			YIPREPHTKAPRGFAFVRFHDRRDAODAEAAMDGAELDGRELBU
J		1	QVARYGRRDLPRSRQGRRHAAGPEAA/RYGRRSRSYGRRSRSPR
1		1	RRHRSRSRGPSCSRSRSRSRSRYRGSRYSRSPYSRSPYSRSRYSRS
		1	PYSRSRYRESRYGGSHYSSSGYSNSRYSRYHSSRSHSKSGSSTS
1			SRSASTSKSSSARRSKSSSVSRSRSRSRSSSMTRSPPRVSKRKS KSRSRSKRPPKSPEEEGQMSS
6837	1	1369	TDGAAVAGNPGSDYFPGGTAP/GGPRTRRP\SGTSSSGSKASGP
i .			PNPPAQGDGTSLSPNYTLESTSGNDGKPVSGGGGRGRRKRDS
Ī	ļ	ĺ.	GHVSPGTPFDKYSAAPDSGGAPGVSPGQQQASGAAVGGSSAGET
Ĭ	ĺ	i	RGAPTPHEKALTSPSWGKGAELLLGDQPDLIGSLDGGAKSDSSS
ĺ			PNVGEFASDEVSTSYANEDEVSSSSDNPQALVKASRSPLVTGSP
			KLPPRGVGAGEHGPKAPPPALGLGIMSNSTSTPDSYGGGGGPGH
	•		PGTPGLEQVRTPTSSSGAPPPDEIHPLEILOAOIOLOROOFSIS
1			EDQPLGLKGGKKGECAVGASGAONGDSELGSCCSEAVKSAMSTI
1			DLDSLMAEHSAAWYMPADKALVDSADDDKTLAPWEKAKPONPNS
1			KEAHDLPANKASASQPGSHLQCLSVHCTDDVGDAKARASVPTWR
6838	16		SLHSDISNRFGTFVAALT
3030	16	499	LTDTPPPKTHMIHHSISDYKATLRCWALGFYPMEITLTWQQDEE
	i	1	DQTRDMELVETRPAGDGTFQKWAAVVVPSGEE/Q/RYMCHVQHE
			GLPEPLTLRWEQSSQPTIPIVGIVAGLVLLGAVVTGAVVSAVMC
6839	1	1195	RKKNSDRVSYSEAASSDHAQGSDVSLTACKV
	_]	1173	AAPAGGGPDPEALSAFPGRHLSGLSWPQVKRLDALLSEPIPIHG
			RGNFPTLSVQPRQIRAGGPQHPGGAG\IHVHRVRLHGSAASHVL
			HPESGLGYKDLDLVFRMDLRSEASFQLTKAVVLACLLDFLPAGV
			SRAKITPLTLKEAYVQKLVKVCTDSDRWSLISLSNKSGKNVELK
			FVDSVRRQFEFSIDSFQIILDSLLLFGQCSSTPMSEAPHPTVTG ESLYGDFTEALFHLEURYIATRS DEFINCEST TYPER A THROUGH
			ESLYGDFTEALEHLRHRVIATRSPEEIRGGGLLKYCHLLVRGFR
]		PRPSTDVRALQRYMCSRFFIDFPDLVEQRRTLBRYLEAHFGGAD AARRYACLVTLHRVVNESTVCLMNHERRQTLDLIAALALQALAE
ľ	1	Ì	QGPAATAALAWRPPGTDGVVPATVNYYVTPVQPLLAHAYPTWLP
		1	CN
6840	4254	2061	ELQGDFSVPDVPKSMAWCENSICVGFKRDYYLIRVDGKGSIKEL
			FPTGKQLEPLVAPLADGKVAVGQDDLTVVLNEEGICTQKCALNW

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A-Alanine, C-Cysteine, D-Aspartic Acid, E-
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
]	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
]	residue of	amino acid	WaTryptophan, YaTvrosine, XaUnknown +-Ston
ł	amino acid	sequence	Codon, /=possible nucleotide deletion
 	sequence		(\=possible nucleotide insertion)
			TDIPVAMEHQPPYIIAVLPRYVEIRTFEPRLLVOSTELOPPET
i			TSGGSNIIYVASNHFVWRLIPVPMATOIOOLLODKOFFI.AI.OI.A
l			EMKDDSDSEKQQQIHHIKNLYAFNLFCOKRFDESMOVFAKIGTD
			PTHVMGLYPDLLPTDYRKQLQYPNPLPVLSGAELEKAHLALTDV
1			LTQKRSQLVKKLNDSDHOSSTSPLMEGTPTIKSKKKLLOTIDTT
İ	ľ		LLKCYLHTNVALVAPLLRLENNHCHIEESEHVLKKAHKYSELII
1			LYEKKGLHEKALQVLVDQSKKANSPLKGHERTVQYLQHLGTENL
i	1		HLIFSYSVWVLRDFPEDGLKIFTEDLPEVESLPRDRVLGFLIEN
Į	1		FKGLAIPYLEHIIHVWEETGSRFHNCLIQLYCEKVQGLMKEYLL
1	1		SFPAGKTPVPAGEEEGELGEYRQKLLMFLEISSYYDPGRLICDF PFDGLLEERALLLGRMGKHEQALFIYVHILKDTRMABEYCHKHY
			DRNKDGNKDVYLSLLRMYLSPPSIHCLGPIKLELLEPKANLQAA
1			LQVLELHHSKLDTTKALNLLPANTQINDIRIFLEKVLEENAQKK
1			RFNQVLKNLLHAEFLRV\QEERILHQQVKCIITEEKVCMVCKKK
			IGNSAFARYPNGVVVHYFCS\KEVNPADT
6841	1	3206	TPSTTGTKSNTPTSSVPSAAVTPLNESLOPLGDYGVGSKNSKRA
			REKRDSRNMEVQVTQEMRNVSIGMGSSDEWSDVODTIDGTBELD
ì			MCPETRLDRTGSSPTQGIVNKAFGINTDSLYHELSTAGSEVIGD
ļ			VDEGADLLGEFSGMGKEVGNLLLENSOLLETKNALNGVKNDLTA
1			KVDQLSGEQEVLRGELEAAKQAKVKLENRIKELEEELKRVKSEA
	1		IIARREPKEEAEDVSSYLCTESDKIPMAQRRRFTRVEMARVLME
	1		RNQYKERLMELQEAVRWTEMIRASREHPSVQEKKKSTIWQFFSR
			LFSSSSSPPPAKRPYPSGNIHYKSPTTAGFSQRRNHAMCPISAG
1	}		SRPLEFFPDDDCTSSARREQKREQYRQVREHVRNDDGRLQACGW SLPAKYKQLSPNGGQEDTRMKNVPVPVYCRPLVEKDPTMKLWCA
1 .	1		AGVNLSGWRPNEDDAGNGVKPAPGRDPLTCDREGDGEPKSAHTS
1	į		PEKKKAKELPEMDATSSRVWILTSTLTTSKVVIIDANQPGTVVD
1 .	i	ĺ	QFTVCNAHVLCISSIPAASDSDYPPGEMFLDSDVNPEDPGADGV
ŀ			LAGITLVGCATRCNVPRSNCSSRGDTPVLDKGOGEVATIANGKV
]		Ì	NPSQSTEEATEATEVPDPGPSEPETATLRPGPLTEHVFTDPADT
İ			PSSGPQPGSENGPEPDSSSTRPEPEPSGDPTGAGSSAAPTMNLC
J			AQNGWLYVHSAVANWKKCLHSIKLKDSVLSLVHVKGRVLVALAD
		j	GTLAIFHRGEDGQWDLSNYHLMDLGHPHHSIRCMAVVYDRVWCG
1			YKNKVHVIQPKTMQIEKSFDAHPRRESQVRQLAWIGDGVWVSIR
1			LDSTLRLYHAHTHQHLQDVDIEPYVSKMLGTGKLGFSFVRITAL
1 1	1	Ĭ	LVAGSRLWVGTGNGVVISIPLTETVVLHRGQ\LLG\LRANKTSP TSGEG\ARPGG\IIHVYG\DDSSDRAARSFIPYCSMAQAQLCFH
		1	GHRDAVKFFVSVPGNVLATLNGSVLDSPAEGPGPAAPASEVEGQ
		1	KLRNVLVLSGGEGYIDFRIGDGEDDETEEGAGDMSQVKPVLSKA
			ERSHIIVWQVSYTPE
6842	3	926	RCQQLSATILTDHQYLERTPLCAILKOKAPOOYRTRAKLBSYKD
		j	RRLFQSVKLHCPKCHLLQEVPHEGDLDIIFODGATKTPDVKLON
1 1		ľ	TSLYDSKIWTTKNQKGRKVAVHFVKNNGILPLSNECLILITEGGT
{			LSEICKLSNKFNSVIPVRSGHEDLELLDLSAPFLIOGTVHHYGC
		1	KQWST*RSIQNLNSLVDKTSWIPSSVAEALGIVPLOYVFVMTFT
		1	LDDGTGVLEAYLMDSDKFFQIPASEVLMDDDLOKSVDMIMDMFC
6843	2	851	PPGIKIDAYPWLECFIKSYNVTNGTDNQ1CYQ1FDTTVAEDVI
	-	The state of the s	NHRKVLSGAKRYECNECGKSFAYTSSLIKHRRIHTGERPYECSE
		1	CGRSFAENSSLIKHLRVHTGERPYECVECGKSFRRSSSLLQHQR
			VHTRERPYECSECGKSFSLRSNLIHHQRVHTGERHECGQCGKSF
		1.	SRKSSLI IHLRVHTGERPYECSDCGKSFAENSSLIKHLRVHTGE
	1	į :	RPYECIDCGKSFRHSSSFRRHQRVHTGMRPYK*SKFWKFSCPGF
			LLLQGQRVHTGSRCYECDKWGIFFS*NASFFT*KSAPTEEVPFE CNECEKAFSPLSLVTTIFT
6844	244	642	EHQLAGFELRKTQTSMSLGTTREKTDRVKSTAYLSPQELEDVFY
			QYDVKSEIYSFGIVLWEIATGDIPFQGCNSEKIRKLVAVKRQQE
			Ασοπομιτικών Αντικόδη

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A-Alanine, C-Cysteine, D-Aspartic Acid, E-
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
[location	corresponding	H-Histidine, I=Isoleucine, K=Lysine,
ł.	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ļ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
- {	amino acid	residue of	Securing members to the state of the state o
ł	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	sequence	Codon, /=possible nucleotide deletion,
	bedaence		\=possible nucleotide insertion)
-{	·	ł	PLGEDCPSELREIIDECRAHDPSVRPSVDEILKKLSTFSK*CIK
6845	ļ		I
1 0043	3	1519	VAVRDECYWRHVFWDQDLWMLLFILMCHPETARARLEYRTRTLD
			GALENAQNLGYQGAKFAWESADSGLEVCPEDIYGVQEVHVNGAV
1			GLAFELYYHTTQDLQLFREAGGWDVVRAVAEFWCSRVEWSPREE
			KYHLRGVMSPDEYHSGVNNSVYTNVLVQNSLRFAAALAQDLGLP
i			IPSQWLAVADKIKVPFDVEQNFHPEFDGYEPGEVVKQADVVLLG
	1		YPVPFSLSPDVRRKNLEIYEAVTSPQGPAMTWSMFAVGWMELKD
		•	AVRARGLLDRSFANMAEPFKVWTENADGSGAVNFLTGMGGFLOA
f			VVFGCTGFRVTRAGVTFDPVCLSGISRVSVSGIFYOGNKLNFSF
	[SEDSVTVEVTARAGPWAPHLEAELWPSQSRLSLLPGHKVSPPRS
,	1		AGRIQMSPPKLPGSSSSEFPGRTFSDVRDPLOSPLWVTLGSSSP
1			TESLTVDPASE*SGTGASETSLGPSLWPRLHPPLLGTLLACHPS
			PAARLSGKVHAAWPEFKAFCL
6846	213	1258	LYFLKTIK*LNRLAEHP*YENEKLTKLRNTIMEQYTRTEESARG
1			IIFTKTROSAYALSOWITENEKFAEVGVKAHHLIGAGHSSEFKP
j			MTQNEQKEVISKFRTGKINLLIATTVAEEGLDIKECNIVIRYGL
1			VTNEIAMVQARGRARADESTYVLVAHSGSGVIEHETVNDFREKM
	1		MYKAIHCVQNMKPEEYAHKILELQMQSIMEKKMKTKRNIAKHYK
			NNPSLITPLCKNCSVLACSGEDIHVIEKMHHVNMTPEFKELYIV
		•	RENKTLQKKCADYQINGEIICKCGQAWGTMMVHKGLDLPCLKIR
1	i		NFVVVFKNNSTKKQYKKWVELPITFPNLDYSECCLFSDED
6847	1450	348	SMCWNSDRLEMPLIDLALILYPPSYVPYTGHLSDDSLSRKYCLT
			WFEDALNGVL*RAEAIQPHCVNAGDRMEKFRQKYWNKLQTLRQQ
			PFAYGTLTVRSLLDTREHCLNEFNFPDPYSKVKQRENGVALRCF
			PGVVRSLDALGWEERQLALVKGLLAGNVFDWGAKAVSAVLESDP
1			YFGFEEAKRKLQERPWLVDSYSEWLQRLKGPPHKCALIFADNSG
1 .			IDIILGVPPFVRELLLRGTEVILACNSGPALNDVTHSESLIVAE
			RIAGMDPVVHSALREERLLLVQTGSSSPCLDLSRLDKGLAALVR
1			ERGADLVVIEGMGRAVHTNYHAALRCESLKLAVIKNAWLAERLG
1 1			GRLFSVIFKYEVPAE
6848	19	16	AMWWNSLDGIRNIVLSNPKKRNTLSLAMLKSLQSDTLHDADSND
1			LKVIIISAEGPVFSSGHDLKELTEEQGRDYHAEVFQTCSKVMMH
			IRNHPVPVIAMVNGLATAAGCQLVASCDIAVASDKSSFATPGVN
ŀ			VGLFCSTPGVALARAVPRKVALEMLFTGEPISAQEALLHGLLNK
1 1			VVPEAELQEETMRIARKIASLSRPVVSLGKATFYKQLPQDLGTA
	ļ		YYLTSQAMVDNLALRDGQEGITAFLQKRKPVWSHEPV*VEH
6849	70	821	SLGVDGSCLEQGSPAPRPQTDTSP*PVGNWATQQEDLYHQSYEC
].			VCVLFASVPDFKEFYSESNINHEGLECLRLLNEI IADFDELLSK
]			PKFSGVEKIKTIGSTYMAATGLNATSGQDAQQDAERSCSHLGTM
		į	VEFAVALGSKLDVINKHSFNNFRLRVGLNHGPVVAGVIGAQKPQ
1 1			YDIWGNTVNVASRMESTGVLGKIQVTEETAWALQSLGYTCYSRG
1 1			VIKVKGKGQLCTYFLNTDLTRTGPPSATLG
6850	2	1235	ARGLNHEWTFEKLRQHISRNAQDKQELHLFMLSGVPDAVFDLTD
	,		LDVI.KLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFL
1 !			RDHLRCLHVKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMI
j j		1	GLESLRELRHLKILHVKSNLTKVPSNITDVAPHLTKLVIHNDGT
		ŀ	KIJAT NGI YYMMULARI RI ONGRE DO TOUT TO THE ONE
	[1	KLLVLNSLKKMMNVAELELQNCELERIPHAIFSLSNLQELDLKS
ļ l			NNIRTIEEIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESL
ļ l	}	İ	YFSNNKLESLPVAVFSLQKLRCLDVSYNNISMIPIEIGLLQNLQ
ļ i		l	HLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLPEKVGQLSQ
1	1		LTQLELKGNCLDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVK
6851	1765		EALNQDINIPFANGI
5551	7,62	660	VSAQVSAREGENCLGWNLADSSQESYKSLEEAEDCYPPSLLTLD
l l]	J	LRDLFNQVEQGPLLSCPKAGTDLSMGRAREVGWMAAGLMIGAGA
<u> </u>			CYCVYKLTIGRDDSEKLEEEGEEEWDDDQELDEEEPDIWFDFET

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F-Phenylalanine, G-Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine.
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ľ	sequence .	sequence	Codon, /=possible nucleotide deletion,
	Beguence 1		\=possible nucleotide insertion)
ļ			MARPWTEDGDWTEPGAPGGTEDRPSGGGKANRAHPIKQRPFPYE HKNTWSAQNCKNGSCVLDLSKCLFIQGKLLFAEPKDAGFPFSQD
1			INSHLASLSMARNTSPTPDPTVREALCAPDNLNASIESQGQIKM
1			YINEVCRETVSRCCNSPLQQAGLNLLISMTVINNMLAKSASDLK
			FPLISEGSGCAKVQVLKPLMGLSEKPVLAGELVGAQMLFSFMSL
			PIRNGNRBILLETPAP
6852	1	407	RTRGEETYANFIKHNDGKNIFYAARTPATLFAVMFAMYIISGLT
j	1		GFIGLNSIAVLCNLVMGLALIFLCTWAYVKYSGEFREIGTVIDQ
			IAETLWEQVLKPLGDNLMEENIRQSVTNSIKAGLTDQVSHHARL
6853	3	469	KTD
""		403	GDSCAVCIELYKPNDLVRILTCNHIFHKTCVDPWLLEHRTCPMC KCDILKALGIEVDVEDGSVSLQVPVSNEIFNSASSHEEDNRSET
ł	Ì		ASSGYASVQGTYEPPLEEHVQSTNESLQLVNHEANSVAVDVIPH
1			VDNPTFEEDETPNOETAVREIKS
6854	1148	585	HESYIGTFDPGELCVCAAIQWLQDNSASYFLNRKLVYBPSTQAK
			PVKNTFLRMWIYSHHIYQQDLRKKILDVGKRLDVTGFCMTGKPG
ŀ			IICVEGFKEHCEEFWHTIRYPNWKHISCKHAESVETEGNGEDLR
1	l i		LFHSFEELLLEAHGDYGLRNDYHMNLGQFLBFLKKHKSEHVFOI
6855	1913	1110	LFGIESKSSDS
0000	1913	1148	GRVGGRVGRICSPLSGANEYIASTDTLKTEEVLLFTDQTDDLAK
	•		EEPTSLFQRDSETKGESGLVLEGDKEIHQIFEDLDKKLALASRF YIPEGCIQRWAAEMVVALDALHREGIVCRDLNPNNILLNDRGHI
			QLTYFSRWSEVEDSCDSDAIERMYCAPEVGAITEETEACDWWSL
			GAVLFELLTGKTLVECHPAGINTHTTLNMPEWVSEEARSLIQQL
			LQFNPLERLGAGVAGVEDIKSHPFFTPVDWAELMR
6856	1617	997	VTQLYVSVDASTKDSLKKIDRPLFKDFWQOFLDSLKALAVKOOR
1			TVYRLTLVKAWNVDELQAYAQLVSLGNPDFIEVKGVTYCGESSA
1 1			SSLTMAHVPWHEEVVQFVRELVDLIPEYEIACEHEHSNCLLIAH
			RKFKIGGEWWTWINYNRFQELIQEYEDSGGSKTFSAKDYMARTP
6857	1	617	HWALFGASERGFDPKDTRHQRKNKSKAISGC
	-	617	KGPEATAMVCVCSHPNCRQNHIKPSHSAAQTWCGSPTPASAPNH KLMAMEQGKTLPSATEDAKEEGLEAQISRLABLIGRLESKALWF
			DLQQRLSDEDGTNMHLQLVRQEMAVCPEQLSEFLDSLRQYLRGT
]			TGVRNCFHITAVRLSDGFTFVIYEFWETEEAWKRHLQSPLCKAF
			RHVKVDTLSQPEALSRILVPAAWCTVGRD
6858	.2	669	RSRGIKDFENDPPLSSCGIFQSRIAGDALLDSGIRISSVFASPA
]]	ł		LRCVQTAKLILEELKLEKKIKIRVEPGIFEWTKWEAGKTTPTLM
	[SLEELKEANFNIDTDYRPAFPLSALMPAESYQEYMDRCTASMVQ
1	1		IVNTCPQDTGVILIVSHGSTLDSCTRPLLGLPPRECGDFAQLVR KIPSLGMCFCEENKEEGKWELVNPPVKTLTHGANAAPNWRNWIS
	ľ		GN CFCEENKEEGKWELVNPPVKTLTHGANAAFNWRNWIS
6859	1	1150	GETMFKKAKTKAKKKPRKRSDSSGGYNLSDI IQSPSSTGLLKSG
1			KTNSVESLPELLTSDSEGSYAGVGSPRDLQSPDFTTGFHSDKIE
			AKVKPYVNGTSPVYSREDLKPWEKSPILKISAPQPIPSNRIDTT
			SSASWVAGSPSPVSPPVVDLRTIMEIEESRQKCGATPKSHLGKT
			VSHGVKLSQKQRKMIALTTKENNSGMNSMETVLFTPSKAPKPVN
			AWASSLHSVSSKSFRDFLLEEKKSVTSHSSGDHVKKVSFKGIEN
			SQAPKIVRCSTHGTPGPEGNHISDLPLLDSPNPWLSSSVTAPSM
			VAPVTFASIVEEELQQEAALIRSREKPLALIQIEEHAIQDLLVF
6860	1889	1515	YEAFGNPEEFVIVERTPQGPLAVPMWNKHGC
		1312	DKDKKRQKKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKQLAQ
	1]	DTGLTILQVNNWFINARRIIVQPMIDQSNRAVSQGAAYSPEGQP MGSFVLDGQQHMGIRPAGPMSGMGMNMGMDGQWHYM
6861	1889	1515	DKDKKRQKKRGI PPKVATNIMRAWLFQHLTHPYPSEEQKKQLAQ
			DTGLTILQVNNWFINARRIIVQPMIDQSNRAVSQGAAYSPEGQP

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L-Leucine, M-Methionine, N-Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence		\=possible nucleotide insertion)
			MGSFVLDGQQHMGIRPAGPMSGMGMNMGMDGQWHYM
6862	2	471	EEIDREFHNKLKLKEDKLEKQEKPVNGEDKGDSGVDTQNSEGNA
İ			DEEDPLGPNCYYDKTKSFFDNISCDDNRBRRPTWAEERRLNAET
ŀ			FGIPLRPNRGRGGYRGRGGLGFRGGRGGGRGGTFTAPRGFRG
			GFRGGRGGREFADFEYRKTTAFGP
6863	2216	487	PQEPALKSEFSQVASNTIPLPLPQPNTCKDNGPCKQVCSTVGGS
1			AICSCFPGYAIMADGVSCEDQDECLMGAHDCSRRQFCVNTLGSF
	1		YCVNHTVLCADGYILNAHRKCVDINECVTDLHTCSRGEHCVNTL
1			GSFHCYKALTCEPGYALKDGECEDVDECAMGTHTCQPGFLCQNT
j			KGSFYCQARQRCMDGFLQDPEGNCVDINECTSLSEPCRPGFSCI
			NTVGSYTCQRNPLICARGYHASDDGTKCVDVNECETGVHRCGEG
			QVCHNLPGSYRCDCKAGFQRDAFGRGCIDVNECWASPGRLCQHT
1			CENTLGSYRCSCASGFLLAADGKRCEDVNECEAQRCSQECANIY
1			GSYQCYCRQGYQLAEDGHTCTDIDECAQGAGILCTFRCLNVPGS YQCACPEQGYTMTANGRSCKDVDECALGTHNCSEAETCHNIQGS
J			FRCLRFECPPNYVQVSKTKCERTTCHDFLECQNSPARITHYOLN
Į.			FQTGLLVPAHIFRIGPAPAFTGDTIALNIIKGNEEGYFGTRRLN
			AYTGVVYLQRAVLEPRDFALDVEMKLWRQGSVTTFLAKMHIFFT
			TFAL
6864	2	2933	LADSSPSNLQIIIKELLSMHHQPDPALTKEFDYLPPVDSRSSSG
			FVGLRNGGATCYMNAVFQQLYMQPGLPESLLSVDDDTDNPDDSV
1			FYQVQSLFGHLMESKLQYYVPENFWKIFKMWNKELYVREQQDAY
i .			EFFTSLIDQMDEYLKKMGRDQIFKNTFQGIYSDQKICKDCPHRY
1			ERBEAFMALNLGVTSCQSLEISLDQFVRGEVLEGSNAYYCEKCK
			EKRITVKRTCIKSLPSVLVIHLMRFGFDWESGRSIKYDEQIRFP
1			WMLNMEPYTVSGMARQDSSSEVGENGRSVDQGGGGSPRKKVALT
			ENYELVGVIVHSGQAHAGHYYSFIKDRRGCGKGKWYKFNDTVIE
1			EFDLNDETLEYECFGGEYRPKVYDQTNPYTDVRRRYWNAYMLFY
į .			QRVSDQNSPVLPKKSRVSVVRQEAEDLSLSAPSSPEISPQSSPR
}			PHRPNNDRLSILTKLVKKGEKKGLFVEKMPARIYQMVRDENLKP MKNRDVYSSDYFSFVLSLASLNATKLKHPYYPCMAKVSLQLAIQ
1			FLFQTYLRTKKKLRVDTEEWIATIEALLSKSFDACOWLVEYFIS
			SEGRELIKIFLLECNVREVRVAVATILEKTLDSALFYQDKLKSL
<u> </u>			HQLLEVLLALLDKDVPENCKNCAQYFFLFNTFVQKQGIRAGDLL
l			LRHSALRHMISFLLGASRONNQIRRWSSAQAREFGNLHNTVALL
l i			VLHSDVSSQRNVAPGIFKQRPPISIAPSSPLLPLHEEVEALLFM
] [SEGKPYLLEVMFALRELTGSLLALIEMVVYCCFCNEHFSFTMLH
			FIKNQLETAPPHELKNTFQLLHEILVIEDPIQVERVKFVFBTEN
			GLLALMHHSNHVDSSRCYQCVKFLVTLAQKCPAAKEYFKENSHH
)			WSWAVQWLQKKMSEHYWTLQSNVSNETSTGKTFQRTISAQDTLA
}			YATALLNEKEQSGSSNGSESSPANENGDRHLQQGSESPMMIGEL
6865	1930	1575	RSDLDDVDP
0005	1820	1242	DPERWKHLSKVTPPGSSVSTTPVQVVRLQSPQSQGSMMPSCNRS
			CSCSRGPSVEDGKWYGVRSYLHLFYEGYAVPPKLEGIGEGEFLV
]]	ļ		LDQRAADYNQALGTCRLAGTALCVAAGVLLAICLFWAMIGWLSQ
	ł		DTKAEPLDPEADSHVEVFGDEPEQQLSPIFRNASGQSWFSPPAS
6866	1571	495	PFGQSSVQTIQPKRDS DCPRPRYTLYGLRATCMRDLDWAWINAVSAFKALEQDLPVNIKF
		•	IIEGMBEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISORKP
	ļ		AITYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLG
]			SLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLDLEEYRNSSR
	1	j	VEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRV
	l	l	IGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTL
	ĺ		GLHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMF
	Į		QEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKLFAAFFL
L			EMAQLH

SEO	Predicted	I honey and	
ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A-Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
l	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
ļ	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
İ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	1	\=possible nucleotide insertion)
6867	2833	1704	GTRIMSQPKQKELAGFVRQKMLLDYSVYMGRCVPQESRSPQRSP
1			LOSAESSPTAGKKLPEVPPSEEBEQEAWVNALLGRIFWDFLGEK
}		ļ	YWSDLVSKKIQMKLSKIKLPYFMNBLTLTBLDMGVAVPKILQAF
1	ĺ		KPYVDHQGLWIDLEMSYNGSFLMTLETKMNLTKLGKEPLVEALK
ł			VGEIGKEGCRPRAFCLADSDEESSSAGSSEEDDAPEPSGGDKQL
	ļ		LPGAEGYVGGHRTSKIMRFVDKITKSKYFQKATETEFIKKKIEE,
ł			VSNTPLLLTVEVQECRGTLAVNIPPPPTDRVWYGFRKPPHVELK
			ARPKLGEREVTLVHVTDWIEKKLEQEFQKVFVMPNMDDVYITIM
			HSAMDPRSTSCLLKDPPVEAADOP
6868	1	346	RPTRPPTRPEEIKNLILPYISDMNFVQDLCEDFYELFKTDKGFD
			KATFESQMSVMRGQILNLTQALRDGKSPFQLVQIPCVIVERSQG
			GSQGRIVHLSNSFTQTVNCRKPFFSSW
6869	3	1619	MYMERMDKRALISFWESVEHLKNANKNEIPQLVGEIYQNFFVES
1			KEISVEKSLYKEIQQCLVGNKGIEVFYKIOEDVYETIKDRYYPS
}			FIVSDLYEKLLIKEEEKHASQMISNKDEMGPRDEAGBEAVDDGT
! .			NQINEQASFAVNKLRELNEKLEYKRQALNSIQNAPKPDKKIVSK
1	j		LKDEIILIEKERTDLQLHMARTDWWCENLGMWKASITSGEVTEE
			NGEQLPCYFVMVSLQEVGGVETKNWTVPKRLSEFHNLHRKLSEC
			VPSLKKDQLPSLSKLPFKSIDHTFMEKFENOLNKFLONLLSDER
			LCQSEALYAPLSPSPDYLKVIDVOGKKNSFSLSSFLERLPRDFF
			SHQEEETEEDSDLSDYGDDVDGRKDALAEPCFMLIGETFELRGM
1			FKWVRRTLIALVQVTFGRTINKQIRDTVSWIFSEQMLVYYINIF
			RDAFWPNGKLAPPTTIRSKEQSQETKQRAQQKLLENIPDMLQSL
1			VGQQNARHGIIKIFNALQETRANKHLLYALMELLLIELCPELRV
6870	1	1566	HLDQLKAGQV
	-	1300	MAAVVAATRWWQLLLVLSAAGMGASGAPQPPNILLLLMDDMGWG
1 1	1		DLGVYGEPSRETPNLDRMAAEGLLFPNFYSANPLCSPSRAALLT
1			GRLPIRNGFYTTNAHARNAYTPQEIVGGIPDSEQLLPELLKKAG
	}		YVSKIVGKWHLGHRPQFHPLKHGFDEWFGSPNCHFGPYDNKARP
]]			NIPVYRDWEMVGRYYEEPPINLKTGEANLTQIYLQEALDFIKRQ ARHHPFFLYWAVDATHAPVYASKPFLGTSQRGRYGDAVREIDDS
1 1			IGKILELLQDLHVADNTFVFFTSDNGAALISAPEQGGSNGPFLC
1. 1			GKQTTFEGGMREPALAWWPGHVTAGQVSHQLGSIMDLFTTSLAL
1 1			AGLTPPSDRAIDGLNLLPTLLQGRLMDRPIFYYRGDTLMAATLG
	}		QHKAHFWTWTNSWENFRQGIDFCPGQNVSGVTTHNLEDHTKLPL
			IFHLGRDPGERPPLSFASAEYQEALSRITSVVQQHQEALVPAQP
			QLNVCNWAVMNWAPPGCEKLGKCLTPPESIPKKCLWSH
6871	209	1126	RMSLNPPIFLKRSEENSSKFVETKOSOTTSIASEDPLONLCLAS
jĺ			QEVLQKAQQSGRSKCLKCGGSRMFYCYTCYVPVENVPIEOIPLV
			KLPLKIDIIKHPNETDGKSTAIHAKLLAPEFVNIYTYPCIDEYE
			EKDHEVALIFPGPQSISIKDISFHLOKRIONNVRGKNDDPDKDS
	ļ		FKRKRTEEQEFCDLNDSKCKGTTLKKIIFIDSTWNOTNKIFTDE
	. 1		RLQGLLQVELKTRKTCFWRHQKGKPDTFLSTIEAIYYFLVDYHT
6872	995		DILKEKYRGQYDNLLFFYSFMYQLIKNAKCSGDKETGKLTH
00/2	880	459	FGLLMVVLSLIFMKGNCVREDLIFNFLFKLGLDVRETNGLFGNT
			KKLITEVFVRQKYLEYRRIPYTEPAEYEFLWGPRAFLETSKMLV
			LRFLAKLHKKDPQSWPFHYLEALAECEWEDTDEDEPDTGDSAHG
6873	1020		PTSRPPPR
00/3	1929	955	DEQAVLCSKDKTYDLKIADTSNMLLFIPGCKTPDQLKKEDSHCN
			IIHTEIFGFSNNYWELRRRRPKLKKLKKLLMENPYEGPDSOKEK
J			DSNSSKYTTEDLLDQIQASEEEIMTQLQVLNACKIGGYWRILEF
	[1	DYEMKLLNHVTQLVDSESWSFGKVPLNTCLQELGPLEPEEMIEH
-			CLKCYGKKYVDEGEVYFELDADKICRAAARMLLQNAVKFNLAEF
		}	QEVWQQSVPEGMVTSLDQLKGLALVDRHSRPEIIFLLKVDDLPE
1			DNQERFNSLFSLREKWTEEDIAPYIQDLCGEKQTIGALLTKYSH SSMQNGVKVYNSRRPIS

Millo Beginning Contion Contion Contion Contion Cortion Contion Contion Contion Continuo Contragonding Continuo Contragonding Cont	SEQ	Predicted	Predicted end	
Docation Corresponding to first amino acid residue of samino acid residue of amino acid sequence Service of the sequence Service of amino acid sequence Service of the sequence Service of	_			Amino acid segment containing signal peptide
location corresponding to first amino acid m	1			Glutamic Reid P. Phonelelenia C. Clutamic Reid P. Phonelelenia
corresponding to first amino acid residue of residue of amino acid sequence should be amino acid sequence seque	""			W-Wight ding T-Taglewater W. T. Taglewater
to first amino acid residue of amino acid residue of amino acid residue of amino acid sequence of security. The present of the control of amino acid sequence of security. The control of the control of amino acid sequence of the control of the con	1			Televoice Memorbiosis V Paris
amino acid residue of amino acid sequence acid sequence acid s	ŀ		3	D-Droline O-Clutarine D Turk
residue of amino acid sequence	ļ	1	1	S-Coving M. Mhanarian M. Marginine,
amino acid sequence 6874 1 307 ESTADNINSARI/WESTKINICHAMIKUMI, **SCOP STADNINSARI/WESTKINICHAMIKUMI, **SCOP STADNINSARI/WESTKINICHAMIKUMIALIVAGALIGGWWG CPIGLIAGFKYAGIAALGGWUSPTGKILIGKKKKMMKKLTS SCEDLISGTONKK. 6875 1688 349 VIGTGERGNSASERKEIMFINELGDFFIIHSISLLARGHKINKKYEIKKRQ LRKKVPHYAALEPDGMGKUMIKYKSLIFTVQAQQDEBMINDEI SEKKEPHYWQDTEDLITVIIRJEDHINEDIG UQELPHPHINI VLKONGPILEGKLYSSIDHESSTWIIKESNSLEISLIKKNGKYEIKKDI LRKKVPHYAALEPDGMGKUMIVSYKSLIFTVQAQQDEBMINDEI SEKKEPHYWQDAYDADEBMINDEI SEKKEPHYWQDAYDADEBMINDEI SEKKEPHYWQDAYDADEBMINDEISLIKKNGKOPHINDE VLKONGPILEGKLYSSIDHESSTWIIKESNSLEISLIKKNGKUME VLKONGPILEGKLYSSIDHESSTWIIKESNSLEISLIKKNGKUME VLKONGPILEGKLYSSIDHESSTWIIKESNSLEISLIKKNGKUME VLKONGPILEGKLYSSIDHESSTWIIKESNSLEISLIKKNGKUME REGROGGOVAKQOVAXCOVASLETNDEI INFORMIKETYPHOKPEKPP CNAQELBECDIFFEESSLICRDONTILKTHVUNISSNOYLEGHD REGROGGOVAXCOVASLETNDEI INFORMIKETYPHOKPEKPP CNAQELBECDIFFEESSLICRDONTILKTHVUNISSNOYLEGHD REGROGGOVAXCOVASLETNDEI INFORMIKETYPHOKPEKPP VANSTIEM 1285 VGENTLINRHLERPLCUVTSAPRILEMHPFLSLGTSRTSVTKLS LHTKPRMPPDCDPMPERVQVIFLVSSSSBARLAMIMARAHAND LHTKPRMPPDCDPMPERVQVIFLVSSSSBARLAMIMARAHAND LHTKPRMPPDCDPMPERVQVIFLVSSSSBARLAMIMARAHAND REGROGGSRCBSPVOTIRKCSCADDCOARDOY IEQFKOTISTE VARSIAGPFARPICQUVIFLVVSSSSBARLAMIMARAHAND REVOTOFICKUS STADENTAMIC INFORMICATION INFORMICATION REVOTOFICKUS STADENTAMICATION INFORMICATION INFORMICATION REVOTOFICKUS STADENTAMICATION INFORMICATI	Į.			S-Serine, leinreonine, vevaline,
Sequence N-possible nucleotide Insertion	1			Codon /wassible surlantide A stop
1 307 DETADIWASANAWVEEGTRNICKARKYKARAIPVAGALIGGWWG PICLLAGFKWAGIAAAKGGWLOPTGGKLIGKKGGWMEKTE. 6875 1688 349 VIGTGERGNSAEFKWEIMFNEELGDFFITHESISLIAAEHBIST TILLARE RESIDMINGSOFTVOSKENONIKKYE I KROI LAGKSVPHYAALEPDGNGKIVSYKSLIFTVQAGQLEENNOMIK YE IKKDI LRGKSVPHYAALEPDGNGKIVSYKSLIFTVQAGQLEENNOMIK YUKUNGOTEDDLIVTIR PEDENTKEDI QUGHPHHINI VUKUNGOTEGKURUPSKIVATURA VUKUNGOTEGKURUPSKATURA VUKUNGOTEGKURUPSKATURA VUKUNGOTEGKURUPSKATURA VUKUNGOTEGKURUPSKATURA VUKUNGOTEGKURUPSKATURA VUKUNGOTEGKURUPSKATURA VUKUNGOTEGKURUPSKATURA VUKUNGOTEGKURUPSKATURA VUKUNGOTEGKURUPSKATURA VUKUNGOTEGKURUPSKATURA VUKUNGOTEGKURUPSKATURA VUKUNGOTEGKURUPSKATURA VUKUNGOTEGKURUPSKATURA VUKUNGOTEGKURUPSKATURA VUKUNGOTEGKURUPSKATURA VUKUNGOTEGKURUPSKATURA VUKUNGOTEGKURUPSKATURA VUKUNGOTEGKURUPKA VUKUNGOTE	ĺ	i e	bequence	_magaible nucleotide deletion,
GPIGLIAGFKYNGIAALIGGGUIFPTGKKI QRKKMMKKUTS GPIGLIAGFKYNGIAALIGGGUIFPTGKKI QRKKMMKKUTS SCDLLSGJTOKKCS 1688 349 VIGTGERGNSASEKKEIMFNEELGDFFIIHSISLINAELHSIA TULLRIEREELDMKGSGFYVSLEWYISKINQDNKKYEIIKAG LRGKSYHYAALEPDGNGLMIVSKSLTTVQAGQLEENNDEDI SEKIKSPLYWQOTEDLTVTIRLPEDNYKSLITVQAGQLEENNDEDI SEKIKSPLYWQOTEDLTVTIRLPEDNYKSLITVQAGQLEENDEDI SEKIKSPLYWQOTEDLTVTIRLPEDNYKSLITVQAGQLEENDEDI SEKIKSPLYWQOTEDLTVTIRLPEDNYKSLITVQAGQLEENDEDI SEKIKSPLYWQOTEDLTVTIRLPEDNYKSLITVQAGQLEENDEDI SEKIKSPLYWQOTEDLTVTIRLPEDNYKSLITVQAGQLEENDEDI VUNKOGGELIRDSAQCAAIASRIMMILTSELMPNDOKENGUT VUNKOGGELIRDSAQCAAIASRIMMILTSELMPNDOKENGUT VUNKOMERCTLIRHDVALLMQPISSKODDMSHITATFRALEYV QASKROKKFPACHYSYAALCELRRVETYRQPSTVLYBNINGSNQVLSV LVDPKEMBCFCLRHDVALLMQPISSKODDMSHITATFRALEYV QASKROKKFPACHYSYAALCELRRVETYRQPSTVLYBNINGSNQVLSV KEGRQVGQVAKQQVASQLETNDPILGPQATNERLLPVLTTKNILFIL KVYPTEN 1015FRGATHGCSTPTYSTYALCHTVALLAGUTTIRLEMPFLSGTSTTSVTKLS LHTYRPRIPPCDPMPERYQVIFLUNSSSEANILAMMARAHSINT DIISFRGATHGCSTPTLIGLTNOYTYRMLIGGTGCOPTHCPDVIF RSPWGGSSICRDSPVCTIRKCSCAPDCCQARQYIEQPENDUT RSPWGGSSICRDSPVCTIRKCSCAPDCCQARQYIEQPENDUT RSPWGGSSICRDSPVCTIRKCSCAPDCCQARQYIEQPENDUT PETAKSLAKCLOHNTGGONAGCAIGSALLEVITARAGGVOTIAN EVYTOFGRILSSHFWGFCTHBULDDIVTMAGIGNOFPMAAVIT PETAKSLAKCLOHNTGGONAGCAIGSALLEVITARAGGVOTIAN EVYTOFGRILSSHFWGFCTHBULTTCTCTSCHOP PREWVOIHBDCKMGLUNGGSISTSGTFTAIAPSCITTPRUD PREWVOIHBDCKMGLUNGGSISTSGTTMARAGIGNENGON PTORNKOLLIFARAVEDDOOTITYTHHLTTCTTSCHOP AVEVPRSALLAVATENDSQODTIKYTHHLTTCTTSCHOP PTORNKOLLIFARAVEDDOOTITYTHHLTTCTTCTSCHOP PTORNKOLLIFARAVEDDOOTITYTHHLTTCTTCTSCHOP PTORNKOLLIFARAVEDDOOTITYTHHLTTCTTCTCHOP PTORNKOLLIFARAVEDDOOTITYTHHLTTCTTCTCHOP PTORNKOLLIFARAVEDDOOTITYTHHLTTCTTCTCHOP PTORNKOLLIFARAVEDDOOTITYTHHLTTCTTCTCHOP PTORNOLLIFARAVEDDOOTITYTHHLTTCTTCTCHOP PTORNCOLLIFARAVEDDOOTITYTHHLTTCTTCTCHOP PTORNCOLLIFARAVEDDOOTITYTHHLTTCTTCTCHOP PTORNCOLLIFARAVEDDOOTITYTHHLTTCTTCTCHOP PTORNCOLLIFARAVEDDOOTITYTHHLTTCTTCTCHOP PTORNCOLLIFARAVEDDOOTITYTHHLTTCTTCTCHOP PTORNCOLLIFARAVEDDOOTITYTHHLTTCTTCTCHOP PTORNCOLLIFARAVEDDOOTITYTHHLTTCTTCTCHOP PTORNCOLLIFARAVEDDOOTITYTHHLTTC	6874		307	\copposition nucleotide insertion)
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PELVIGNKGGELIRDSAQCAAIAREMHLTSEELNPNDPKEKPP CNAQELEECL FYFEESSLERDENTLATVAULGSNOYLPSV LVAPKEMPCFCLRRUVBALLWQPHSSKQDDMWEHIATFNALGYV QASKRDKKFFACAPNYSYAALCECLRRVFITRQDARMETVLYNR REGRQVGQVARQQVASLETNDPILGPCATRRELEVLTTENLFLI KVATTEN 1285 41 1285 VGEMTLINRHLLRELGLVTSAPRILEMHPFLSLGTSRTSVTKLS LHTKPRMPPCDPMPERYQUIFLVNSGSRANKLAMLMARAHSNNI LHTKPRMPPCDPMPERYQUIFLVNSGSRANKLAMLMARAHSNNI LHTKPRMPPCDPMPERYQUIFLVNSGSRANKLAMLMARAHSNNI BVQTGVGRLGSHFWGPCTHDVLPDIVTMAKGIGNGFPMAAVIT PEIAKSLAKCLQHFNTFGGNBMACAIGSAVLEVIKERLGNNSQ EVETYMLKAPKALRDFEIFUGDVRGKUMIGLEWVQDKISCRPL PREVNQIHBDCHMMGLUFGNSTFSOTFRIAPSMCITKPEVDF AVEVPRSALITOHMERAK 6877 1 778 GTSSSPARAYAPPTEEKRRYQNVSITQGGGFEINLDHRKLKTP QAKLPTVPSEALAIAVATEWDSQODTIKYYTMHLTTLCNTSLON PTQRKRQLIRAAVKELDTDTICTKVEEFELLQRREMMPII EMABKRYGVEISSSTSIMGPSIPAKTREVLUSHLASYTWALQG IEPVAQLKSRVLTUGLIDLBLTVEGAVLLSPLEEFYGIQKMCM IEMAHDYBLGBLRARTAGGTFHHLCSSSTTVKHKLLKR 6878 931 263 CTCGGSFKRRAEMTDBNIGKROWTDLSHLESPYGIKKCM IEMAHDYBLGBLRARTAGGTFHHLCSSSTTVKHKLLKR CTCGGSFKRRAEMTDBNIGKROWTDLSHLESPYGIKKCM IEMAHDYBLGBLRARTAGGTFHHLCSSSTTVKHKLLKR TGYSGCRARKSVOTRGENGRWYDLDHAISIAIAVAVVALVIS VCGLGVCYAQRKSYFSKETSFQKSNSSKATTMSENDFKHTKSFI II 6879 3 845 IKVIGSSDIMGPFLSSSDENYNGVSDVELRVALPFGTFTVTYVKK PPPKLYIQNYTSAVPGTCLTIRKWLFTESETILLBKDNDLAVTYP FRQANDOVKKGYIKABEKSVQLQKLYBGROWMYLLANGTCEGY NEITPHICAGDSRRGHHIVTAISITHFCHISFDVKKLAPNE PPKLYIQNYTSAVPGTCLTIRKWLFTESETILLBKDNDLAVTYP FRQANDOVKKGYIKABEKSVQLQKLYBGROWMYLLANGTCEGY NEITPHICAGDSRRGHGHITAISITHFCHISFDVKKLAPNE PPKLYIQNYTSAVPGTCLTIRKWLFTESETILLBKDNDLAVTYP FRQANDOVKKGYIKABEKSVQLQKLYBGROWMYLLANGTCEGY NEITPHICAGGSRRGHGHITAISITHFCHISFDVKKLAPNE PPKLYIQNYTSAVPGTCLTIRKWLFTESETILLBKDNDLAVTYP FRQANDOVKGYIKABERSVALIFYTPFGSQLEMQVIA FRENDEMGRODTDEEGMARCFEYARGEKPRWVKIFTPYFNYMHE CERRYFCELKWREESY NRDQIKCGFFTGHRASVALIFVTAFGGSAFFILKFKBNDEN NRDQIKCGFFTGHRASVALIFVTAFGGSAFFILKFKBNDEN PROGRENGERGRINGTFRENDVIN VANAQVTTVITITVSVLVPFFRSEEFFLEBSVLLSEFTRESBED GROWNAVEDLERGERGRINGTSFRENDVIN OSGMWYARQEBRILVISLTCCODTLITLSAATTROLLLEFKFT TANAVHKCKFURGLETESGERGRATAGNTSFRENDVIN OSGMWYARQEBRILVISLTC	1			SEATAEPLYYWQQTEDDLTVTIRLPEDNTKEDIQIQFLPDHINI
CNAGELESCO IFFESSISLERBORITATIVATURALISMOTIFS IVOPREMBEGECLIRRUPISS KODDMMENIATIVALIGY QASKRIKKF FACARIN'SYAALCECLIRRUFI'KQPAPMSTVLYNR REGROWGOVAKQVAS LETNID ILGFQATIBELFULTKINFIL 6876 41 1285 VGENTLIWRHLIRPLCUTTSAFRILEMHEPISLGTSRTSVTKLS LHTYRPMBPCDFMERRYOU'FLUNSGSEANBLAMLARARASINI DISFRGAYHGCSPYTLGLTNVGIYKMELPGGTTCOPTMCDDVF RGPWGGSHCRDSPOYTIRKGSCSAPCCAROOV'I EQFKDTLSTS VAKSIAGPPAPIGONGVOYPKGELREAFELVRARGOVCIAN EVOTOFGRILGSHFWGFOTIDULPDI'VTRAGIGORPHAAVITT PEIAKSLAKCLQHFNTFGGNPMACAIGSAVLEVIKEENLQENSG EVGTYMLLKFAKLRGEFEI VCDVRGKGSI FSGTFALTSBMCITKFVDF ANEVPRSALTCHMERRAK 6877 1 778 GTSFSFARAYAPFTERKRYRYON'SITYGGGGFEINLDHRKLKTP QALLFTVPSEALAIAVATENDSQODTIKYYTMHLTTLCNTSLON PTORNKODLIRAAVKELDTDI'CTRVEEPTSMCITKFVDF ANEVPSALITANAVATENDSQODTIKYYTMHLTTLCNTSLON PTORNKODLIRAAVKELDTDI'CTRVEEPTSMCITKFVDP EMBERRYGVEISSSTSIMDSIPAKTREULVSHLASYNTWALQG IEWAHDYELGELRAATRAGTLFHLCSSSTTVCHKILKE GERBYTULVLAPAVPSECUFSSALSSTVCHKILLER CHECHTVTLEU'LVAPAVPSECUFSSALSSTVCHKILLER ETTWRGGIRLLENDRICSGSTNSSTVNTKTGTLGFTOTOKMCN LEWAHDYELGELRAATRAGTLFHLCSSTTVCHKILLER ETTWRGGIRLLENDRICSGSTNSSTVNTKTGTLGFTTVTKKL CELECTVTLEU'LVAPAVPSECUFSSALSSTVCHKILLER ETTWRGGIRLLENDRICSGSTNSSTVNTKTGTLGFTTVTKVK VCCLGGVCAQRKGYFSKETSFQXSNSSSKATTMSENDFKHTKSF II 6879 3 645 IRVIGESDIMGETLSESDENYNGVSDVELRVALPPDGTTVTVRVK KNSTTDQV'QAIAAVKODSTTVNTFALFEVISHSFVNLAPVNR FPRIKLYIQNTSASPGGTCLITKRWLFTTEEBELLIANDNLAVTYF FRIQANDDVKKGYIKAEEKSVOLKLYEGRKWAVILLINERTEEGY NEITPHICAGORSRIGHUTTAISTHFFLHAGTESGOLENQVILA FENDBMORNDTDESGMARCFEYARGEKKPRWVKIFTPYPYNMHE CERRYFCELKHKEEY CERRYFCELKHKEEY ANNIYNSKILKRSNQLTESTFIQNSKLYFGGLINGLITLGLGRS NEDGIRGCGFFGRAFGSVALIFTARGEFFLERGOLENQVILA FRIDDINGCGFFGRAFGSVALIFTARGEFFLERGOLENQVILA NEITPHICAGORRIGHUTTAISTHFFLHAHATESGOLENQVILA FREDEMRORDTDESGMARCFEYARGEKKPRWVLIFTPYNALD ANNIYNSKILKRSNQLTESTFIQNSKLYFFGLIFNGLTHLGLGRS NEDGIRGCGFFGGRAFGSVALIFTARGEFFLERGOLENGVTOG REGOLFFYTYNSKLUTHGOLFTHAHERODFVNAIKGEPR ORVAAVKDLIRGLFFREIGNIANTFREUVIN OGGMNVTARGERTANTAVORDIVELILLESSFCR 6881 2638 2244 NOSKWEDIHATIGLETGGOLENGVTINFHE	1	}		VEKUNGFLEGKLYSSIDHESSTWIIKESNSLEISLIKKNEGLTW
TVDPKEMPCFCLRHUVDALLMCPHSKGDDMWRITATINATEVY QASKRIKKFRACANYSYAALCECURRYTYRQDAMSTVLYNN KEGROVGOVAKQOVAS LETNDPILOFQATNERLFVLTTKNLFLI KVANTEN 1285 VGEMTLIWRHLRPLCIVTSAPRILEMHPFLSLGTSRTSVTKLS LHYKPRMPPCDPMERRYQVIFIJUNGGSEANELAMLMARAHSNNI DIISPRGAYHGCSPYTLGINNGIYKMEGGGGCOPTMCCPUV RGPWGGSHCRDSPVQTITRKCSCAPDCCQAKQOYLGPKDTLSTS VAKSIAGPFARPIGGNVOVYPKGHEAPELVRARGGVCIAN EVQTGIGRIGSHFWCFQTHDVLPDIVTMAKGIGNGFPRAAVITT PEIAKSLAKCLQHPNTFGGNWGVOVYPKGHEAPELVRARGGVCIAN EVQTGIGRIGSHFWCFQTHDVLPDIVTMAKGIGNGFPRAAVITT PEIAKSLAKCLQHPNTFGGNWGACAIGSAVLEVIKERLGENSO EVGTYMLKFAKLRDEFEIVGDVRKGMIGGIEMVQDKISCREL PREEVWQLHEDCKHMGLLVGRGSIFSOTFFIAPSMCITKFEVDF PREEVWQLHEDCKHMGLLVGRGSIFSOTFFIAPSMCITKFEVDF AVEVFRSALTOHMERRAK AVEVFRSALTOHMERRAK AVEVFRSALTOHMERRAK PTORNKDQLIRAAVKPLDTDTICYRVEEPETLVELQRNEMDPII EWAEKRYGVEISSSTSIMGPSIFPAKTREVLVSHLASNYTWALGG IEPVAAQLKSNVLTLGLIDLRLTVEDAYKRCEVSAPSEQGON LEEDTVATLEULVAPAVPSCEVDSSALSGTVVSLRCODKEGNPAP EYTWFKLGILILENERVINIKIKAVTRESKYRCEVSAPSEQGON LEEDTVTLEVLVAPAVPSCEVDSSALSGTVVSLRCODKEGNPAP EYTWFKLGILILENERVINIKIKAVTRESKYRCEVSAPSEQGON LEEDTVATLEVLVAPAVPSCEVDSSALSGTVVSLRCODKEGNPAP EYTWFKLGIRLILENERVINIKIKAVTRESHTKGTLQRNTVSKLD TGEYSCEARNSVGYRRCPGKRNQVDLINISGIIAAVVVVALVIS VCGLGVCVAGRKGYFSKETSFCKSNSSSKATTMSENDFKKTKSF II 6879 3 845 IRVIGESDIMOFFISESDENYNGVSDVDLERVALPDGTTVVTVKV NSITPDICACDSARKGHVITAISITHRKHAFTEEILLINDNDLAVTYP FHOAVDDVKKGYIKAEEKSYQLOKLYFGRILVNIKLRETCGDY NSITPDICACDSARKGHVITAISITHRKHAFTEEGLLENDVALA FENDEMORMDTDEEGMAFCFEVARGEKKRWKLITFPYNYMHE CFERFYGELWKREESV CFERFYGELWKREESV ANNIVARGHTFLKENONLTRS IFIQNSKLYFFGILFNGITLGLGR NRDQIKNCGPFYGHRAFVALIFVTARGCLSVAPILLEFITYMAS KROVPETAPRGREIRDSGLWERSGOGGELERLITTPKSBDSD BTTP VIJAAQVTVITITTVSVLVPDFRSELEFFLEAPSVLLSIFTYMAS KROVPETAPRGREIRDSGLWERSGOGGELERLITTPKSBDSD BTTP ONSKKEDIHVITGALKMFFRELPEPPLFTFNHENDFVNATKGBER ONSKKEDIHVITGALKMFFRELPEPPLFTFNHENDFVNATKGBER ORDSKEDIHVITGALKMFFRELPEPPLFTFNHENDFVNATKGBER ORDSKEDIHVITGALKMFFRELPEPLTFNAMKLSGGBER ORDSKEDIHVITGALKMFFRELPERPSTAKFNINING OSGMWTARGBERLVLISLITCDGGTLATAVHTVYQNGIVELILLELSSIFGR TAMHKKRYGHGELFISCHGGGBATAONTEKSGO	1	}		PELVIGURGELIRDSAQCAAIAERLMHLTSEELNPNPDKEKPP
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6879 3 845 IRVIGESDIMQEFLSESDENYNGVSDVELRVALPDGTTVTVRVK KNSTTDQVYQAIAAKVGMDSTTVNYFALFEVISHSFVRKLAPNE FPHKLYIQNYTSAVPGTCLTIRKWLFTTEEILLINDNDLAVTYP FHQAVDDVKKGYIKAEEKSYQLQKLYEQRKMYMYLMMLRTCEGY NEIIFPHCACOSRRKGHVITAISITHFKLHACTEEGQLENQVIA FEWDEMQRWDTDEEGMAFCFEYARGEKKPRWVKIFTPYPNYMHE CFERVFCELKWRKEEY 6880 2110 1437 RKDNCTAKEWTFPEAKWNTTARVFSHIRLGMGHVLIIVQCFISS MANIYNEKILKEGNQLTESIFIQNSKLYFFGILFNGLTLGLQRS NRDQIKNCGFFYGHRAFSVALIFVTAFQGLSVAFILKFLDNMFH VLMAQVTTVIITTVSVLVFDFRPSLEFFLEAPSVLLSIFIYNAS KPQVPEYAPRQERIRDLSGNLWERSSGDGEBLERLTKPKSDESD EDTF 6881 2638 2244 NDSKWEDIHVITGALKMFFRELPEPLFTFNHFNDFVNAIKQEPR QRVAAVXDLIRQLPKPNQDTMQILPRHLRRVIENGEKNRMTYQS IAIVFGPTLLKPEKETGNIAVHTVYQNQIVELILLELSSIFGR GIPEAQLWIYPVKSCKGVPVSEAECTAMGLRSGNLRDRFMUVIN QEGNNWTARQEPRLVLISLTCDGDTLTLSAAYTKDLLLPIKTPT TNAVHKCRVHGLEIEGRDCGEATAQWITSFLKSOPYRLVHFEPH	!	1		II
KNSTTDQVYQAIAAKVGMDSTTVNYFALFEVISHSFVRKLAPNE FPHKLYIQNYTSAVPGTCLTIRKWLFTTEEILLNDNDLAVTYF FHQAVDDVKKGYIKAEEKSYQLQKLYEQRKMVMYLNMLRTCEGY NEIIFPHCACDIRKKGHVITAISITHFKLHACTEEGQLENQVIA FEWDEMQRWDTDEEGMAFCFEYARGEKKPRWVKIFTPYFNYMHE CFERVFCELKWRKEEY 1437 RKDNCTAKEWTFPEAKWNTTARVFSHIRLGMGHVLIIVQCFISS MANIYNEKILKEGNQLTESIFIQNSKLYFFGILFNGLTLGLQRS NRDQIKNCGFFYGHRAFSVALIFVTAFQGLSVAFILKFLDNMFH VLMAQVTTVIITTVSVLVFDFRPSLEFFLEAPSVLLSIFIYNAS KPQVPEYAPRQERIRDLSGNLWERSSGDGEBLERLTKPKSDESD EDTF 6881 2638 2244 NDSKWEDIHVITGALKMFFRELPEPLFTFNHFNDFVNAIKQEPR QRVAAVXDLIRQLPKPNQDTMQILFRLRRVIENGEKNRMTYQS IAIVFGPTLLKPEKETGNIAVHTVYQNQIVELILLELSSIFGR GIPEAQLWIYPVKSCKGVPVSBAECTAMGLRSGNLRDRFMUVIN QEGNNWTARQBPRLVLISLTCDGDTLTLSAAYTKDLLLPIKTPT TNAVHKCRVHGLEIEGRDCGEATAQWITSFLKSOPYRLVHFEPH	6879	3	845	I ==
FPHKLYIQNYTSAVPGTCLTIRKWLFTTEEILLINDNDLAVTYP PHQAVDDVKKGY IKAEEKS YQLQKLYEQRKWMYXIMMLRTCEGY NEIIFPHCACDSRRKGHVITAISITHFKLHACTEEGQLENQVIA FEWDEMQRWDTDEEGMAFCFEYARGEKKPRWVKIFTPYPNYMHE CFERVFCELKWRKEEY RKDNCTAKEWTFPEAKWNTTARVFSHIRLGMGHVLIIVQCFISS MANIYNEKILKEGNQLTESIFIQNSKLYFFGILFNGLTLGLQRS NRDQIKNCGFFYGHRAFSVALIFVTAFQGLSVAFILKFLDNMFH VLMAQVTTVIITTVSVLVFDFRPSLEFFLEAPSVLLSIFIYNAS KPQVPEYAPRQERIRDLSGNLWERSSGDGEBLERLTKPKSDESD EDTF 6881 2638 2244 NDSKWEDIHVITGALKMFFRELPEPLFTFNHFNDFVNAIKQEPR QRVAAVXDLIRQLPKPNQDTMQILPRHLRRVIENGEKNRMTYQS IAIVFGPTLLKPEKETGNIAVHTVYQNQIVELILLELSSIFGR GIPEAQLWIYPVKSCKGVPVSEAECTAMGLRSGNLRDRFMUVIN QEGNNWTARQEPRLVLISLTCDGDTLTLSAAYTKDLLLPIKTPT TNAVHKCRVHGLEIEGRDCGEATAQWITSFLKSOPYRLVHFEPH		ļ		KNSTTDOVYOAIAAKVGMDSTTMVEALEDITOUGEUDET STOOL
FHQAVDDVKKGYIKAEEKSYQLQKLYEQRKMVMYLNMLRTCEGY NEIIFPHCACDSRRKGHVITAISITHFKLHACTEEGQLENQVIA FEWDEMQRWDTDEEGMAFCFYARGEKKPRWVKIFTPYFNYMHE CFERVFCELKWRKEEY 6880 2110 1437 RKDNCTAKEWTFPEAKWNTTARVFSHIRLGMGHVLIIVQCFISS MANIYNEKILKEGNQLTESIFIQNSKLYFFGILFNGLTLGLQRS NRDQIKNCGFFYGHRAFSVALIFVTAFQGLSVAFILKFLDNMFH VLMAQVTTVIITTVSVLVFDFRPSLEFFLEAPSVLLSIFIXNAS KPQVPEYAPRQERIRDLSGNLWERSSGDGEBLERLTKPKSDESD EDTF 6881 2638 2244 NDSKWEDIHVITGALKMFFRELPEPLFTFNHFNDFVNAIKQEPR QRVAAVKDLIRQLPKPNQDTMQILPRHLRRVIENGEKNRMTYQS IAIVFGPTLLKPEKETGNIAVHTVYQNQIVELILLELSSIFGR 6882 1 850 GIPEAQLWIYPVKSCKGVPVSEAECTAMGLRSGNLRDRFWLVIN QEGNMVTARQBPRLVLISLTCDGDTLTLSAAYTKDLLLPIKTPT TNAVHKCRVHGLEIEGRDCGEATAQWITSFLKSOPYRLVHFEPH	}			FPHKLYIONYTSAVPGTCLTTRKWI.PTTPDDTTIANDADA
NEIIFPHCACDSRRKGHVITAISITHFKLHACTEEGQLENQVIA FEWDEMQRWDTDEEGMAFCFEYARGEKKPRWVKIFTPYFNYMHE CFERVFCELKWRKEEY RKDCTAKEWTFPEAKWNTTARVFSHIRLGMGHVLIIVQCFISS MANIYNEKILKEGNQLTESIFIQNSKLYFFGIIFNGLTLGLQRS NRDQIKNCGFFYGHRAFSVALIFVTAFQGLSVAFILKFLDNMFH VLMAQVTTVIITTVSVLVFDFRPSLEFFLEAPSVLLSIFIYNAS KPQVPEYAPRQERIRDLSGNLWERSSGDGEBLERLTKPKSDESD EDTF 6881 2638 2244 NDSKWEDIHVITGALKMFFRELPEPLFTFNHFNDFVNAIKQEPR QRVAAVKDLIRQLFKPNQDTMQILFRHLRRVIENGEKNRMTYQS IAIVFGPTLLKPEKETGNIAVHTVYQNQIVELILLELSSIFGR 6882 1 850 GIPEAQLWIYPVKSCKGVPVSEAECTAMGLRSGNLRDRFWLVIN QEGNNVTARQBPRLVLISLTCDGDTLTLSAAYTKDLLLPIKTPT TNAVHKCRVHGLEIEGRDCGEATAQWITSFLKSOPYRLVHFEPH				PHOAVDDVKKGYIKAREKSYOLOKI.VEODIMIMYI XIMI.DEGDOV
FEWDEMQRWDTDEEGMAFCFEYARGEKKPRWVKIFTPYPNYMHE CFERVFCELKWRKEEY RKDNCTAKEWTFPEAKWNTTARVFSHIRLGMGHVLIIVQCFISS MANIYNEKILKEGNQLTESIFIQNSKLYFFGILFNGLTLGLQRS NRDQIKNCGFFYGHRAFSVALIFVTAFQGLSVAFILKFLDNMFH VLMAQVTTVIITTVSVLVFDFRPSLEFFLEAPSVLLSIFIYNAS KPQVPEYAPRQERIRDLSGNLWERSSGDGEBLERLTKPKSDESD EDTF 6881 2638 2244 NDSKWEDIHVITGALKMFFRELPEFLFTFNHFNDFVNAIKQEPR QRVAAVKDLIRQLFKPNQDTMQILFRHLRRVIENGEKNRMTYQS IAIVFGPTLLKPEKETGNIAVHTVYQNQIVELILLELSSIFGR 6882 1 850 GIPEAQLWIYPVKSCKGVPVSEAECTAMGLRSGNLRDRFWLVIN QEGNNVTARQEPRLVLISLTCDGDTLTLSAAYTKDLLLPIKTPT TNAVHKCRVHGLEIEGRDCGEATAQWITSFLKSOPYRLVHFEPH				NEIIFPHCACDSRRKGHVITAISTTHPKI.NACTPPGOT.PNOST
CFERVFCELKWRKEEY RKDNCTAKEWTFPEAKWNTTARVFSHIRLGMGHVLIIVQCFISS MANIYNEKILKEGNQLTESIFIQNSKLYFFGILFNGLTLGLQRS NRDQIKNCGFFYGHRAFSVALIFVTAFQGLSVAFILKFLDMFH VIMAQVTTVIITTVSVLVFDFRPSLEFFLEAPSVLLSIFIYNAS KPQVPEYAFRQERIRDLSGNLWERSSGDGEBLERLTKPKSDESD EDTF 6881 2638 2244 NDSKWEDIHVITGALKMFFRELPEFLFTFNHFNDFVNAIKQEPR QRVAAVKDLIRQLFKPNQDTMQILFRHLRRVIENGEKNRMTYQS IAIVFGPTLLKPEKETGNIAVHTVYQNQIVELILLELSSIFGR GIPEAQLWIYPVKSCKGVPVSEAECTAMGLRSGNLRDRFWLVIN QEGNNWTARQEPRLVLISLTCDGDTLTLSAAYTKDLLPJKTPT TNAVHKCRVHGLEIEGRDCGEATAQWITSFLKSOPYRLVHFEPH				FEWDEMORWDTDEEGMAFCFEVADGREEDGRIET CTDURAGE
6880 2110 1437 RKDNCTAKEWTFPEAKWNTTARVFSHIRLGMGHVLIIVQCFISS MANIYNEKILKEGNQLTESIFIQNSKLYFFGILFNGLTLGLQRS NRDQIKNCGFFYGHRAFSVALIFVTAFQGLSVAFILKFLDNMFH VLMAQVTTVIITTVSVLVFDFRPSLEFFLEAPSVLLSIFIYNAS KPQVPEYAPRQERIRDLSGNLWERSSGDGEBLERLTKPKSDESD EDTF 6881 2638 2244 NDSKWEDIHVITGALKMFFRELPEPLFTFNHFNDFVNAIKQEPR QRVAAVKDLIRQLPKPNQDTMQILPRHLRRVIENGEKNRMTYQS IAIVFGPTLLKPEKETGNIAVHTVYQNQIVELILLELSSIFGR GIPEAQLWIYPVKSCKGVPVSEAECTAMGLRSGNLRDRFMUVIN QEGNMVTARQEPRLVLISLTCDGDTLTLSAAYTKDLLLPIKTPT TNAVHKCRVHGLEIEGRDCGEATAQWITSFLKSOPYRLVHFEPH				CFERVFCELKWRKEEY
MANIYNEKILKEGNQLTESIFIQNSKLYFFGILFNGLTLGLQRS NRDQIKNCGFFYGHRAFSVALIFVTAFQGLSVAFILKFLDNMFH VLMAQVTTVIITTVSVLVFDFRPSLEFFLEAPSVLLSIFIXNAS KPQVPEYAPRQERIRDLSGNLWERSSGDGEBLERLTKPKSDESD EDTF 6881 2638 2244 NDSKWEDIHVITGALKMFFRELPEPLFTFNHFNDFVNAIKQEPR QRVAAVKDLIRQLPKPNQDTMQILFRHLRRVIENGEKNRMTYQS IAIVFGPTLLKPEKETGNIAVHTVYQNQIVELILLELSSIFGR 6882 1 850 GIPEAQLWIYPVKSCKGVPVSEAECTAMGLRSGNLRDRFPMLVIN QEGNNVTARQBPRLVLISLTCDGDTLTLSAAYTKDLLLPIKTPT TNAVHKCRVHGLEIEGRDCGEATAQWITSFLKSOPYRLVHFEPH	6880	2110	1437	
NRDQI KNCGFFYGHRAFSVALIFVTAFQGLSVAFILKFLDNMFH VIMAQVTTVIITTVSVLVFDFRPSLEFFLEAPSVLLSIFIYNAS KPQVPEYAPRQERIRDLSGNLWERSSGDGEBLERLTKPKSDESD EDTF NDSKWEDIHVITGALKMFFRELPEPLFTFNHFNDFVNAIKQEPR QRVAAVKDLIRQLPKPNQDTMQILFHLRRVIENGEKNRMTYQS IAIVFGPTLLKPEKETGNIAVHTVYQNQIVELILLELSSIFGR GIPEAQLWIYPVKSCKGVPVSEAECTAMGLRSGNLRDRFWLVIN QEGNNVTARQBPRLVLISLTCDGDTLTLSAAYTKDLLLPIKTPT TNAVHKCRVHGLEIEGRDCGEATAQWITSFLKSOPYRLVHFEPH				MANIYNEKII.KRGNOLTRETETONEKI VEDGIT BYGT TI G-
VLMAQVTTVIITTVSVLVFDFRPSLEFFLEAPSVLLSIFIYNAS KPQVPEYAPRQERIRDLSGNLWERSSGDGEBLERLTKPKSDESD EDTF NDSKWEDIHVITGALKMFFRELPEPLFTFNHFNDFVNAIKQEPR QRVAAVKDLIRQLPKPNQDTMQILPRHLRRVIENGEKNRMTYQS IAIVFGPTLLKPEKETGNIAVHTVYQNQIVELILLELSSIFGR GIPEAQLWIYPVKSCKGVPVSEAECTAMGLRSGNLRDRFWLVIN QEGNNVTARQBPRLVLISLTCDGDTLTLSAAYTKDLLLPIKTPT TNAVHKCRVHGLEIEGRDCGEATAQWITSFLKSOPYRLVHFEPH		}		NRDOIKNCGFFYGHRARSVALIFUMA BOOLGVA BIT VOT
KPQVPEYAPRQERIRDLSGNLWERSSGDGEBLERLTKPKSDESD BDTF 6881 2638 2244 NDSKWEDIHVITGALKMFFRELPEPLFTFNHFNDFVNAIKQEPR QRVAAVKDLIRQLPKPNQDTMQILPRHLRRVIENGEKNRMTYQS IAIVFGPTLLKPEKETGNIAVHTVYQNQIVELILLELSSIFGR 6882 1 850 GIPEAQLWIYPVKSCKGVPVSEAECTAMGLRSGNLRDRPWLVIN QEGNNVTARQBPRLVLISLTCDGDTLTLSAAYTKDLLLPIKTPT TNAVHKCRVHGLEIEGRDCGEATAQWITSFLKSOPYRLVHFEPH		1		VIMAOVTTVI ITTVSVI UPDEDDOI PEDI DE DOME I CEDE
6881 2638 2244 NDSKWEDIHVITGALKMFFRELPEPLFTFNHFNDFVNAIKQEPR QRVAAVKDLIRQLPKPNQDTMQILFRHLRRVIENGEKNRMTYQS IAIVFGPTLLKPEKETGNIAVHTVYQNQIVELILLELSSIFGR 6882 1 850 GIPEAQLWIYPVKSCKGVPVSEAECTAMGLRSGNLRDRFWLVIN QEGNNVTARQBPRLVLISLTCDGDTLTLSAAYTKDLLLPIKTPT TNAVHKCRVHGLEIEGRDCGEATAQWITSFLKSOPYRLVHFEPH		ŀ		KPOVPEYAPROER TRDI.SCAT.WEBSCCOCORD TOT MUNICIPAL
6881 2638 2244 NDSKWEDIHVITGALKMFFRELPEPLFTFNHFNDFVNAIKQEPR QRVAAVKDLIRQLPKPNQDTMQILFRHLRRVIENGEKNRMTYQS IAIVFGPTLLKPEKETGNIAVHTVYQNQIVELILLELSSIFGR 6882 1 850 GIPEAQLWIYPVKSCKGVPVSEAECTAMGLRSGNLRDRFWLVIN QEGNMVTARQBPRLVLISLTCDGDTLTLSAAYTKDLLPIKTPT TNAVHKCRVHGLEIEGRDCGEATAQWITSFLKSOPYRLVHFEPH			l	RDTP
QRVAAVKDLIRQLPKPNQDTMQILPRHLRRVIENGEKNRMTYQS IAIVFGPTLLKPPKETGNIAVHTVYQNQIVELILLELSSIFGR 6882 1 850 GIPEAQLWIYPVKSCKGVPVSEAECTAMGLRSGNLRDRFWLVIN QEGNNVTARQBPRLVLISLTCDGDTLTLSAAYTKDLLLPIKTPT TNAVHKCRVHGLEIEGRDCGEATAQWITSFLKSOPYRLVHFEPH	6881	2638	2244	· · · · · · · · · · · · · · · · · · ·
IAIVFGPTLLKPEKETGNIAVHTVYQNQIVELILLELSSIFGR 6882 1 850 GIPEAQLWIYPVKSCKGVPVSEAECTAMGLRSGNLRDRPWLVIN QEGNMVTARQBPRLVLISLTCDGDTLTLSAAYTKDLLLPIKTPT TNAVHKCRVHGLEIEGRDCGEATAQWITSFLKSOPYRLVHFEPH			22.23	OPVARVKDI TOOLDKDNODTMOTI PRITT BOTTONIA TOOLOGO
GIPEAQLWIYPVKSCKGVPVSEAECTAMGLRSGNLRDRFWLVIN QEGNMVTARQBPRLVLISLTCDGDTLTLSAAYTKDLLLPIKTPT TNAVHKCRVHGLEIEGRDCGEATAQWITSFLKSOPYRLVHFEPH		į.	ľ	INTURCEDITAL PRESENCE A TRUMBUCKO TENT TO THE PROPERTY OF THE
QEGNMVTARQEPRLVLISLTCDGDTLTLSAAYTKDLLLPIKTPT TNAVHKCRVHGLEIEGRDCGEATAQWITSFLKSOPYRLVHFRPH	6882	1	850	GIPPIOLHTYDUYCCYCUDUGDD CONTUCTOR CO
TNAVHKCRVHGLEIEGRDCGEATAOWITSFLKSOPYRLVHFEPH		- 1		ORGNMUTA POPPEL VILLE I MODORNI III GARANTERE PER CENTURE IN CARREST IN CARRE
MRPRRPHQIADLFRPKDQIAYSDTSPFLILSEASLADLNSRLEK	1		1	TNAVHYCOVIGLE I ECONOGRAM COLTEGE TO THE TOTAL
	j			MPDPP PHOTADLE PROPERTY AND
		<u>-</u>		

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, T=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R≈Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			KVKATNFRPNIVISGCDVYAEDSWDELLIGDVELKRVMACSRCI
			LTTVDPDTGVMSRKEPLETLKSYRQCDPSERKLYGKSPLFGQYF
6000			VLENPGTIKVGDPVYLLGQ
6883	2794	2256	NSKLKLNONLKLFITLTYQVLSLHGWGPGIHLQKEGAFPVTQNR
1			ALQLLYDLRYLNIVLTAKGDEVKSGRSKPDSRIEKVTDHLEALI
	·	1	DPFDLDVFTPHLNSNLHRLVQRTSVLFGLVTGTENQLAPRSSTF
	1		NSQEPHNILPLASSQIRFGLLPLSMTSTRKAKSTRNIETKAQYD
C004			ANC
6884	2	99	BFERVTAEAVKPRETSEPRAAAQRFCEKFPFL
6885	297	1554	STGQFWHVTDLHLDPTYHITDDHTKVCASSKGANASNPGPFGDV
			LCDSPYQLILSAFDFIKNSGQEASFMIWTGDSPPHVPVPELSTD
	1		TVINVITNMTTTIQSLFPNLQVFPALGNHDYWPQDQLSVVTSKV
.[1		YNAVANLWKPWLDEEAISTLRKGGFYSQKVTTNPNLRIISLNTN
	1		LYYGPNIMTLNKTDPANQFEWLESTLNNSQQNKEKVYIIAHVPV
1			GYLPSSQNITAMREYYNEKLIDIFQKYSDVIAGQFYGHTHRDSI
	l '		MVLSDKKGSPVNSLFVAPAVTPVKSVLEKQTNNPGIRLFQYDPR
[DYKLLDMLQYYLNLTEANLKGESIWKLEYILTQTYDIEDLQPES
	1		LYGLAKOFTILDSKOFIKYYNYFFVSYDSSVTCDKTCKAFQICA IMNLDNISYADCLKOLYIKHNY
6886	2	1341	QCGGIPGREGGSSRPLEEGTGSSPACVRGAAPGSEDAFYPTRAK
	[1341	QCGGIPGREGGSSRPLBEGTGSSPACVRGAAPGSEDAFYPTRAK QARVSQELKKAAKRTVSISEGPDTLGDGMRERRETLALAPEPEP
	[LEKEACEKWKRPFRSASATSLTLSHCVDVVKGLLDFKKRRGHSI
'			GGAPEQRYQIIPVCVAARLPTRAQDVLDAHLSEVNAVRFGPNSS
			LLATGGADRLIHLWNVVGSRLEANOTLEGAGGSITSVDFDPSGY
			QVLAATYNQAAQLWKVGEAQSKETLSGHKDKVTAAKFKLTRHOA
]		VTGSRDRTVKEWDLGRAYCSRTINVLSYCNDVVCGDHIIISGHN
-			DQKIRFWDSRGPHCTQVIPVQGRVTSLSLSHDQLHLLSCSRDNT
			LKVIDLRVSNIRQVFRADGFKCGSDWTKAVFSPDRSYALAGSCD
	<u> </u>		GALYIWDVDTGKLESRLQGPHCAAVNAVAWCYSGSHMVSVDQGR
	1		KVVLWO
6887	1047	116	WTARPSQKPFWEAGAVPGDPLSTGCSQAOLGGCCPRGPWGPOHG
			GOORAAGPTLPRGERGGPQQSGPGLAAQTPPTSKOVAWRAPLTG
]			TYRSQSPRSPAGPFRGGTGWWPEPAVCLCVAVGPQRLSSPGLVY
			NASGSEHCYDIYRLYHSCADPTGCGTGPDARAWDYQACTEINLT
	·		PASNNVTDMFPDLPFTDELRQRYCLDTWGVWPRPDWLLTSFWGG
	·		DLRAASNIIFSNGNLDPWAGGGIRRNLSASVIAVTIQGGAHHLD
		*	LRASHPEDPASVVEARKLEATIIGEWVKAARREQOPALRGGPRL
<u> </u>			SL
6888	1	992	FVAYVKKEIPHIVVTHCLLNPHALVIKTLPTKLRDALFTVVRVI
] .]	- ,	NFIKGRAPNHRLFQAFFEEIGIEYSVLLFHTEMRWLSRGQILTH
			IFEMYBEINQFLHHKSSNLVDGFENKEFKIHLAYLADLFKHLNE
			LSASMORTGMNTVSAREKLSAFVRKFPFWOKRIEKRNFTNFPFL
Ì	· .		EEIIVSDNEGIFIAAEITLHLQQLSNFFHGYFSIGDLNEASKWI
	[]		LDPFLFNIDFVDDSYLMKNDLAELRASGQILMEFETMKLEDFWC
			AQFTAFPNLAKTALEILMPFATTYLCELGFSITFTFQNKVPEAA
			LILSDDIRVAISKKVPSFLGHH
6889	1	1534	LTLENQIKEEREQDNSESPNGRTSPLVSQNNEQGSTLRDLLTTT
			AGKLRVGSTDAGIAFAPVYSMGAPSSKSGRTMPNILDDIIASVV
			ENKIPPSKTSKINVKPELKEEPEESIISAVDENNKLYSDIPHSW
			ICEKHILWLKDYKNSSNWKLFKECNKQGQPAVVSGVHKKMNISL
			WKAESISLDFGDHQADLLNCKDSIISNANVKEFWDGFEEVSKRQ
			KNKSGETVVLKLKDWPSGEDFKTMMPARYEDLLKSLPLPEYCNP
			EGKFNLASHLPGFFVRPDLGPRLCSAYGVVAAKDHDIGTTNLHI
	' .		EVSDVVNILVYVGIAKGNGILSKAGILKKFEEEDLDDILRKRLK
			DSSEIPGALWHIYAGKDVDKIRBFLQKISKBQGLEVLPEHDPIR
			DQSWYVNKKLRQRLLBEYGVRTWTLIQFLGDAIVLPAGALHQVQ

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide '	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, FaPhenylalanine, GaGlycine,
i	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
ļ	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
}	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	sequence	Codon, /-possible nucleotide deletion,
		 	\=possible nucleotide insertion)
])		NFHSCIQVTEDFVSPEHLVESFHLTQELRLLKEEINYDDKLQVK
6890	3	667	NILYHAVKEMVRALKIHEDEVDDMEKN
1	•	867	THACGMWIPLYLHRALVVHKTAETCNSPPCGAKDSLIFGAITCF
1		j	TGFLGVDTGAGATRWCRLKTQRADPLVCAVGMLGSAIFICLIFV
i			AAKSSIVGAYICIFVGETLLFSNWAITADILMYVVIPTRRATAV
1	ł		ALQSFTSHLLGDAGSPYLIGFISDLIRQSTKDSPLWEFLSLGYA
1			LMLCPFVVVLGGMFFLATALFFVSDRARAEQQVNQLAMPPASVK
6891	1980	1262	-
	1	1202	LRIHQELLSKELKLLRGITIESIIHIGLAAGKEQFMQDASNVMQ
1			LLLKTQSHLYNMEDNNPEVRQAAAYGLGVMAQFGGDDYRSLCSE
ı			AVPLLVKVIKRAHSKTKKNVIATENCISAIGKILKFKPNCVNVD
1			EVLPHWLSWLPLHEDKEEAIQTLSFLCDLIESNHPVVIGPNNSN
İ			LPKIISIIAEGKINETINYEDPCAKRLANVVRQVQTSEDLWLEC
6892	3	876	VSQLDDEQQEALQELLNFA
1]	910	RSVAAASGPGAWGTDHYCLELLRKRDYEGYLCSLLLPAESRSSV
			FALRAFNVELAQVKDSVSEKTIGLMRMQFWKKTVEDIYCDNPPH
]			QPVAIELWKAVKRHNLTKRWLMKIVDEREKNLDDKAYRNIKELE
1			NYAENTQSSLLYLTLEILGIKDLHADHAASHIGKAQGIVTCLRA
1 .			TPYHGSRRKVFLPMDICMLHGVSQEDFLRRNQDKNVRDVIYDIA
1	,		SQAHLHLKHARSFHKTVPVKAFPAFLQTVSLEDFLKKIQRVDFD
6893	1	842	IPHPSLQQKNTLLPLYLYIQSWRKTY
i i	_	012	DGBRKSMSVERTFSEINKAEEQYSLCQELCSELAQDLQKERLKG
			RTVTIKLKNVNFEVKTRASTVSSVVSTABEIFAIAKELLKTEID ADFPHPLRLRLMGVRISSFPNBEDRKHQQRSIIGFLQAGNQALS
]]			ATECTLEKTDKDKFVKPLEMSHKKSFFDKKRSERKWSHQDTFKC
1 1			FAUNYOS POTSO DEGLE VYVINTENT DE CONTROL DE
1 1			EAVNKQSFQTSQPFQVLKKKMNENLEISENSDDCQILTCPVCFR AQGCISLEALNKHVDECLDGPSISENFKMFSCSHVSATKVNKKE
			NVPASSLCEKODYEAH
6894	1742	1463	TTLCKPLVPREHQFYETLPAEMRKFTPQYKGKSQLLEGLPHWRG
1 1		2.03	DVRDRGHGRPWQPSLEPSLPPTLCPPSLSSFSSSWPSAQHLTPS
1 1			VFNPW VFNPW
6895	2379	478	VTYVELCDLASPTALLIMRTVLDLIVEDLQSTSEDKEQQYTSQT
1 1		170	TRLLALLYALASHKACKLAILHLINGTIKGDERYAEIFQDLLAL
]	1		VRSPGDSVIRQQCVEYVTSILQSLCDQDIALILPSSSEGSISEL
	1		EQLSNSLPNKELMTSICDCLLATLANSESSYNCLLTCVRTMMFL
1 1	j		AEHDYGLFHLKSSLRKNSSALHSLLKRVVSTFSKDTGELASSFL
}			EFMRQILNSDTIGCCGDDNGLMEVEGAHTSRTMSINAAELKQLL
			QSKEESPENLFLELEKLVLEHSKDDDNLDSLLDSVVGLKQMLES
}	}		SGDPLPLSDQDVEPVLSAPESLQNLFNNRTAYVLADVMDDQLKS
1		l	MWFTPFQAEEIDTDLDLVKVDLIELSEKCCSDFDLHSELERSFL
1			SEPSSPGRTKTTKGFKLGKHKHETPITSSGKSEYIEPAKRAHVV
] 1	j	ļ	PPPRGRGGGGGGGIRPHDIFRQRKQNTSRPPSMHVDDFVAAES
			KEVVPQDGIPPPKRPLKVSQKISSRGGFSGNRGGRGAFHSQNRF
1			FTPPASKGNYSRREGTRGSSWSAQNTPRGNYNESRGGQSNFNRG
]]			PLPPLRPLSSTGYRPSPRDRASRGRGGLGPSWASANSGSGGSRG
1. 1		ļ	KFVSGGSGRGRHVRSFTR
6896	1	. 555	GNIVIQKKKYNKQHIIPLENVTIDSIKDEGDLRNGWLIKTPTK8
]]	İ		FAVYAATATEKGEWMNUTNKOUTDI I OKOOVIDONOMII KTPTKS
[ĺ	.	FAVYAATATEKSEWMNHINKCVTDLLSKSGKTPSNEHAAVWVPD
]	SEATVCMRCQKAKFTPVNRRHHCRKCGFVVCGPCSEKRFLLPSQ
1	!]	SSKPVRICDFCYDLLSAGDMATCQPARSDSYSQSLKSPLNDMSD DDDDDDSSD
6897	3	920	
	-	120	GDGLMHEVVNGLMERPDWETAIQKPLCSLPAGSGNALAASLNHY
1		1	AGYEQVTNEDLLTNCTLLLCRRLLSPMNLLSLHTASGLRLFSVL
		ĺ	SLAWGFIADVDLESEKYRRLGEMRFTLGTFLRLAALRTYRGRLA YLDYGDYGSYTDD CDUDYNGGGDDD MANDY DED YN DDOG
1]	ŀ	YLPVGRVGSKTPASPVVVQQGPVDAHLVPLEEPVPSHWTVVPDB
			DFVLVLALLHSHLGSEMFAAPMGRCAAGVMHLFYVRAGVSRAML

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
1	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
-	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
İ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
}	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ŀ	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	1	\=possible nucleotide insertion)
		-	LRLFLAMEKGRHMEYECPYLVYVPVVAFRLEPKDGKGVFAVDGE
1		ł	LMVSEAVQGQVHPNYFWMVSGCVEPPPSWKPQQMPPPEEPL
6898	919	346	QKTVTAVASLLKGRQGIYTENERRMGAVIKIRFFKIMLVLIICW
i			LSNIINESLLFYLEMQTDINGGSLKPVRTAAKTTWFIMGILNPA
1	1		QGFLLSLAPYGWTGCSLGFQSPRKEIQWESLTTSAAEGAHPSPL
ì			MPHENPASGKVSQVGGQTSDEALSMLSEGSDASTIEIHTASESC
			NKNEGDPALPTHGDL
6899	120	827	MKVRKNNDAYLLDKNKINMDCFISCFFKKMLTTLMFSHSGILSL
i			LEHGEEYTFSLPCAYARSILTVPWVELGGKVSVNCAKTGYSASI
1	i		TFHTKPFYGGKLHRVTAEVKHNITNTVVCRVQGEWNSVLEFTYS
I	}		NGETKYVDLTKLAVTKKRVRPLEKQDPFESRRLWKNVTDSLRES
			EIDKATEHKHTLEERORTEERHRTETGTPWKTKYFIKEGDGWVY
4.0			HKPLWKIIPTTQPAE
6900	3	451	TEVLGSKGIHELRSSTSALHHALEESASLLTMFWRAALPSTHIP
1			VLPGKVGESTERELLELRTKVSQQEQLLQSTTEHLKNANOOKES
			MEQFIVSQLTRTHDVLKKARTNLEVRKLLHQSEAPSLSPTHHHP
6901			LADLVGDSWPALRFQEK
6901	1	201	DDNMVQRLETDFKMTLQQQSTLEQWAAWLDNVMMQALKPYEGRP
6902			SFPKAARQFLLKWSFYRYHLGFS
0302	2	267	GAPPPPPSQPPRQPPQAAPSSHPHSDLTFNPSSALEGQAGAQGA
6903	1		SDMPEPSLDLLPELTNPDELLSYLDPPDLPSNSNDDLLSLFENN
0,03	+	149	RINQVYRQGPTGIHILVIDQMVQNFQDESCFLFSTVKAESSDGI
6904	464		HIILK
1 0504	404	2092	MEASLPVSLSCVLACGDVEGKFDILFNRVQAIQKKSGNFDLLLC
1 1			VGNFFGSTQDAEWEEYKTGIKKAPIQTYVLGANNQETVKYFQDA
1			DGCELAENITYLGRKGIFTGSSGLQIVYLSGTESLNEPVPGYSF
1 1			SPKDVSSLRMMLCTTSQFKGVDILLTSPWPKCVGNFGNSSGEVD
1	1		TKKCGSALVSSLATGLKPRYHFAALEKTYYERLPYRNHIILQEN
]			AQHATRFIALANVGNPEKKKYLYAFSIVPMKLMDAAELVKQPPD VTENPYRKSGQEASIGKQILAPVEESACQFFFDLNEKQGRKRSS
1 1			TGRDSKSSPHPKQPRKPPQPPGPCWFCLASPEVEKHLVVNIGTH
1 1			CYLALAKGGLSDDHVLILPIGHYQSVVELSAEVVEEVEKYKATL
1			RRFFKSRGKWCVVFERNYKSHHLQLQVIPVPISCSTTDDIKDAF
1 1			ITQAQEQQIELLEIPEHSDIKQIAQPGAAYFYVELDTGEKLFHR
]]	i		IKKNFPLQFGREVLASEAILNVPDKSDWRQCQISKEDEETLARR
			FRKDFEPYDFTLDD
6905	1	226	FRKDFEPYDFTLDD VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLTAT
			FRKDFEPYDFTLDD VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAI VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA
6905	3	226	FRKDFEPYDFTLDD VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAI VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA SYDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKIIPAT
			FRKDFEPYDFTLDD VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAI VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA SYDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKIIPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVFTRT
			FRKDFEPYDFTLDD VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAI VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA SYDDHNGHIDFITAASNLRAKMYSIEPADFKTKRIAGKIIPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNWPLNLAIPIVVFTET TEVRKTKIRNGISFTIWDRWTYHGKEDFTILDFINAVERYGIR
			FRKDFEPYDFTLDD VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAI VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA SYDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKIIPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVFTET TEVRKTKIRNGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE PTMVVQGVKMLYVPVMPGHAKRLKLTMHKLVKPTTEKKYVDLTV
6906	3	611	FRKDFEPYDFTLDD VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAI VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA SYDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKIIPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVFTET TEVRKTKIRNGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE PTMVVQGVKMLYVPVMPGHAKRLKLTMHKLVKPTTEKKYVDLTV SFAPDIDGDEDLPGPPVRYYFSHDTD
			FRKDFEPYDFTLDD VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAI VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA SYDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKIIPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVFTET TEVRKTKIRNGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE PTMVVQGVKMLYVPVMPGHAKRLKLTMHKLVKPTTEKKYVDLTV SFAPDIDGDEDLPGPPVRYYFSHDTD LRGVPVWAAGAFRFSSGEESTSHLIMSRRSQRLTRYSQGDDDGS
6906	3	611	FRKDFEPYDFTLDD VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAI VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA SYDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKIIPAI ATTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVFTET TEVRKTKIRNGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE PTMVVQGVKMLYVPVMPGHAKRLKLTMHKLVKPTTEKKYVDLTV SFAPDIDGDEDLPGPPVRYYFSHDTD LRGVPVWAAGAFRFSSGEESTSHLIMSRRSQRLTRYSQGDDDGS SSSGGSSVAGSQSTLFKDSPLRTLKRKSSNMKRLSPAPOLGPSS
6906	3	611	FRKDFEPYDFTLDD VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAI VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA SYDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKIIPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVFTET TEVRKTKIRNGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE PTMVVQGVKMLYVPVMPGHAKRLKLTMHKLVKPTTEKKYVDLTV SFAPDIDGDEDLPGPPVRYYFSHDTD LRGVPVWAAGAFRFSSGEESTSHLIMSRRSQRLTRYSQGDDDGS SSSGGSSVAGSQSTLFKDSPLRTLKRKSSNMKRLSPAPQLGPSS DAHTSYYSESLVHESWFPPRSSLEELHGDANWGEDLRVRRRRGT
6906	3	611	PRKDFEPYDFTLDD VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAI VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA SYDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKIIPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVFTET TEVRKTKIRNGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE PTMVVQGVKMLYVPVMPGHAKRLKLTMHKLVKPTTEKKYVDLTV SFAPDIDGDEDLPGPPVRYYFSHDTD LRGVPVWAAGAFRFSSGEESTSHLIMSRRSQRLTRYSQGDDDGS SSSGGSSVAGSQSTLFKDSPLRTLKRKSSNMKRLSPAPQLGPSS DAHTSYYSESLVHESWFPPRSSLEELHGDANWGEDLRVRRRRGT GGSESSRASGLVGRKATEDFLGSSSGYSSEDDYVGYSDVDOOSS
6906	3	611	FRKDFEPYDFTLDD VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAI VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA SYDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKIIPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVFTET TEVRKTKIRNGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE PTMVVQGVKMLYVPVMPGHAKRLKLTMHKLVKPTTEKKYVDLTV SFAPDIDGDEDLPGPPVRYYFSHDTD LRGVPVWAAGAFRFSSGEESTSHLIMSRRSQRLTRYSQGDDDGS SSSGSSVAGSQSTLFKDSPLRTLKRKSSNMKRLSFAPQLGPSS DAHTSYYSESLVHESWFPPRSSLEELHGDANWGEDLRVRRRGT GGSESSRASGLVGRKATEDFLGSSSGYSSEDDYVGYSDVDQQSS SSRLRSAVSRAGSLLWMVATSPGRLFRLLYWWAGTTWYRLTTAA
6906	3	2228	FRKDFEPYDFTLDD VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAI VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA SYDDHNGHIDFITAASNLRAKMYSIEPADFKTKRIAGKIIPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVFTET TEVRKTKIRNGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE PTMVVQGVKMLYVPVMPGHAKRLKLTMHKLVKPTTEKKYVDLTV SFAPDIDGDEDLPGPPVRYYFSHDTD LRGVPVWAAGAFRFSSGEESTSHLIMSRRSQRLTRYSQGDDDGS SSSGGSSVAGSQSTLFKDSPLRTLKRKSSNMKRLSPAPQLGPSS DAHTSYYSESLVHESWFPPRSSLELHGDANWGEDLRVRRRGT GGSESSRAGGLVGRKATEDFLGSSGYSSEDDYVGYSDVDQQSS SSRLRSAVSRAGSLLMWVATSPGRLFRLLYWWAGTTWYRLTTAA SLLDVFVLTRRFSSLKTFLWFLLPLLLLTCLTYGAWYFYPYGLO
6906	3	2228	PRKDFEPYDFTLDD VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAI VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA SYDDHNGHIDFITAASNLRAKMYSIEPADFKTKRIAGKIIPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVFTET TEVRKTKIRNGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE PTMVVQGVKMLYVPVMPGHAKRLKLTMHKLVKPTTEKKYVDLTV SFAPDIDGDEDLPGPPVRYYFSHDTD LRGVPVWAAGAFRFSSGEESTSHLIMSRRSQRLTRYSQGDDDGS SSSGGSSVAGSQSTLFKDSPLRTLKRKSSNMKRLSPAPQLGPSS DAHTSYYSESLVHESWFPPRSSLEELHGDANWGEDLRVRRRGT GGSESSRASGLVGRKATEDFLGSSGYSSEDYVGYSDVDQQSS SSRLRSAVSRAGSLLMWVATSPGRLFRLLYWWAGTTWYRLTTAA SLLDVFVLTRRFSSLKTFLWFLLPLLLLTCLTYGAWYFYPYGLQ TFHPALVSWWAAKDSRRADEGWEARDSSPHFQAECRYMSRVHSL
6906	3	2228	FRKDFEPYDFTLDD VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAI VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA SYDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKIIPAI ATTTATVSGLVALEMIKVTGGYPFEAYRWFLNLAIPIVVFTET TEVRKTKIRNGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE PTMVVQGVKNLYVPVMPGHAKRLKLTMHKLVKPTTEKKYVDLTV SFAPDIDGDEDLPGPPVRYYFSHDTD LRGVPVWAAGAFRFSSGEESTSHLIMSRRSQRLTRYSQGDDDGS SSSGGSSVAGSQSTLFKDSPLRTLKRKSSNMKRLSPAPQLGPSS DAHTSYYSESLVHESWFPPRSSLEELHGDANWGEDLRVRRRGT GGSESSRASGLVGRKATEDFLGSSSGYSSEDDYVGYSDVDQQSS SSRLRSAVSRAGSLLWWVATSPGRLFRLLYWWAGTTWYRLTTAA SLLDVFVLTRFFSSLKTFLWFLLPLLLLTCLTYGAWYFYPYGLQ TFHPALVSWWAAKDSRRADEGWEARDSSPHFQAEQRVMSRVHSL ERRLEALAAEFSSNWQKEAMRLERLELRQGAPGOGGGGLSHRD
6906	3	2228	VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAI VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAI VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA SYDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKIIPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVFTET TEVRKTKIRNGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE PTMVVQGVKMLYVPVMPGHAKRLKLTMHKLVKPTTEKKYVDLTV SFAPDIDGDEDLPGPPVRYYFSHDTD LRGVPVWAAGAFRFSSGEESTSHLIMSRRSQRLTRYSQGDDDGS SSSGGSSVAGSQSTLFKDSPLRTLKRKSSNMKRLSPAPQLGPSS DAHTSYYSESLVHESWFPPRSSLEELHGDANWGEDLRVRRRRGT GGSESSRASGLVGRKATEDFLGSSSGYSSEDDYVGYSDVDQQSS SSRLRSAVSRAGSLLWMVATSPGRLFRLLYWWAGTTWYRLTTAA SLLDVFVLTRRFSSLKTFLWFLLPLLLLTCLTYGAWYFYPYGLQ TFHPALVSWWAAKDSRRADEGWEARDSSPHFQAEQRWSRVHSL ERRLEALAAEFSSNWQKEAMRLERLELRQGAPGQGGGGLSHBD TLALLEGLVSRREAALKEDFRRETAARIOEELSALRAEHOODSE
6906	3	2228	VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAI VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA SYDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKIIPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVFTET TEVRKTKIRNGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE PTMVVQGVKMLYVPVMPGHAKRLKLTMHKLVKPTTEKKYVDLTV SFAPDIDGDEDLPGPPVRYYFSHDTD LRGVPVWAAGAFRFSSGEESTSHLIMSRRSQRLTRYSQGDDDGS SSSGGSSVAGSQSTLFKDSPLRTLKRKSSNMKRLSPAPQLGPSS DAHTSYYSESLVHESWFPPRSSLEELHGDANWGEDLRVRRRRGT GGSESSRASGLVGRKATEDFLGSSSGYSSEDDYVGYSDVDQQSS SSRLRSAVSRAGSLLWMVATSPGRLFRLLYWWAGTTWYRLTTAA SLLDVFVLTRRFSSLKTFLWFLLPLLLLTCLTYGAWYFYPYGLQ TFHPALVSWWAAKDSRRADEGWEARDSSPHFQAEQRVMSRVHSL ERRLEALAAEFSSNWQKEAMRLERLELRQGAPQGGGGGGLSHED TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAEHQQDSE DLFKKIVRASQESEARIQQLKSEWQSMTOESFOESSVKELRRLE
6906	3	2228	VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAI VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAI VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA SYDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKIIPAI ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVFTET TEVRKTKIRNGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE PTMVVQGVKMLYVPVMPGHAKRLKLTMHKLVKPTTEKKYVDLTV SFAPDIDGDEDLPGPPVRYYFSHDTD LRGVPVWAAGAFRFSSGEESTSHLIMSRRSQRLTRYSQGDDDGS SSSGGSSVAGSQSTLFKDSPLRTLKRKSSNMKRLSPAPQLGPSS DAHTSYYSESLVHESWFPPRSSLEELHGDANWGEDLRVRRRRGT GGSESSRASGLVGRKATEDFLGSSSGYSSEDDYVGYSDVDQQSS SSRLRSAVSRAGSLLWMVATSPGRLFRLLYWWAGTTWYRLTTAA SLLDVFVLTRRFSSLKTFLWFLLPLLLLTCLTYGAWYFYPYGLQ TFHPALVSWWAAKDSRRADEGWEARDSSPHFQAEQRWSRVHSL ERRLEALAAEFSSNWQKEAMRLERLELRQGAPGQGGGGLSHBD TLALLEGLVSRREAALKEDFRRETAARIOEELSALRAEHOODSE

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	Halistidine, IaIsoleucine, Kabysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine.
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	WaTryptophan, YaTyrosine, XaUnknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	5542555	\=possible nucleotide insertion)
			AREAAASLSLTLQKEGVIGVTREQVHHIVKQALQRYSEDRIGLA
1		Į.	DYALESGGASVISTRCSETYETKTALLSLFGIPLWYHSOSPRVI
1			LQPDVHPGNCWAFQGPQGFAVVRLSARIRPTAVTLEHVPKALSP
			NSTISSAPKDFAIFGFDEDLQQEGTLLGKFTYDODGEPIQTPHF
•			QAPTMATYQVVELRILTNWGHPEYTCIYRFRVHGEPAH
6908	3	780	QVPSAAWLMAVCGLGSRLGLGSRLGLOGCFGAARLLYPRFOSRG
1	_	1	PQGVEDGDRPQPSSKTPRIPKIYTKTGDKGFSSTFTGERRPKDD
			QVFEAVGTTDELSSAIGFALELVTEKGHTFAEELOKIOCTLODV
1			GSALATPCSSAREAHLKYTTFKAGPILELEQWIDKYTSQLPPLT
1	1		AFILPSGGKISSALHFCRAVCRRAERRVVPLVOMGETDANVAKF
į	İ		LNRLSDYLFTLARYAAMKEGNQEKIYKKNDPSAESEGL
6909	3	409	GRLLAVGTDLYGQRSSAPEQELLVQDATPVSNSLLPEKAFSDIP
	_		SPYLRGTIKMMQAVRQAFQDQDDRRTWDGRPLTMAATFDDCLYA
			LCVVDTIKRSSQTGEWQNIAIMTEEPELSPAYLISEAMRRSRMS
		ļ	LYC
6910	1	1068	LVPVVVIDSYYYGKLVIAPLNIVLYNIFTPHGPDLYGTEPWYFY
ľ			LINGFLNFNVAFALALLVLPLTSLMEYLLQRFHVQNLGHPYWLT
1 .	}		LAPMYIWFIIFFIQPHKEERFLFPVYPLICLCGAVALSALQHSF
į	ł	,	LYFQKCYHFVFQRYRLEHYTVTSNWLALGTVFLFGLLSFSRSVA
j			LFRGYHGPLDLYPEFYRIATDPTIHTVPEGRPVNVCVGKEWYRF
			PSSFLLPDNWQLQFIPSEFRGQLPKPFAEGPLATRIVPTDMNDO
	}		NLEEPSRYIDISKCHYLVDLDTMRETPREPKYSSNKEEWISLAY
J	j	•	RPFLDASRSSKLLRAFYVPFLSDQYTVYVNYTILKPRKAKQIRK
1			KSGG
6911	1184	966	GEDAEEMETGNVANLISIFGSSFSGLLRKSPGGGREEEEGEESG
			PEAAEPGQICCDKPVLRDMNPWSTAIVAF
6912	1	844	AMKPVETHSFQMLFTILSTGSALKAQSYEDAYRCIKSSILLGSI
1	,		SGGTDIISCFMGHNFSLPVYKGEIQARNLGMAVEAWNEEGKAVW
			GESGELVCTKPIPCQPTHFWNDENGNKYRKAYFSKFPGIWAHGD
			YCRINPKTGGIVMLGRSDGTLNPNGVRFGSSEIYNIVESFEEVE
	i		DSLCVPQYNKYREERVILFLKMASGHAFQPDLVKRIRDAIRMGL
			SARHVPSLILETKGIPYTLNGKKVEVAVKQIIAGKAVEQGGAFS
			NPETLDLYRDIPELQGF
6913	1643	. 1558	KKSHEESHKEELSYGAQASLPLPCSDFR
6914	1251	615	ELAAECKSAGYPGTLIPYRCDLSNEEDILSMFSAIRSQHSGVDI
			CINNAGLARPDTLLSGSTSGWKDMFNVNVLALSICTREAYQSMK
			ERNVDDGHIININSMSGHRVLPLSVTHFYSATKYAVTALTEGLR
			QELREAQTHIRATCISPGVVETQFAFKLHDKDPEKAAATYEQMK
			CLKPEDVAEAVIYVLSTPAHIQIGDIQMRPTEQVT
6915	254	652	GRSLSFKTFLIWVLISIYQGGILMYGALVLFBSEFVHVVAISFT
			ALILTELLMVALTVRTWHWLMVVAEFLSLGCYVSSLAFLNEYFD
			VAFITTVTFLWKVSAITVVSCLPLYVLKYLRRKLSPPSYCKLAS
6916	254	652	GRSLSFKTFLIWVLISIYQGGILMYGALVLFESEFVHVVAISFT
			ALILTELLMVALTVRTWHWLMVVAEFLSLGCYVSSLAFLNEYFD
			VAFITTVTFLWKVSAITVVSCLPLYVLKYLRRKLSPPSYCKLAS
6917	254	652	GRSLSFKTFLIWVLISIYQGGILMYGALVLFESEFVHVVAISFT
			ALILTELLMVALTVRTWHWLMVVAEFLSLGCYVSSLAFLNEYFD
			VAFITTVTFLWKVSAITVVSCLPLYVLKYLRRKLSPPSYCKLAS
6918	28	921	PEAGTRSWREPDPEDLRRFLLSAACRSFPQWLPGGGGGQVSSCS
			DTDVPYLLLAVKSEPGRFAERQAVRETWGSPAPGIRLLFLLGSP
			VGEAGPDLDSLVAWESRRYSDLLLWDFLDVPFNQTLKDLLLLAW
			LGRHCPTVSFVLRAQDDAFVHTPALLAHLRALPPASARSLYLGE
			VFTQAMPLRKPGGPFYVPESFFEGGYPAYASGGGYVIAGRLAPW
			LLRAAARVAPFPFEDVYTGLCIRALGLVPQAHPGFLTAWPADRT
<u> </u>			ADHCAFRNLLLVRPLGPQASIRLWKQLQDPRLQC

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ĺ	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
6919	850	41	QGRRELSGSVFCPFIQQEPKEMLTLSEYHERVRSQGQQLQQLQA
}			ELDKLHKEVSTVRAANSERVAKLVFQRLNEDFVRKPDYALSSVG
1	}		ASIDLQKTSHDYADRNTAYFWNRFSFWNYARPPTVILEPHVFPG
	1		NCWAPEGDQGQVVIQLPGRVQLSDITLOHPPPSVEHTGGANSAP
			RDFAVFFLLSFFTHQGLQVYDETEVSLGKFTFDVEKSEIOTFHL
1			QNDPPAAFPKVKIQILSNWGHPRFTCLYRVRAHGVRTSEGAEGS
6000			AQGPH
6920	1418	591	EAQGPSKVHLTLKKKK
6921	2	1711	MNATRSEEQFHVINHAEQTLRKMENYLKEKQLCDVLLIAGHLRI
İ			PAHRLVLSAVSDYFAAMFTNDVLEAKOEEVRMEGVDPNALNSLV
i	1		QYAYTGVLQLKEDTIESLLAAACLLQLTQVIDVCSNFLIKOLHP
1			SNCLGIRSFGDAQGCTELLNVAHKYTMEHFIEVIKNQEFLLLPA
			NEISKLLCSDDINVPDEETIFHALMQWVGHDVQNRQGELGMLLS
			YIRLPLDPPQLLADLETSSMFTGDLECQKLLMEAMKYHLLPERR
			SMMQSPRTKPRKSTVGALYAVGGMDAMKGTTTIEKYDLRTNSWL
1	}		HIGTMNGRRLQFGVAVIDNKLYVVGGRDGLKTLNTVECFNPVGK
ļ			IWTVMPPMSTHRHGLGVATLEGPMYAVGGHDGWSYLNTVERWDP
1			EGRQWNYVASMSTPRSTVGVVALNNKLYAIGGRDGSSCLKSMEY FDPHTNKWSLCAPMSKRRGGVGVATYNGFLYVVGGHDAPASNHC
l			SRLSDCVBRYDPKGDSWSTVAPLSVPRDAVAVCPLGDKLYVVGG
1	j		YDGHTYLNTVESYDAQRNEWKEEVPVNIGRAGACVVVVKLP
6922	1075	369	LTPPAGIRHEVRDRBREREREREREKEFPLDSTGSELKQNIHSIT
			GLPPAMQKVMYKGLAPEDKTLREIKVTSGAKIMGGGSTINDVLA
[VNTPKDAAQQDAKAEENKKEPLCRQKQHRKVLDKGKPEDVMPSV
			KGAQERLPTVPLSGMYNKSGGKVRLTFKLEQDQLWIGTKERTEK
1 1			LPMGSIKNVVSEPIEGHEDYHMMAFQLGPTEASYYWVYWVPTQY
		_	VDAIKDTVLGKWQYF
6923	2469	1660	LGLFCILPIDTLCAVLERDTLSIRESRLFGAVVRWAEAECQRQQ
1 1	İ		LPVTFGNKQKVLGKALSLIRFPLMTIEEFAAGPAQSGILSDREV
1 1			VNLFLHFTVNPKPRVEYIDRPRCCLRGKECCINRFOOVESRWGY
1 1	į		SGTSDRIRFTVNRRISIVGFGLYGSIHGPTDYQVNIQIIEYEKK
i 1	l		QTLGQNDTGFSCDGTANTFRVMFKEPIEILPNVCYTACATLKGP
	l		DSHYGTKGLKKVVHETPAASKTVFFFFSSPGNNNGTSIEDGQIP
6924	2210	1235	EIIFYT
		1233	PEERVICFVEYYLTAFHEGRKGALAKKPYNPIIGETFHCSWEVP
		ļ	KDRVKPKRTASRSPASCHEHPMADDPSKSYKLRFVAEQVSHHPP
		1	ISCFYCECEBKRLCVNTHVWTKSKFMGMSVGVSMIGEGVLRLLE HGFFYVFTLDSAVARSILTINGER
		ļ	HGEEYVFTLPSAYARSILTIPWVELGGKVSINCAKTGYSATVIF HTKPFYGGKVHRVTAEVKHNPTNTIVCKAHGEWNGTLEFTYNNG
			ETKVIDTTTLPVYPKKIRPLEKQGPMESRNLWREVTRYLRLGDI
			DAATEQKRHLEEKQRVEERKRENLRTPWKPKYFIQEGDGSGILQ
			SPLESTLMGLEVQSFPV
6925	2	1653	RGGAAGAAMBPDSVIEDKTIELMCSVPRSLWLGCANLVESMCAL
	1	İ	SCLQSMPSVRCLQISNGTSSVIVSRKRPSEGNYQKEKDLCIKYF
	• 1		DQWSESDQVEFVEHLISRMCHYQHGHINSYLKPMLQRDFITALP
	į.]	EQGLDHIAENILSYLDARSLCAAELVCKEWQRVISEGMLWKKLI
		ļ	ERMVRTDPLWKGLSERRGWDQYLFKNRPTDGPPNSFYRSLYPKI
	ł	1	IQDIETIESNWRCGRHNLQRIQCRSENSKGVYCLOYDDEKIISG
	į]	LRDNSIKIWDKTSLECLKVLTGHTGSVLCLQYDERVIVTGSSDS
		_	TVRVWDVNTGEVLNTLIHHNEAVLHLRFSNGLMVTCSKDRSIAV
		l	WDMASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVW
		1	STSTCEFVRTLNGHKRGIACLOYRDRLVVSGSSDNTIRLWDIRC
			GACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLOAALDP
		· 1	RAPASTLCLRTLVEHSGRVFRLOFDEFOIISSSHDDTILIWDFL
6926			NVPPSAQNETRSPSRTYTYISR
0,20	1	733	SGRVAMDGLGLQFPEQGFPAGPPLLPPHMGGHYRDCQSLGAPPL

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ł	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	ı •	\=possible nucleotide insertion)
			DGYPLPTPDTSPLDGVDPDPAFFAAPMFGDCPAAGTYSYAQVSD
			YAGPPEPPAGPMHPRLGPEPAGPSIPGLLAPPSALHVYYGAMGS
		1	PGAGGGRGFQMQPQHQHQHQHQHPPGPGQPTPPPEALPCRDGT
Į	1		DPSQPABLLGEVDRTEFEQYLHFVCKPEMGLPYQGHDSGVNLPD
	1		SHGAISSVVSDASSAVYYCNYPDV
6927	2	1484	LTLCGDIQLMLAQNANNRAAHLEEFHYQTKEDQEILHSLHRESS
}	1		CQGFAWATDLSTDLESQLSVSCKCYEAANBILQFRDLKSQNPEH
			YVQVLKRMGNIRNEIGVFYMNQAAALQSERLVSKSVSAAEQQLW
			KKSFSCFEKGIHNFESIEDATNAALLLCNTGRLMRICAQAHCGA
ł			GDELKREFSPEEGLYYNKAIDYYLKALRSLGTRDIHPAVWDSVN
	}		WELSTTYFTMATLQQDYAPLSRKAQEQIEKEVSEAMMKSLKYCD
			VDSVSARQPLCQYRAATIHHRLASMYHSCLRNQVGDEHLRKQHR
			VLADLHYSKAAKLFQLLKDAPCELLRVQLERVAFAEFQMTSQNS
1	1		NVGKLKTLSGALDIMVRTEHAFQLIQKELIEEFGQPKSGDAAAA
			ADASPSLNREEVMKLLSIFESRLSFLLQSIKLLSSTKKKTSNN
	ĺ		IEDDTILKTNKHIYSQLLRATANKTATLLERINVIVHLLGQLAA
			GSAASSNAVQ
6928	1086	777	EAIDLINNLLQVKMRKRYSVDKTLSHPWLQDYQTWLDLRELECK
			IGERYITHESDDLRWEKYAGEQGLQYPTHLINPSASHSDTPETE
			ETEMKALGERVSIL
6929	1749	607	RDQRGYRDDRSPAREPGDVSARTRSGGGGGRSATTAMPPPVPNG
			NLHQHDPQDLRHNGNVVVAGRPSCSRGPRRAIQKPQPAGGRRSG
			RGPAAGGLCLQPPDGGTCVPEEPPVPPMDWEALEKHLAGLQFRE
·			QEVRNQGQARTNSTSAQKNERESIROKLALGSFFDDGDGTVTCC
			SKSGKPSLSSRLQSGMNLQICFVNDSGSDKDSDADDSKTETSLD
-			TPLSPMSKQSSSYSDRDTTEEESESLDDMDFLTROKKT.OAFAKM
			ALAMAKPMAKMQVEVEKQNRKKSPVADLLPHMPHISECLMKPSI.
	ì		KPTDLRDMTIGQLQVIVNDLHSOIESLNEELVOLLITEDELHTR
<u> </u>			QDAMLVDIEDLTRHAESOOKHMAEKMPAK
6930	131	545	FKDTANVFVSLFQMRNNFRHYFIBPSQLKLFYDVITWIVTQVAI
	ŀ		SYTVVPFVLLSIKPSLTFYSSWYYCLHILGILVLLLDUKKTOD
			RKNTHENIQLSQSKKFDEGENSLGQNSFSTTNNVCNONOEIASR
6931			HSSLKQ
9331	2	659	FVERLPNRPACLLVASGAAEGVSAQSFLHCFTMASTAFNLQVAT
		1	PGGKAMEFVDVTESNARWVQDFRLKAYASPAKLESIDGARYHAI.
			LIPSCPGALTDLASSGSLARILOHFHSESKPICAVGHGVAALCC
			ATNEDRSWVFDSYSLTGPSVCELVRAPGFARLPLVVEDFUKDSG
6932	2		ACFSASEPDAVHVVLDRHLVTGONASSTVPAVONLLFLCGSPK
-552	4	1131	FVDSPGQGEQAEEEEGGIQMNSRMRAHSPAEGASVESSSPGPKK
J			SDMCEGCRSLAAGHPGYISHDKETSIKYVSHOHPSHDOLDGTVD
	ļ		QACVRSLSCEVCPGREGPIFFGDEOHGFVFSHTFFIKDSLARGE
1	1		QRWYSIITIMMDRIYLINSWPFLLGKVRGIIDELOGKALKVFFA
i			EQFGCPQRAQRMNTAFTPFLHORNGNAARSLTSLTSDDNI.Wact.
,	1	ļ	HTSFAWLLKACGSRLTEKLLEGAPTEDTLVOMEKLADI.EFFSFS
1	1	. 1	WDNSEAEEEEKAPVLPESTEGRELTQGPAESSSLSGCGSWQPRK
		•	LPVFKSLRHMRQVGGRGTAHHELRRRANHGLCLPTRLASGPSTL
6933	1431	890	KTLQEVTDSLLGGWLMAQGVGGII
		070	SLNLHCTLPPPPHQYPAGYPSDKEGKKPKGQSKKQPSGTTKRPI
			SDDDCPSASKVYKASDSAEAIEAFQLTPQQQHLIREDCQNQKLW
1	j		DEVLSHLVEGPNFLKKLEQSFMCVCCQELVYQPVTTECFHNVCK
l l		1	DCLQRSFKAQVFSCPACRHDLGQNYIMIPNEILQTLLDLFFPGY
6934	3030	2502	SKGR
7,5,2	3030	2588	DRDHSQCGGIRRVALARVSSVKLISKAKIRTVKMTFIIVLAFIV
1	İ		CWTPFFFVQMWSVWDANAPKRASAFIIVMLLASLNSCCNDWTVM
- 1		İ	LFTGHLFHELVQRFLCCSASYLKGRRLGETSASKKSNSSSFVLS
			HRSSSQRSCSQPSTA

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1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	70423330	\=possible nucleotide insertion)
6935	886	543	NSALYVAGGNDGTSCLNSVERYSPKAGAWESVAPMNIRRSTHDL
		1	VAMDGWLYAVGGNDGSSSLNSIEKYNPRTNKWVAASCMFTRRSS
			VGVAVLELLNFPPPPSSPTLSVSSTSL
6936	1347	567	RSHRRQFLSRALLEFFGKSHPPPHRLFRKSLNVGLHYSHIPFLT
1			TCLHFLRKRLQKGEVGLSVETSKPQVPVGGLSRKKVPQEPWATV
			MEKRLQEAQLYKEEGNQRYREGKYRDAVSRYHRALLQLRGLDPS
l			LPSPLPNLGPQGPALTPEQENILHTTQTDCYNNLAACLLQMEPV
		1	NYERVREYSQKVLERQPDNAKALYRAGVAFFHLQDYDQARHYLL
1			AAVNRQPKDANVRRYLQLTQSELSSYHRKEKQLYLGMFG
6937	1	727	AVEFRCCPGRDPACFARGWRLDRVYGTCFCDQACRFTGDCCFDY
1			DRACPARPCFVGEWSPWSGCADQCKPTTRVRRRSVQQEPQNGGA
			PCPPLEERAGCLEYSTPQGQDCGHTYVPAFITTSAFNKERTRQA
l .			TSPHWSTHTEDAGYCMEFKTESLTPHCALENRPLTRWMQYLREG
j			YTVCVDCQPPAMNSVSLRCSGDGLDSDGNQTLHWQAIGNPRCQG
L			TWKKVRRVDQCSCPAVHSFIFI
6938	3	719	NSRKLELAERVOTDFMQLKKRRQSSEKENDSGTLDTVGAVVVDH
İ			EGNVAAAVSSGGLALKHPGRVGQAALYGCGCWAENTGAHNPYST
1		•	AVSTSGCGEHLVRTILARECSHALQAEDAHQALLETMONKFISS
1			PFLASEDGVLGGVIVLRSCRCSAEPDSSONKOTLLVEFLWSHTT
1		ı	ESMCVGYMSAQDGKAKTHISRLPPGAVAGQSVAIEGGVCRLGEP
		L	SELTLQAECEASQRHFRT
6939	3	810	KVTAPRRPQRYSSGHGSDNSSVLSGELPPAMGRTALFHHSGGSS
į.]		GYESLRRDSEATGSASSAPDSMSESGAASPGARTRSLKSPKKRA
İ			TGLQRRRLIPAPLPDTTALGRKPSLPGQWVDLPPPLAGSLKEPF
ł			EIKVYEIDDVERLQRPRPTPREAPTQGLACVSTRLRLAERRQQR
}			LREVQAKHKHLCEELAETQGRLMLEPGRWLEQFEVDPELEPESA
			EYLAALERATAALEQCVNLCKAHVMMVTCFDISVAASAAIPGPQ
6940	1000		EVDV
6540	1188	496	GKMAAQPLRHRSRCATPPRGDFCGGTERAIDQASFTTSMEWDTQ
	! . !		VVKGSSPLGPAGLGAEEPAAGPQLPSWLQPERCAVFQCAQCHAV
			LADSVHLAWDLSRSLGAVVFSRVTNNVVLKAPFLVGIEGSLKGS
	}		TYNLLFCGSCGIPVGFHLYSTHAALAALRGHFCLSSDKMVCYLL
			KTKAIVNASEMDIQNVPLSEKIAELKEKIVLTHNRLKSLMKILS
6941	1	713	EVTPDQSKPEN
*****	•	/13	SLSRADSDPHGPHTCGHVLNVIIGSNVLALAEAQRQAEALGYQA
			VVLSAAMQGDVKSMAQFYGLLAHVARTRLTPSMAGASVEEDAQL HELAAELQIPDLQLEEALETMAWGRGPVCLLAGGEPTVQLQGSG
			RGGRNOELALRVGAELRRWPLGPIDVLFLSGGTDGQDGPTEAAG
			AWYTPELASQAAAEGLDIATFLAHNDSHTFFCCLQGGAHLLHTG
			MTGTNVMDTHLLFLRPR
6942	1	246	GDYVERYDPKTDTWTMGAPLSMPTNAVGGCLLGDRLYADGGYDG
	1		QTYLNTMESYDPQTNEWTQMASLNIGRAGACVVVIKQP
6943	. 1	739	PMATGDGAKTLATHVKALTADSIRITWKATLPASSFRLSWLRLG
	[HSPAGGSITETLVQGDKTEYLLTALEPKPTYIICMVTMETTNAY
			VADETPVCAKAETADSYGPTTTLNQEQNAGPMASLPLAGIIGGA
	ŀ		VALVFLFLVLGAICWYVHQAGELLTRERAYNRGSRKKDDYMESG
	•	İ	TKKDNSILBIRGPGLQMLPINPYRAKEEYVVHTIFPSNGSSLCK
	ĺ		ATHTIGYGTTRGYRDGGIPDIDYSYT
6944	960 .	156	VANILLNGVKYESELTGSSERAEQPLSVGRLCSTICNMPKALRT
J	}		LCVNHFLGWLSFEGMLLFYTDFMGEVVFQGDPKAPHTSEAYOKY
		İ	NSGVTMGCWGMCIYAFSAAFYSAILEKLEEFLSVRTLYFIAYLA
}			FGLGTGLATLSRNLYVVLSLCITYGILFSTLCTLPYSLLCDYYO
1			SKKFAGSSADGTRRGMGVDISLLSCQYFLAQILVSLVLGPLTSA
			VGSANGVMYFSSLVSFLGCLYSSLFVIYEIPPSDAADEEHRPLL
		1	LNV

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NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
į.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
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ł	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence	_	\=possible nucleotide insertion)
6945	2067	179	EGEDRGLPRTMGAALGTGTRLAPWPGRACGALPRWTPTAPAQGC
	[İ	HSKPGPARPVPLKKRGYDVTRNPHLNKGMAFTLEERLQLGIHGL
	1	l	IPPCFLSQDVQLLRIMRYYERQQSDLDKYIILMTLQDRNEKLFY
l			RVLTSDVEKFMPIVYTPTVGLACQHYGLTFRRPRGLFITIHDKG
1		ł	HLATMLNSWPEDNIKAVVVTDGERILGLGDLGCYGMGIPVGKLA
ſ			LYTACGGVNPQQCLPVLLDVGTNNEELLRDPLYIGLKHQRVHGK
ł		į	AYDDLLDEFMQAVTDKFGINCLIQFEDFANANAFRLLNKYRNKY
1	1		CMFNDDIQGTASVAVAGILAALRITKNKLSNHVFGFQGAGEAAM
1		}	G\IAHLLVMALE\KEGVPKA\EATRKIW\MVDF\KGLIVQGRDH
			LNHEKEMFAQD\HPEVNSLEEVVRLVKPTAIIGVAAIAEA\FTE
1			QILRDMASFHERP\IIFALSNPTSKAECTA\EKCYRVTEGPRGF
1	1		FAS\GSPF+GVLIWEMGKTFIPGGRGNNA+RVPRGWQLGVHSPG
1			GDPGHIP\DEIFLPDSRAKLPQEVSEQHLSQGRLYP\PLST\IR
1			NVFLRIAIKVFD*GYKHNLV\SYYPEPKD\KEAFCKIPGSYTPD
			YDSFYT/VDSYIWAQGKAMNVQTV
6946	133	2551	SCEYSGITVAPGDPCPGVAHLLAPSMASDTPESLMALCTDFCLR
			NLDGTLGYLLDKETLRLHPDIFLPSEI\CDRLVNEYVBLVNAAC
			NF\EPHE\SFFNPLFRDPRKQPASRRIHL\RED\LVQD\QD\LE
			AIRKQDL\VEL\YLTN\CEKLSAKSLQTLRSFSHTLGVP*AFFG
1			C\TNILLLRKENPGGL/CEDEYLFNPTCQVLVKDFTFEGFSRLR
			F\LKLGRMIDWVPVES\LLRPLNSLAALDLSGIQTSDAA\FLTQ
1			WKDSL\VSLVL\YNMDLSDDHIR\VIVQLHKLRHLDISRDRLSS
			YYKFKLTREVLSLFVQKLGNLMSLDISG\HMILENCSISKIGKR
			EAGQTSI\EPSK\SSIIPFRGFEGGPLQF\LGVF*GIFCGRLTH
]			IPAYKVSGDKNEEQVLNAIEAYTEHRPEITSRAINLLFDIARIE
1 1			RCNQLLRALKLVITALKCHKYDRNIOVTGSAALFYLTNSEVPSE
i i			QSVKLRRQVIQVVLNGMESYQEVTVORNCCLTLCNFSIPERIER
			QYRRVNELLLSILNPTRQDESIQRIAVHLCNALVCQVDNDHKEA
I i			VGKMGFVVTMLKLTQKKLLDKTCDOVMEFSW\SALWNTTDETPD
1	ì		NCEMFLNPNGMKLFLDCLNEFPEKQELHRNMLGLLGNVARVKEL
,	i		RPQLMTSQFISVFSNLLESKADGIEVSYNACGVLSHIMFDGDEA
1 1	j		WGVCEPQREEVEERMWAAIQSWDINSRRNINYRSFEPILRLLPO
i i	į		GISPVSQHWATWALYNLVSVYPDKYCPLLIKEGGMPLLRDIIKM
			ATARQETKEMARKVIEHCSNFKEENMDTSR
6947	2	1682	TSVSTIPRGLASARPOSRSWRCCPVWRRSPGRARGRGLKMINUD
			SQSFPAPRSQQRVASGGRSKVPLKOGRSLMDWIRLTKSGKDLTG
			LKGRLIEVTEEELKKHNKKDDCWICIRGFVYNVSPYMEYHPGGE
			DELMRAAGSDGTELFDQVHRWVNYESMLKECLVGRMATKPAVI.K
l J			DYREEEKKVLNGMLPKSQVTDTLAKEGPSYPSYDWFOTDSLVTI
	1		/EHIY*TEGYQFRLNNS*SSE*FLYSRNNY*GLLISYTYW/p*A
			MRFRKIFLCGL/CESVGKIEIVLOKKENTSWDFLGHPLKNHWST.
	1		IPRKDTGLYYRKCQLISKEDVTHDTRLFCLMLPPSTHLOVPIGO
1		İ	HVYLKLPITGTEIVKPYTPVSGSLLSEFKEPVLPNNKYTVFLTK
		1	IYPTGLFTPELDRLQIGDFVSVSSPEGNFKISKFOELEDLFLLA
1		ļ	AGTGFTPMVKILNYALTDIPSLRKVKLMFFNKTEDDIIWRSOLE
1			KLAPKDKRLDVEFVLSAPISEWNGKOGHISPALLSEFLKRNIDK
6948	104		SKVLVCICGPVPFTEQGVRLLHDLNFSKNEIHSFTA
0340	104	58	PDGAHSFFPDEYFTCSSLCLSCGVGCKKSMNHGKEGVPHEAKSP
ł			CRYSHQYDNRVYTCKACYERGEEVSVVPKTSASTDSPWMGLAKY
- 1		1	AWSGYVIECPNCGVVYRSRQYWFGNQDPVDTVVRTEIVHVWPGT
			DGFLKDNNNAAQRLLDGMNFMAQSVSELSLGPTKAVTSWLTDOT
	ļ	i	APAYWRPNSQILSCNKCATSFKDNDTKHHCRACGEGFCDSCSSK
	1	[TRPVPERGWGPAPVRVCDNCYEAR/TRPVSCYRGTSGR*RRRRT
6949			QETVE
0343	152	4656	GLRLCLSRPLTRPGDDSVGGSAMASGAGGVGGGGGGKIRTRRCH
			QGPIKPYQQGRQQHQGILSRVTESVKNIVPGWLQRYFNKNEDVC

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	amino acid	sequence	Codon, /=possible nucleotide deletion,
<u> </u>	sequence	1 -	\=possible nucleotide insertion)
			SCSTDTSEVPRWPENKEDHLVYADEESSNITDGRITPEPAVSNT
1	[i	BEPSTTSTAST\YPDVLTRVSLYRSHLNFSMLESPALHCQPSTS
			SAPPIGSSGFSLVKEIKDSTSQHDDDNISTTSGFSSRASDKDIT
1	í '	1	VSKNTSI DRI MCDENERGURI SOUTH TOOMS TO STANDARD TO
	Ì		VSKNTSLPPLWSPEAERSHSLSQHTATSSKKPAFNLSAFGTLSP SLGNSSILKTSQLGDSPFYPGKTTYGGAAAAVRQSKLRNTPYQA
1]	PVRROMYAKOLGAGGYGUMGGMARATIGGAAAAVRQSKLRNTPYQA
ľ		[PVRRQMKAKQLSAQSYGVTSSTARRILQSLEKMSSPLADAKRIP SIVSSPLNSPLDRSGIDITDFQAKREKVDSQYPPVQRLMTPKPV
			SIATNRSVYPKPSLTPSGEFRKTNQRIDKKCSTGYEKNMTPGQN
ļ			REQRESGFSYPNFSLPAANGLSSGVGGGGGKMRRERHAFVASKP
			LEEEEMEGPVLPKISLPITSSSLPTFNFSSPEITTSSPSPINSS
	1		QALTNKVQMTSPSSTGSPMFKFSSPIVKSTEANVLPPSSIGFTF
			SVPVAKTAELSGSSSTLEPIISSSAHHVTTVNSTNCKKTPPEDC
	1		EGPFRPAEILKEGSVLDILKSPGFASPKIDSVAAQPTATSPVVY
1			TRPAISSFSSSGIGFGESLKAGSSWQCDTCLLQNKVTDNKCIAC
1			QAAKLSPRDTAKQTGIETPNKSGKTTLSASGTGFGDKFKPVIGT
1			WDCDTCLVQNKPEAIKCVACETPKPGTCVKRALTLTVVSESAET
1			MTASSSSCTVTTGTLGFGDKFKRPIGSWECSVCCVSNNAEDNKC
1			VSCMSEKPGSSVPTSSSSTVPVSLPSGGSLGLEKEKKPGGTWDG
1			ELCLVQNKADSTKCLACESAKPGTKSGFKGFDTSSSSSNEARS
			SFREGVSSSSSGPSQTLTSTGNFKFGDOGGFKTGVSSDSGVIND
i			MSEGF*FSKHIVGFKFGVSSESKPEEVKKDSKNDNFKFGLSFGL
j			SNPVFLTPFQFGVSNLGQEEKKEELLKSSCAGFRFGTGVINGTB
1	j		VPANTIVTSENKSSFNLGTIETKSVSVAPIKCOTSEAKKEEMDA
1			TRUGFSFGNVBPASLPSASVFVLGRTEEKOOEPVTSTSLVPGPG
			KLTMKEPKC\QPVFSFGEFOROTKDENSSKSTFSFSMTKDGFVF
]		SEQPAKATFAFGAQTNTTADOGAAKPDLSYLNNSSSSSSTDATE
1	! [AGGG \ I FGSSTSSSNPPVATFVFGOSSNPGSSS \ AFGNTAFGCT
			SQSLLFSQDSKLATTSSTGTAVTPFVFGPGASSNNTTTSGEGEG
		ļ	ATTTSSSAGSSFVFGTGPSAPSASPAFGANOTPTFGOSOGASOR
1			NPPGFGSISSSTALFPTGSOPAPPTFGTVSSSSOPPVFGOODSO
}	1		SAFGSGTTPNSSSAFOFGSSTTNFNFTNNSPSGVFTFGDNSGTD
1			AASAQPSGSGGPPFNQSPAAFTVGSNGKNVFSSSGTSFSGPKIK
6950	2585		TAVRRK
	2303	411	PRPGSRSGLCRRAGERGAVRAGGLSRRTRAE*IMDELHYQDTDS
1		i	DVPEQRDSKCKVKWTHEEDEOLRALVROFGOODWKFIACHPBND
[i	TDQQCQYRWLRVLNPDLVKGPWTKEEDOKVTELVKKYGTVOWTI
1 1			TAKHLKGRLGKQCRERWHNHLNPEVKKSCWTEEEDRIICEAUG
1	İ		LGNRWAEIAKMLPGRTDNAVKNHWNSTIKRKVDTGGFLSESKDC
1 1		1	KPPVYLLELEDKDGLQSAQPTEGQGSLLTNWPSVPPTIKEEEN
1 1	1	1	SEEELAAATTSKEQEPIGTDLDAVRTPEPLEEFPKREDQEGSPP
1 1			ETSLPYKWVVEAANLLIPAVGSSLSEALDLIESDPDAWCDLSKF
1 }			DLPEEPSAEDSINNSLVQLQASHQQQVLPPRQPSA\LVPSVTEY
, ,	J		RLDGHTISDLSRSSRGELIPISPSTEVGGSGIGTPPSVLKRQRK
1			RRVALSPVTENSTSLSFLDSCNSLTPKSTPVKTLPFSPSQFLNF
		-	WNKQDTLELESPSLTSTPVCSQKVVVTTPLHRDKTPLHQKHAAF
		1.	VTPDQKYSMDNTPHTPTPFKNALEKYGPLKPLPQTPHLEEDLKE
		1.	VLRSEAGIELIIEDDIRPEKQKRKPGLRRSPIKKVRKSLALDIV
			DEDMKLMMSTLPKSLSLPTTAPSNSSSLTLSGIKEDNSLLNQGF
		1:	LQAKPEKAAVAQKPRSHFTTPAPMSSAWKTVACGGTRDQLFMQE
6951	1940	239	KARQLLGRLKPSHTSRTLILS
-			AGPDDTMKRSLQALYCQLLSFLLILALTEALAFAIQEPSPRESL
1	1	[]	QVLPSGTPPGTMVTAPHSSTRHTSVVMLTPNPDGPPSQAAAPMA
i	1	13	TPTPRAEGHPPT\TPSPPSLRQ*PPPILKAP/SSTGPAPAAMAT
}	İ	13	ISSKPEGRPRGQAAPTILLTKPPGATSRPTTAPPPTTTPDDDDD
		[;	PGSSRKGAGNSSRPVPPAPGGHSRSKEGQRGRNPSSTPLGQKRP
		L	LGKIFQIYKGNFTGSVEPEPSTLTPRTPLWGYSSSPQPQTVAAT

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ì	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
1	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
- 1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ì	sequence	Joquecc	Codon, /=possible nucleotide deletion,
		 	\=possible nucleotide insertion)
1	1	1	TVPSNTSWAPTTTSLGPAKDKPGLRRAAQGGGSTFTSQGGTPDA
j	•		TAASGAPVSP/PSCPSAFSAPPPR*PTGWPQP**LLAYCYP\CT
ı	1	1	SRPLSTSSGVFTAATGPTPAAFDTSVSAPSQGIPQGASTTPQAP
			THPSRVSESTISGAKEETVA\PSP*PTGCPVLSPQWYPQPQAIS
1			STAWSPPGPGSLGQQGTSPMWPRGTNRSTEPPSA*ARWISPG*S WPSACPSPP\LCPADGVLHEBEEEDRQPGEQPEAYGNNTHHPGT
1		1	TFQQAC\RGAAPGEIPVPLKPLRTQLSEPRSPANGDYRDTGMVP
			C C C COMPANDED POPER PER PER PER PER PER PER PER PER PER
6952	658	304	PESEGESGEMTDRYTIHSQLEHLQSKYIGT\ATPTPPSGSG\CE
			PTPRLVLLHGPLRPSQLLRHCGE*EQSASPLQLDGKDASALWT
			ASRQARGELRLCLTTAVRGTSPSVSPVCQSS
6953	1512	349	NWGKTRALASGKHVPFGKQTNPNKS/VHCDS*G**RRETTQDES
1	1		FSPHFRGKMGGVV\KLEKELENTEOPVGGNEG+FUEUTGNI NCD
			PLLELCQCPLCQLDCGSREOLIAHVYOHTAAVVSAKSVM\ CDVC
1			GRALSSPESLERHLLIHSEDORSNCAVCGAPFTSHATENGERID
ſ			BVLNMESLPTVHNEGPSSAEGKDIAFSPDVVPAGTLIVCNNCAR
1	ĺ		YKKLLEAQTPSVRKWALRRONEPLEVRLORLERERTAKKERDOM (
	1		ETPECKEVRRMRDREAKRLORMOETDEORARDI.ODDREAMDI VD
1			ALETPEKRQARLIREREAKRLKRRLEKMDMMI.RAOFGODBCAMA
6954	819		ALAAEMNFFQLPVSGVELDSOLLGKMAFERONSSSLU
****	""	1	PPPPFIIPSHPREAGT*AG*KRSGDSECSPPVEO*A*TPAAAON
ĺ			"PQK"RWIEGNSPQASAVATPGOGASPAAPRC"PD+DGDDUBDID
			PGARPPAG*AAPAPTKPWLAGPASAPOPGAAPI.SDDADDI TDTD
ł	1		*CAGAAARGRPRRDRSPRPRTPGGCSWSEPRTPPAVSASAQTPS
	1		DAG*AGGR*GQRQRPSTGR*PPGVGGAGRSHRREGTIPGNPHPR
			AS*RAGWQR*PGP/REWGL*EPQGEEMSGPGGPGGAPPNQVGSS
6955	1968	782	
Į.	[· · · -	PPGRRQVRAQVAGAPVGHWGTRARQVKTGGRRRARRTMPFLGQD WRSPGWSWIKTEDGWKRCESCSQKLERENNHCNISHSIILNSED
ŀ		i	GEIFNNEEHEYASKKRKKDHFRNDTNTQSFYREKWIYVHKESTK
ļ			ERHGYCTLGEAFNRLDFSSAIQDIRRFNYVVKLLQLIAKSQLTS
			LSGVAQKNYFNILDKIVQKVLDDHHNPRLIKDLLQDLSSTLCIL
i			/N*RSREVCISGKHQYLDLPIRNYSRLATTATGSSDD*ASE\NG
1			LTLSDLPLHMLNNILYRPSDGWDIITLGQVTPTLYMLSEDRQLW
ĺ			ARLCVIHFAEKOFCRHLILSEKGHTEWKIMVERI OVUVDRYBOY
[GDTLHFCRHCSILFWKDSGHPCTAADPDSCFTPVSPQHFIDLFK
6956	0665		•
9236	8605	3839	QTSTS I FASPTSPPVLGESVLQDNSFDLNNGSDAEQEEMETQSS
l j	ł	I	DFFFSLTQPAPDQSSTIOLHPATSPAVSPTTSDAVSTITIODARS
	j	ĺ	PEISPEVCPAASTVVSPAVFSVVSPASSAVI, DAVST, EVDT TO CV
			TSPKASPVTSPAAAFPTASPANKDVSSFLETTADVFFTTOFCT m
		1	ASGSGDVMRRRIATPEEVRLPLOHGWRRRVRTKKGGUPWOGRAW
1			11GPCGARMAQEPEVIKYLSRNVVHSVRREHFSESDDMDUCDER
Í		ı	BERDTPEGLQWVQLSAEEIPSRIOAITGKRGRPPNTFKADTVPV
J		ļ	PKVKRGRGRPPKVKITELLNKTDNRPLKKLEAQETLNEEDKAKI
J		1	AKSKKKMRQKVQRGECQTTIQGQARNKRKQETKSLKQKEAKKKS
[ĺ	1	KAEKEKGKTKQEKLKEKVKREKKEKVKMKEKEEVTKAKPACKAD
		1	KTLATORRLEERQRQQMILEEMKKPTEDMCLTDHQPLPDFSRVP
J	İ	j :	GLTLPSGAFSDCLTIVEFLHSFGKVLGFDPAKDVPSLGVLQEGL
į			LCQGDSLGEVQDLLVRLLKAALHDPGFPSYCQSLKILGEKVSEI
ŀ	[1 ;	PLTRDNVSEILRCFLMAYGVEPALCDRLRTQPFQAQPPQQKAAV
[ļ	1;	LAFLVHELNGSTLIINEIDKTLESMSSYRKNKWIVEGRLRRLKT
į	ſ	1 :	VLAKRTGRSEVEMEGPEECLGRRRSSRIMEVTSGMEEEBEESI AAVPGRRGRRDGEVDATASSIPELERQIEKLSKRQLFFRKKLLH
		13	SSQMLRAVSLGQDRYRRRYWVLPYLAGIFVEGTEGNLVPEEVIK
		i	KETDSLKVAAHASLNPALFSMKMELAGSNTTASSPARARGRPRK
			- CHICALIAGONTTASSPARAKGRPRK

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ı	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine.
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine.
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, +=Ston
1	amino acid	sequence	Codon, /=possible nucleotide delerion
	sequence		\=possible nucleotide insertion)
			TKPGSMQPRHLKSPVRGQDSEQPQAQLQPEAQLHAPAQPQPQLQ
1	· ·	}	LQLQSHKGFLEQEGSPLSLGQSQHDLSQSAFLSWLSQTQSHSSI.
			LSSSVLTPDSSPGKLDPAPSQPPEEPEPDEAESSPDPQALWFNI
J			SAQMPCNAAPTPPPAVSEDQPTPSPQQLASSKPMNRPSAANPCS
	1	1	PVQFSSTPLAGLAPKRRAGDPGEMPQSPTGLGQPKRRGRPPSKF
1			FKQMEQRYLTQLTAQPVPPEMCSGWWWIRDPEMLDAMLKALHPR GIREKALHKHLNKHRDFLQEVCLRPSADFIFEPRQLPAFQEGIM
			SWSPKEKTYETDLAVLQWVEBLEQRVIMSDLQIRGWTCPSPDST
1		,	REDLAYCEHLSDSQEDITWRGRGREGLAPQRKTTNPLDLAVMRL
			AALEQNVERRYLREPLWPTHEVVLEKALLSTPNGAPEGTTTEIS
i	1		YEITPRIRVWRQTLERCRSAAQVCLCLGOLERSIAWEKSUNKUT
İ			CLVCRKGDNDEFLLLCDGCDRGCHIYCHRPKMEAVPEGDWECTV
1			CLAQQVEGEFTQKPGFPKRGQKRKSGYSLNFSEGDGRRRRVLLR
	1		GRESPAAGPRYSEEGLSPSKRRRLSMRNHHSDLTFCEITLMEME
1			SHDAAWPFLEPVNPRLVSGYRRIIKNPMDFSTMRERLLRGGVTS
			SEEFAADALLVFDNCQTFNEDDSEVGKAGHIMRRFFE\SRWEEF
	1		YQGKQGQSVRQGRWGVTLWHLPPTFQTKTCHFHLLMLPWVQTQV RYNPDF
6957	82	3514	HLIVAMPEPTKKEENEVPAPAPPPEEPSKEKEAGTTPAKDWTLV
[]		ETPPGEEQAKQNANSQLSILFIEKPQGGTVKVGEDITFIAKVKA
]		EDLSEKPTINGSRKWMDLASKAGKHLQLKETFERHSRVYTFEMQ
1			IIKAKDNFAGNYRCEVTYKDKFDSCSFDLKVHESTGTTPNIDID
1			SAFKRSGEGQEDAGELDFSGLLKRREVKOOEEEPOVDVWELLKN
			TKPSEYEKIAPQYESPTCSGMLKRLKRSIREEKKSAAFAKTIDD
1			VYQVDKGGRVRFVVELADPKLEVKWNKNGOELRPSTKYIFRDTD
1	ľ		CQSILNIDNCQMTDDSEYYVTAGDEKCSTELLVREPPIMVTKQL
1	1		EDTTDYCGERVELECEVSEDDAQVKWFKNGEEIILVQTRYRIRV
	1		EGKKHILIIEGATKADAADYSVMTTGGQSSAKLSVDLKPLKILT
1	1	ĺ	PLTDQTVNLGKEICLKCEISENIPGKWTKNGLPVQESDRLKVVH KGRIHKLVIDHALTEDEGDYVFAPDAYNVTLPAKVHVIDPPKII
	}		LDGLDADNTVTVIAGNKLRLEIPISGEPPPKAMWSRGDKAIMEG
1	1	j	SGRIRTESYPDSSTLVIDIAERDDSGVYHINLKNEAGEAHASIK
			VKVVDFPDPPVAPTVTEVGDDWCIMNWEPPAYDGGSPILGYFIE
Ì	ŀ		RKKKQSSRWMRLNFDLCKETTFEPKKMIEGVAYEVRIPAVNA\T
l	}		GISKPSMPSRPFVPLAVTSPPTLLTVDSVTDTTVTMRWRPPDHT
			GAAGLDGYVLEYCFEGSTSAKOSDENGEAAYDLPAEDWIVANKD
}		-	LIDKTKFTITGLPTDAKIFVRVKAVNAAGASEPKYYSQPILVKE
1		}	IIEPPKIHSPKHLKQTYIRRVGDRVILVIPFQGKPRPELTWKKD
		1	GAEIDKNQINIRNSETDTIIFIRKAERSHSGKYDLQVKVDKFVE TASIDIRIIDRPGPPQIVKIEDVWGRNVALTWTPPKDDGNAAIT
j i		ł	GYTIQKADKKSMEWLRVIEHIIEPVPHTELVIGNEYYFRVFSEN
	1	.	MCGLSEDATMTKESAVIARDGKIYKNPVYEDPDFSEAPMFTQPL
		i	VNRLCHSGYMATLNCSVRGNPKPKITWMKNKVAIVDDPPVPMFG
			NQGVCTLEIRKPSPYDGGTYCCKAVNDLGTVEIECKLEVKVIAO
6958	274	1003	PRTSRVKTEGSQGSSAMDFSVKVDIEKEVTCPICLELLTEPLST.
		ı	DCGHSFCQACITAKIKESVIISRGESSCPVCOTRFOPGNIRDND
	•	1	HLANIVERVKEVKMSPQEGQKRDVCEHHGKKLOIFCKEDGKVTC
]	ŀ	WVCELSQEHQGHQTFRINEVVKECOEKLOVALORLIKENOEAEK
	1	[LEDDIRQERTAWKNYIQIBROKILKGFNEMRVILDNEEORELOK
	ľ	į.	LEEGEVNVLDNLAAATDOLVOORODASTLISDLORRLRGSSVEM (
		l	LODVIDVMKRSESWTLKKPKSVSKKLKSVFRVPDLSGMLQVLKE
1		İ	LTDVQYYWVDVMLNPGSATSNVAISVDQRQVKTVRTCTPKNSNP
{].	CDFSAFGVFGCQYFSSGKYYWEVDVSGKIAWILGVHSKISSLNK RKSSGFAFDPSVNYSKVYSRYRPQYGYWVIGLQNTCEYNAFEDS
		f :	SSSDPKVLTLFMAV\LPVVLGFS
6959	1	1469	SLVHVVEFGRGIEDFPYLFFQLTHCQQRICSVTQAGVQWCDHSS
			THE AUTHONOMICS AT AUCUMS

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
j	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Ì	amino acid	sequence	Codon, /=possible nucleotide deletion,
ł	sequence	Doguesie	\=possible nucleotide insertion)
		<u> </u>	LQPQTPGLNQSSHLSLLSSRDYRMLSSFNEWFWQDRFWLPPNVT
İ		•	WTELEDRDGRVYPHPQDLLAALPLALVLLAMRLAFERFIGLPLS
1			RWLGVRDQTRRQVKPNATLEKHFLTEGHRPKEPQLSLLAAQCGL
ĺ	!		TLQQTQRWFRRRRNQDRPQLTKKFCEASWRFLFYLSSFVGGLSV
İ			
ŀ		ľ	LYHESWLWAPVMCWDRYPNQLTLSCPAADSEA\SLYWWYLLELG FYLSLLIRLPFDVKRKGGGPSSIKPRPHYDPPSTA\DFKEQVIH
]		<u> </u>	HFVAVILMTFSYSANLLRIGSLVLLLHDSSDYLLRACKMVNYMO
1	1		YQQVCDALFLIFSFVFFYTRLVLFPTQILYTTYYESISNRGPFF
1		i	
ì	ł		GYYFFNGLLMLLQLLHVFWSCLILRMLYSFMKKGQMEKDIRSDV EESDSSEEAAAAQEPLQLKNGTAGGPRPAPTDGPRSRVAGRLTN
1]		RHTTAT
6960	387	2068	1 "
	707	2000	AKWAREKEMQEF\TRSFF\RGRPDLSTLTHSIVRRRYLAHSGRS
[[HLEPEEKQALKRLVEEEPLKMQVDEAASREDKLDLTKKGKRPPT PCSDPERKRFRPNSESESGSEASSPDYFGPPAKNGVASRSHTHP
			KEENPRRA\SKAVEBSSDEERQRDLPAQRGEESSEEEEKGYKGK
j	l .		TRKKPVVKKQAPGKASVSRKQAREESEBSEAEPVQRTAKKVEGN KGTKSLKESEQESEBEILAQKKEQREEEVEEEEKEEDEEKGDWK
Ì			PRTRSNGRRKSAREERSCKQKSQAKRLLGDSDSEEEQKEAASSG
l			DDSGRDREPPVQRKSEDRTQLKGGKRLSGSSEDEEDSGKGEPTA
İ			KGSRKMARLGSTSGEESDLEREVSDSEAGGGPQGERKNRSSKKS
}	!		SRKGRTRSSSSSDGSPEAKGGKAGSGRRGEDHPAVMRLKRYIR
			ACGAHRNYKKLLGSCCSHKERLSILRAELEALGMKGTPSLGKCR
			ALKEQREEAAEVASLDVANIISGSGRPRRRTAWNPLGEAAPPGB
Į.			LYRRTLDSDEERPRPAPPDWSHMRGIISSDGESN
6961	340	1646	RPWSSPTMKPNFSLRLRIFNLNCWGIPYLSKHRADRMRRLGDFL
	* • • • • • • • • • • • • • • • • • • •	1010	NQESFOLALLEEVWSEQDFQYLRQKLSPTYPAAHHFRSGIIGSG
			LCVFSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLLVLHL
			SGMVLNAYVTHLHAEYNRQKDIYLAHRVAQAWELAQFIHHTSKK
ĺ			ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEEG
	i i	•	NTMVPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFET
			TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGP\AERS
			PL/MCVCLKEALDGSLGLGMA\QARWWA\TFA\SYVIGLGL\LL
			LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG
			LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ
6962	340	1646	RPWSSPTMKPNFSLRLRIFNLNCWGIPYLSKHRADRMRRLGDFL
			NQESFDLALLEEVWSEQDFQYLRQKLSPTYPAAHHFRSGIGSG
			LCVFSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLLVLHL
			SGMVLNAYVTHLHAEYNRQKDIYLAHRVAQAWELAQFIHHTSKK
			ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEEG
		i	NTMVPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFET
			TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGP\AERS
			PL/MCVCLKEALDGSLGLGMA\QARWWA\TFA\SYVIGLGL\LL
			LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAPYLFHVQEVNG
			LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ
6963	374	2618	RVTPLILKLLKKPKTAENOKASEENEITOPGGSSAKPGLPCLNF
	-		EAVLSPDPALIHSTHSLTNSHAHTGSSDCDISCKGMTERIHSIN
			LHNFSNSVLETLNEQRNRGHFCDVTVRIHGSMLRAQRCVLAAGS
ľ			PFFQDKLLLGYSDIEIPSVVSVQSVQKLIDFMYSGVLRVSOSEA
			LQILTAASILQIKTVIDECTRIVSQNVGDVFPGIQDSQQDTPRG
	•		TPESGTSGQSSDTESGYLQSHPQHSVDRIYSALYACSMQNGSGE
	ļ		
1	ľ	ĺ	RSFYSGAVVSHHETALGLPRDHHMEDPSWITRIHERSQQMERYL STTPETTHCRKQPRPVRIQTLVGNIHIKQEMEDDYDYYGQQRVQ
		1	
		ĺ	ILERNESEECTEDTDQAEGTESEPKGESFDSGVSSSIGTEPDSV
J	ł	Ì	EQQFGPGAARDSQAEPTQPEQAAEAPAEGGPQTNQLETGASSPE
	j		RSNEVEMDSTVITVSNSSDKSVLQQPSVNTSIGQPLPSTQLYLR
			QTETLTSNLRMPLTLTSNTQVIGTAGNTYLPALFTTQPAGSGPK

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	nemistraine, reisoreucine, Kebysine,
Ì	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid		P=Proline, Q=Glutamine, R=Arginine,
}	residue of	residue of	S=Serine, T=Threonine, V=Valine,
		amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
1			PFLFSLPQPLAGQQTQFVTVSQPGLSTFTAQLPAPQPLASSAGH
]	STASGQGEKKPYECTLCNKTFTAKQNYVKHMFVHTGEKPHQCSI
ļ			CWRSFSLKDYLIK\HMVTHTGVRAYQCSICNKRFTQKSSLNVHM
l	1	[RLHRGEKSYBCYICKKKFSHKTLLERHVALHSASNGTPPAGTPP
	1		GARAGPPGVVACTEGTTYVCSVCPAKFDQIEQFNDHMRMHVSDG
6964	1	178	SGRPFFFFFSNTDVYFIKKVTNRWTAGSSYKMTRMKSIGKILLL
	1 -		QIFIG\NCSMFVLVI
6965	757	208	1
""	1 '3'	200	NVFIEPRIQGFMKTSAHPGQKHPDFSMGLLFPLLAALEVCSCGS
	1		SGSLGYNLPQNH\GLLGRNTLVLLGQMRRISPFLCLKDRSDFRF
1	į.		PQEKVEVSQLQKA\QAMSFLYDVLQQVFNFSHKALL\CCMEHDL
	İ		PGPTPHFTSSAAGTPGDLLGAGDGRRRSWGQWVIEGSTLALRRY
<u></u>			FQESISTLE
6966	820	1867	IITALGVRGMPGCPCPGCGMAGPRLLFLTALALELLGRAGGSQP
1	\		ALRSRGTATACRLDNKESESWGALLSGERLDTWICSLLGSLMVG
1	1		LSGVFPLLVIPLEMGTMLRSEAGAWRLKQLLSFALGGLLGNVFL
1	1		HLLPEAWAYTCSASPGGEGQSLQQQQQLGLWVIAGILTFLALEK
j			/HVPGQQGGDQPGPQQRPHCCCRRAQWRPLSGPAGCRARPRCR
		,	GP\DIKVSGYLNLLANTIDNFTHGLAVAASFLVSKKIGLLTTMA
			ILLHEIPHEVGDFAILLRAGFDRWSAAKLQLSTALGGLLGAGFA
i			ICTQSPKGVBETAAWVLPFTSGGFLYIALVNVLPDLLEEEDPW
6967	162	633	
""		033	GFLPFKYWILDLSASSRMETDCNPMELSSMSGFEEGSELNGFEG
1			TDMKDMRLEAEAVVNDVLFAVNNMFVSKSLRCADDVAYINVETK
1	ĺ		ERNRYCLELTEAGLKVVGYAFDQVDDHLQTPYHETVYSLLDTL\
6968			SPAYREAFGKR\LLQRLEALKRDGQS
6968	1	2265	RGGGGGGGGGARERERPGEPERTMEAAAGGRGCFQPHPGLQKT
			LEQFHLSSMSSLGGPAAFSARWAQEAYKKESAKEAGAAAVPAPV
]		PAATEPPPVLHLPAIQPPPPVLPGPFFMPSDRSTERCETVLEGE
1	į		TISCFVVGGEKRLCLPQILNSVLRDFSLQQINAVCDELHIYCSR
			CTADQLEILKVMGILPFSAPSCGLITKTDAERLCNALLYGGAYP
}			PPCKKELAASLALGLELSERSVRVYHE\CFGKCKGL\LVPELYS
1			SPSAACIQCLD\CRLMYPPHKFVVHSHKALENRTCHWGF\DSA\
			NWRAYILLSQDYTGKEEQARLGR\CLDDVKEKFDYGNKYKRRVP
f I			RVSSEPPASIRPKTDDTSSQSPAPSEKDKPSSWLRTLAGSSNKS
			LGCVHPRQRLSAFRPWSPAVSASBKELSPHLPALIRDSFYSYKS
			PETAVAPNVALAPPAQQKVVSSPPCAAAVSRAPEPLATCTQPRK
	İ		RKLTVDTPGAPETLAPVAAPEEDKDSEAEVEVESREEFTSSLSS
		•	
, 1			LSSPSFTSSSSAKDLGSPGARALPSAVPDAAAPADAPSGLEAEL
]]			EHLRQALEGGLDTKEAKEKFLHEVVKMRVKQEEKLSAALQAKRS
[LHQELEFLRVAKKEKLREATEAKRNLRKEIERLRAENEKKMKEA
1 1			NESRLRLKRELEQARQARVCDKGCEAGRLRAKYSAQIEDLQVKL
1 1	}		QHAEADREQLRADLLREREAREHLEK\VVK\ELQEQLWPRARPE
 			AAGSEG\AAELEP
6969	1855	118	AGTMHGRLKVKTSEEQAEAKRLEREQKLKLYQSATQAVFQKRQA
			GELDESVLELTSQILGANPDFATLWNCRREVLQQLETQKSPEEL
		İ	AALVKAELGFLESCLRVNPKSYGTWHHRCWLLGRLPEPNWTREL
, ,	ļ		ELCARFLEVDERNFHCWDYRRFVATQAAVPPAEELAFTDSLITR
, ,			NFSNYSSWHYRSCLLPQLHPQPDSGPQGRLPEDVLLKELELVON
	ſ		AFFTDPNDQSAWFYHRWLLGRADPQDALRCLHVSRDEACLTVSF
	•		SRPLLVGSRMEILLLMVDDSPLIVEWRTPDGRNRPSHVWLCDLP
	1		
	ļ		AASLNDQLPQHTFRVIWTAGDVQKECVLLKGRQEGWCRDSTTDE
	1		QLFRCELSVEKSTVLQSELESCKELQELEPENKWCL\LTIILLM
	İ		RALDPLLYEKETLQYFQTLK\AWDPKRATY\LDDLRSKFLLENS
			VLKMEYAEVRVLHLAHKDLTVLCHLEQLLLVTHLDLSHNRLRTL
ļ [ł		PPALAALRCLEDPPPRT\VLQASDNAIESLDGVTNLPRLQELLL
l l			CNNRLQQPAVLQPLASCPRLVLLNLQGNPLCQAVGILEQLAELL
			PSVSSVLT

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
ио:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ì	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine.
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ľ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ł	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	j -	\=possible nucleotide insertion)
6970	3	1528	SFPPLLSSPSAVGEGKVAVAAPCPGRSECARAKMAYIQLEPLNE
i			GFLSRISGLLLCRWTCRHCCQKCYESSCCQSSEDEVBILGPFPA
			QTPPWLMASRSSDKDGDSVHTASEVPLTPRTNSPDGRRSSSDTS
			KSTYSLTRRISSLESRRPSSPLIDIKPIEFGVLSAKKEPIOPSV
1			LRRTYNPDDYFRKFEPHLYSLDSNSDDVDSLTDEEILSKYQLGM
1			LHFSTQYDLLHNHLTVRVIEARDLPPPISHDGSRQDMAHSNPYV
1			KICLLPDQKNSKQTGVKRKTQKPVFEERYTFEIPFLEAQRRTLL
}			LTVVDFDKFSRHCVIGKVSVPLCEVDLVKGGHWWKALIPSSQNE
1			VELGELLLSLNYLPSAGRLNVDVIRAKQLLQTDVSQGSDPFVKI
ŀ			QLVHGLKLVKTKKTSFLRGTIDPFYNESFSFKVPQEELENASLV
}			FTVFGHNMKSSNDFIGRIVIG\QYSSGP\SEPNHWRRMLNTHRT
1			AVEQWHSLRSRAECDRVSPASLEVT
6971	37	3702	ACFYVPGSRSFKLIPRHGLVNMGRSGKLPSGVSAKLKRWKKGHS
			SDSNPAICRHRQAARSRFFSRPSGRSDLTVDAVKLHNELQSGSL
			RLGKSEAPETPMEEEAELVLTEKSSGTFLSGLSDCTNVTFSKVQ
	·		RFWESNSAAHKEICAVLAAVTEVIRSQGGKETETEYFAALIRKA
			AQHGVCSVLKGSEFMFEKAPAHHPAAISTAKFCIQEIEKSGGSK
İ			EATTTLHMLTLLKDLLPCFPEGLVKSCSETLLRVMTLSHVLVTA
ŀ			CAMQAFHSLFHARPGLSTLSAELNAQIITALYDYVPSENDLQPL
I			LAWLKVMEKAHINLVRLQWDLGLGHLPRFFGTAVTCLLSPHSQV
l .			LTAATQSLKEILKECVAPHMADIGSVTSSASGPAQSVAKMFRAV
1			EEGLTYKFHAAWSSVLQLLCVFFEACGRQAHPVMRKCLQSLCDL
1			RLSPHFPHTAALDQAVGAAVTSMGPEVVLQAVPLEIDGSEETLD
			FPRSWLLPVIRDHVQETRLGFFTTYFLPLANTLKSKAMDLAQAG
			STVESKIYDTLQWQMWTLLPGFCTRPTDVAISFKGLARTLGMAI
			SERFDLRVTVCQALRTLITKGCQAEADRAEVSRFAKNFLPILFN
1			LYGQPVAAGDTPAPRRAVLETIRTYLTITDTQLVNSLLEKASEK
1			VLDPASSDFTRLSVLDLVVALAPCADEAAISKLYSTIRPYLESK
1			AHGVQKKAYRVLEEVCASPQGPGALFVQSHLEDLKKTLLDSLRS
i i			TSSPAKRPRLKCLLHIVRKLSAEHKEFITALIPEVILCTKEVSV
i i			GARKNAFALLVEMGHAFLRFGSNQEEALQCYLVLIYPGLVGAVT
}			MVSCSILALTHLLFEFKGLMGTSTVEQLLENVCLLLASRTRDVV
1			KSALGFIKVAVTVMDVAHLAKHVQLVMEAIGKLSDDMRRHFRMK
	[LRNLFT\KFIPK\FGILTWGKKAVGPKEYHRVLVNIRKAEARAK
			RHRALSQAAVEEEEEEEEEEPAQGKGDSIEEILADSEDEEDNE
			EEERSRGKEQRKLARQRSRAWLKEGGGDEPLNFLDPKVAQRVLA
]	J		TOPGPGRGRKKDHSFKVSADGRLIIREEADGNKMEEEEGAKGED
	Ì		EEMADPMEDVIIRNKKHQKLKHQKEAEEEELEIPPQYQAGGSGI
			HRPVAKKAMPGAEYKAKKAKGDVKKKGRPDPYAYIPLNRSKLNR
6972	2179	973	RKKMKLQGQFKGLVKAAQRGSQVGHKNRRKDRRP
~~/~	41.3	7/3	PGGAILLPLWRRTRPREATVPRGAAQRGRARSAEGRIPSSQSPS
	[PAEAGGATRSPPPRPPRPPRPARPPGPSAPPLLRSDAGPGATVSAAA
			AAATERARRGATMGAQLSTLGHMVLFPVWFLYSLLMKLFQRSTP
1	ľ		AITLESPDIKYPLRLIDREIISHDTRRFRFALPSPQHILGLPVG
			QHIYLSARIDGNLVVRPYTPISSDDDKGFVDLVIKVYFKDTHPK
			FPAGGKMSQYLESMQIGDTIEFRGPSGLLVYQGKGKFAIRPDKK
		ł	SNPIIRTVKSVGMIAGGTGITPMLQVIRAIMKDPDDHTVCHLLF
] [ĺ	I	ANOTEKDILLRPELEELRNKHSARFKLWYTLDRAPEAWDYGQG\
	Į.	ļ	FVNBEMIRDHLPPPE\EEPLVLMCGPPPMIQYACLPNL\DHVGH
6973	1		PTERCFVF
ا "" ا	-	1964	LQPRCAHRGLRAQKCGRPAPGVDAMVLCPVIGKLLHKRVVLASA
	ĺ	ľ	SPRRQEILSNAGLRFEVVPSKFKEKLDKASFATPYGYAMETAKQ
			KALEVANRLYQKDLRAPDVVIGADTIVTVGGLILEKPVDKQDAY
			RMLSRFE/SGREHSVFTGVAIVHCSSKDHQLDTRVSEFYEETKV
			KFSELSEELLWEYVHSGEPMDKAGGYGIQALGGMLVESVHGDFL
			NVVGFPLNHFCKQLVKLYYPPRPEDLRRSVKHDSIPAADTFEDL

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A-Alanine, C-Cysteine, D-Aspartic Acid, E Glutamic Acid, F-Phenylalanine, G-Glycine,
1	location	corresponding	H-Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine.
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine.
1	residue of amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, +=Stop
ł	sequence	sequence	Codon, /=possible nucleotide deletion,
-	00400000	 	\=possible nucleotide insertion)
			SDVEGGSEPTORDAGSRDEKAEAGEAGOATAEAECHRTRETLP PFPTRLLELIEGFMLSKGLLTACKLKVFDLLKDEAPOKAADIAS
1		1	KVDASACGMERLLDICAAMGLLEKTEQGYSNTETANVYLASDGE
1			YSLHGFIMHNNDLTWNLFTYLEFAIREGTNQHHRALGKKAEDLF
f	1		QDAYYQSPETRLRFMRAMHGMTKLTACQVATAFNLSRFSSACDV
I			GGCTGALARELAREYPRMQVTVFDLPDIIELAAHFOPPGPOAVO
1			IHFAAGDFFRDPLPSAELYVLCRILHDWPDDKVHKLLSRVAESC
1	1	1	KPGAGLLLVETLLDEEKRVAORALMOSLNMLVOTEGKERSLGRY
6974	3082		QCLLELHGFHQVQVVHLGGVLDAIL\PPKWPPEAOAACSL
03/4	3002	2172	RSCAAFASFASRPPLELFAPPGSHRSPPGRGVATSAQCALSVRK
			LLAARPGLGTKYQATMVYKTLFALCILTAGWRVQSLPTSAPLSV
			SLPTNIVPPTTIWTSSPONTDADTASPSNGTHNNSVLPVTASAP
	ļ		TSLLPKNISIESREEEITSPGSNWEGTNTDPSPSGFSSTSGGVH LTTTLEEHSLGTPEAGVAATLSQSAAEPPTLISPQAPASSPSSL
1		f	STSPPEVFSASVTTNHSSTVTSTQPTGAPTAPESPTEESSSDHT
			PTSHATAEPVPQEKTPPTTVSGKVMCELIDMET\PPPFPG
6975	2	500	RPRPTVHCCKWALKLETAMETLINVFHAHSGKEGDKYKLSKKEY.
1			KELLQTELSGFLDVKELML*ATEALKTFEEA*KSPIJOCSSSRS
			SLPPAPQPPPYL*LSAVPFPIHLPLPLLPPOAOKDVDAVDKVMK
6976	1216	970	BLDENGDGEVDFQEYVVLVAALTVACNNFFWENS
"""	1210	370	GCQL*VAYGTTENSPVTFAHPPEDTVEQKAESVGRIMPHTEARI
			MNMEAGTLAKLNTPGELCIRGYCVMLGYWGEPQKTERAVDQDKW
1	ŀ		YWTGDVATMNEQGFCKIVGRSKDMIIRGGENIYPAELEDFFHTH PKVQEVQVVGVKDDRMGEEICACIRLKDGBETTVEEIKAFCKGK
1			ISHFKIPKYIVFVTNYPLTISGKIQKFKLREQMERHLNL*IKQQ
			ACPGRLA
6977	1298	588	SLFINTNLLSNQIRKTSFGMCSEPISDNTEDQKGKLKTPDFA*R
			ANKKSKHHVNGNRTVEPFPEGTQMAVFGMGCFWGAERKFWVLKG
(VYSTQVGFAGGYTSNPTYKEVCSEKTGHAEVVRVVYOPEHMSFR
			ELLKVFWENHDPTQGMRQGNDHGTQYRSAIYPTSAKQMEAALSS
1			KENYQKVLSEHGFGPITTDIREGQTFYYAEDYHQQYLSKNPNGY CGLGGTGVSCPVGIKK
6978	3	242	SPPFRDSRRCGCCKGSSLRHTAVAMVKLSKEAKQRLQQLFKGSQ
L	,		FAIRWGFIPLVIYLGFKRGADPGMPEPTVLSLLWG
6979	3917	1146	DEARVRGEAVAAAILSRCRHWSGPPPFPPSPPDRKGLRGTEPWE
ļ			AGPGSGATPGARAMDVRRLKVNELREELORRGLDTRGI,KTELAE
1			RLQAALEAEEPDDERELDADDEPGRPGHINEEVETEGGSELEGT
			AQPPPPGLQPHAEPGGYSGPDGHYAMDNITRONOFYDTOVIKOE
			NESGYERRPLEMEQQQAYRPEMKTEMKQGAPTSFLPPEASQLKP
))]		DRQQFQSRKRPYEENRGRGYFEHREDRRGRSPQPPAEEDEDDFD
			DTLVAIDTYNCDLHFKVARDRSSGYPLTIEGFAYLWSGARASYG VRRGRVCFEMKINEEISVKHLPSTEPDPHVVRIGWSLDSCSTQL
]]			GEEPFSYGYGGTGKKSTNSRFENYGDKFAENDVIGCFADFECGN
1 1	1		DVELSFTKNGKWMGIAFRIQKEALGGQALYPHVLVKNCAVEFNF
			GQRAEPYCSVLPGFTFIQHLPLSERIRGTVGPKSKAECRILMMV
	}	j	GLPAAGKTTWAIKHAASNPSKKYNILGTNAIMDKMRVMGLRROR
l i	ľ		NYAGRWDVLIQQATQCLNRLIQIAARKKRNYILDOTNVYGSAOR
	ļ		RKMRPFEGFQRKAIVICPTDEDLKDRTIKRTDEEGKDVPDHAVI.
			EMKANFTLPDVGDFLDEVLFIELQREEADKLVRQYNEEGRKAGP
		ļ	PPEKRFDNRGGGGFRGRGGGGGGFQRYENRGPPGGNRGGFQNRGG
			GSGGGGNYRGGFNRSGGGYSQNRWGNNNRDNNNSNNRGSYNRA
			PQQQPPPQQPPPPQPPPQQPPPPPSYSPARNPPGASTYNKNSNI PGSSANTSTPTVSSYSPPQSFGFFPSTFQPSYSQPPYNQGGYSQ
			GYTAPPPPPPPPPAYNYGSYGGYNPAPYTPPPPPTAGTYPQPSY
2065			NQYQQYAQQWNQYYQNQGQWPPYYGNYDYGSYSGNTOGGTSTO
6980	1	420	GTRGRKTGRVAAPSTRRRTGNMQKLQTRSPAMSLSDPGLGYHPT

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
aı	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ł	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ĺ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
l	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
l	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ſ	amino acid	sequence	Codon, /=possible nucleotide deletion
	sequence		\=possible nucleotide insertion)
			CWTLRWPPLCSLHALHVFHCLFSSRLGTPVSPRLAMDPNCSCEA
1		ĺ	GGSCACAGSCKCKKCKCTSCKKSCCSCCPLGCAKCAQGCICKGA
			SEKCSCCA
6981	10	1054	PGRGFRRASLRPAFAARGVFQGGLGQAKQARTRACAALPTPHPS
i			APRLLEPQGVFSLFPPPPGPWPNMILTKAOYDEIAOCLVSVPPT
1	1		ROSLRKLKORFPSQSQATLLSIFSOEYOKHIKRTHAKHHTSKAT
1			ESYYQRYLNGVVKNGAAPVLLDLANEVDYAPSIMARIJILERET.O
1			EHEETPPSKSIINSMLRDPSQIPDGVLANQVYOCIVNDCCYGPI.
l			VDCIKHAIGHEHEVLLRDLLLEKNLSFLDEDOLRAKGYDKTPDF
Į.			ILQVPVAVEGHIIHWIESKASFGDECSHHAYLHDQFWSYWNRFG
6982	153	1000	PGLVIYWYGFIQELDCNRERGILLKACFPTNIVTLCHSIA
1 3302	133	1285	FPQQDCSAPAAPGLAGSEPRRLRAYRRRRQRARGLKRVAWLAPP
1			PSLLQGLQGWAQAPVDGTLGPEDSRASSPMIQNSRPSLLQPQDV
1			GDTVETLMLHPVIKAFLCGSISGTCSTLLFQPLDLLKTRLQTLQ
1	į i		PSDHGSRRVGMLAVLLKVVRTESLLGLWKGMSPSIVRCVPGVGI
}	1	 -	YFGTLYSLKQYFLRGHPPTALESVMLGVGSRSVAGVCMSPITVI
1	l i		KTRYESGKYGYESIYAALRSIYHSEGHRGLFSGLTATLLRDAFF
1]		SGIYLMPYNQTKNIVPHDQVDATLIPITNFSCGIPAGILASLVT QPADVIKTHMQLYPLKFQWIGQAVTLIPKDYGLRGFFQGGIPRA
j		•	LRRTLMAAMAWTVYEEMMAKMGLKS
6983	82	773	EMSFLQDPSFFTMGMWSIGAGALGAAALALLLANTDVFLSKPQK
1 1	}		AALEYLEDIDLKTLEKEPRTFKAKELWEKNGAVIMAVRRPGCFL
	Ì		CREEAADLSSLKSMLDQLGVPLYAVVKEHIRTEVKDFQPYFKGE
			IFLDEKKKFYGPQRRKMMFMGFIRLGVWYNFFRAWNGGFSGNLE
1 1			GEGFILGGVFVVGSGKQGILLEHREKEFGDKVNLLSVLEAAKMI
			KPQTLASEKK
6984	1845	1282	GGRSAYSLPAGSLPRVPATAAAKMASGVQVADEVCRIFYDMKVR
1 1			KCSTPEEIKKRKKAVIFCLSADKKCIIVEEGKEILVGDVGVTIT
			DPFKHFVGMLPEKDCRYALYDASFETKESRKEELMFFLWADELA
1			PLKSKMIYASSKDAIKKKFQGIKHECQANGPEDLNRACIAEKLG
6985	1887		GSLIVAFEGCPV
1 0,03	100/	1324	RRTAGIYPCFPKPGRTRHALCSVVLLLLTGQLAFDDFQESCAMM
l I			WQKYAGSRRSMPLGARILFHGVFYAGGFAIVYYLIQKPHSRALY
1 1			YKLAVEQLQSHPEAQEALGPPLNIHYLKLIDRENFVDIVDAKLK
1 1			IPVSGSKSEGLLYVHSSRGGPFQRWHLDEVFLELKDGQQIPVFK
6986	642	1350	LSGENGDEVKKE
		,,,,,	YHLYFKMGDPNSRKKQALNRLRAQLRKKKESLADQFDFKMYIAF VFKEKKKKSALFEVSEVIPVMTNNYEENILKGVRDSSYSLESSL
1 1		ļ	ELLQKDVVQLHAPRYQSMRRDVIGCTQEMDFILWPRNDIEKIVC
i !			LLFSRWKESDEPFRPVQAKFEFHHGDYEKQFLHVLSRKDKTGIV
1 1			VNNPNQSVFLFIDRQHLQTPKNKATIPKLCSICLYLPQEQLTHW
1			AVGTIEDHLRPYMPE
6987	1623	341	LEAAEKASRAFKESQRQTDSKNYETENWSPQKSQRRYDMYNTAC
] }	į		FLGEIEVGLYTIQILQLTPFFHKENELSKKHMVOFLSGKWTIPP
	ļ	ł	DPRNECYLALSKFTSHLKNLQSDLKRCFDFFIDYMVLLKMRYTO
			KEIABIMLSKKVSRCFRKYTELFCHLDPCLLOSKESOLLORENC
		1	RKKLEALRADRFAGLLEYLNPNYKDATTMESIVNEYAFLLOOMS
	1	ł	KKPMTNEKQNSILANIILSCLKPNSKLIOPLTTLKKOLREVLOF
			VGLSHQYPGPYFLACLLFWPENQELDODSKLIEKYVSSI,NRSFP
		}	GQYKRMCRSKQASTLFYLGKRKGLNSIVHKAKIEOYFDKAONTN
1	ł		SLWHSGDVWKKNEVKDLLRRLTGQAEGKLISVEYGTEEKIKIPV
6988			ISVYSGPLRSGRNIERVSFYLGFSIEGPPGL
0700	3	689	TQLLRRPAVFVGSAASGIRSGLWSASSGHWCAPAAGRAHAPVPR
			LVRGLGAASTAAPQDAQTGPQPMPRADCIMRHLPYFCRGOVVRG
	ļ	- 1	FGRGSKQLGIPTANFPEQVVDNLPADISTGIYYGWASVGSGDVH
			KMVVSIGWNPYYKNTKKSMETHIMHTFKEDFYGEILNVAIVGYL

Designing Continue	SEO	Predicted	Predicted end	
NO: nucleotide location corresponding to first amino acid residue of residue of amino acid sequence se				Amino acid segment containing signal peptide
Corresponding to first anino acid amino acid amino acid amino acid residue of amino acid anino acid anino acid anino acid anino acid anino acid anino acid acquence acid sequence acid s	NO:			Glutamic Acid E-Dhomalalania Columnia
corresponding to first amino acid residue of residue of residue of samino acid residue of samino acid sequence	1			Halistidian Tables in the Halistidian Tables in the Halistidian Tables in the Halistidian Tables in the Halistidian in the Hali
to first amino acid am	l l			Indicate, introduction, Kabysine,
residue of amino acid sequence shows a sequence equence shows a sequenc				Paperoline O-Glutanine Nasparagine,
maino acid aequence maino aci	Î	amino acid	1	Susarine Turnonine W. Walling,
amino acid sequence Codon, 'Apposible nucleotide deletion, 'Apposible nucleotide deletion, 'Apposible nucleotide deletion, 'Apposible nucleotide deletion, 'Apposible nucleotide deletion,' RPERNFDSIBELISTAGDETERKEREEPHENIKERDNFFQVS SSKIMMSH IRPERNFDSIBELISTAGDETERKERKEREEPHENIKERDNFFQVS SSKIMMSH ALVOVIEDKKERGENDENTTVVGVGAVGMACASILMKOLDAGE, 'ASKIMSKIL 'AUGULIVALKERGTPGNRITTVGVGAVGMACASILMKOLDAGE, 'AUGULIVALKERGTPGNRITTVGVGAVGMACASILMKOLDAGE, 'AUGULIVALKERGTPGNRITTVGAVGAVGMACASILMKOLDAGE, 'AUGULIVALKERGTPGNRITTVGAVGAVGMACASILMKOLDAGE, 'AUGULIVALKERGTPGNRITTGAGCAGESCHISTARGENGTVAGGENGSVATAGGENGGENGGENGGENGGENGGENGGENGGENGGENGGE				Waltendam Valuedia Value
Appossible nucleotide insertion	1	amino acid		Codon /prossible musl-seld- all wi
RPENSTPBLESLISATIOGDIERAKKRIELEPELKIKEDNFFQVS KKKMMOH LMFSDRPLSSPTHASAGSHCHAPPTTARRAPTIPGSKSMALDEL LOULYNLIKERGYTOPINKTYVUGGVAUGHACAISILMKDLADEL ALVOVIEDULKGSMMDLJOHSSLFLATRIVSGSCONVTANSIGMV LITAGARQGEGESRINLVRANNIFRFITENVKYNSPNCKLILD SNPVDILTYVAKKIGGFPNRWIGGSCULDSARFSLIMGERLGV HPLSCHGWVLGEHGDSSVYWAGGWNVAGVSLKTLHPDLGTDKELGV HPLSCHGWVLGEHGDSSVYWAGGWNVAGVSLKTLHPDLGTDKELGV HPLSCHGWVLGEHGDSSVYWAGGWNVAGVSLKTLHPDLGTDKELGV HPLSCHGWVLGEHGDSSVYWAGGWNVAGVSLKTLHPDLGTDKELGV HPLSCHGWVLGEHGDSSVYWAGGWNVAGVSLKTLHPDLGTDKELGV HPLSCHGWVLGEHGDSSVYWAGGWNVAGVSLKTLHPDLGTDKELGV HPLSCHGWVLGEHGDSSVYWAGGWNVAGVSLKTLHPDLGTDKELGV HPLSCHGWVLGEHGDSSVYWAGGWNVAGVSLKTLHPDLGTDKELGS KNEMENHSOPTISH (SELVE I VERNEWLE I		sequence		\mpossible nucleotide deletion,
SSKIMSH SSKIMSH				RPEKNEDGLEGITGATOCDIRPAYED TV PROVINCE
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EOMEVHKOVVESAYEVIKLKGYTSWAIGLSVADLAESIMKNIK RWHDVSTIK KGLYGI KOUPLSVPCTLGONGI SDLVKVTLTSEE BARLKKSADTLMGI QKELOP THASGMASVULDERTEAVISLEFTPATALAVRYASKKSGSS NLAGKSSGRRQGI KKMEGHYVHAGNI LATGRIFRHHPGAHVGV GKNKCLYALESGI VRITKEVYVPPRNTEAVDLITRLPKGAVLY KTFYHVVPAKPEGTFIKLVAML 6991 169 451 RESSDFHNFGFLSRFVSLREN HHGVICSTKNKRRNFKKAYLL CGRHVH 6992 944 510 ROADGCSLALRGURGVYGGLVRAPGVQTRFLSSRFVBRRGALY RSPMONDRP PPY PROGPTAPYPPY PP QWRGPGMGGPYPPPGGY PYGSTPQISTQUGNGGGPGPPKTTVTVVEDQRRDELGFSTCLTACUT ALCCCLUMULT 6993 1 374 GWCVTCFOGNARGGPAYPPGI QAYGAAPFEDLQVFTMSKCRG DWVELKMINVASLCPLWKOPOTVULSPPTAVKUEGI PAMIHHSH VKPAARETWEARPSPONFFRTTLKKTTSPAPVTPGS RDFAPPGQOKREAPVDVLTQIGRSVRGTLDAMI GDETMHLVSS SSQULMAISSAISVAFFALSGI ARQLLMALGLLAGILAGISK RDFAPPGQOKREAPVDVLTQIGRSVRGTLDAMI GDETMHLVSS SSQULMAISSAISVAFFALSGI ARQLLMALGLLAGILAGIKLUF LAGFVALMRSVPDPSTRALLLLALLILLALLILALLAGIKAGK RDFAPPGQOKREAPVDVLTQIGRSVRGTLDAMI GDETMHLVSS SSQULMAISSAISVAFFALSGI ARQLLMALGLAGILAGIKLUF LAGFVALMRSVPDPSTRALLLLALLILLALLILALLAGIKAGK RDFAPPGQOKREAPVDVLTQIGRSVRGTLDAMI GDETMHLVSS SSQULMAISSAISVAFFALSGI ARQLLMALGLAGILAGIKLUF LAGFVALMRSVPDPSTRALLLLALLILLALLICALLAGIKAGKKUTF LAGFYALMRSVPDPSTRALLLLALLILLALLICALLAGIKAGKKUTF LAGFYALMRSVPDPSTRALLLLALLILLALLICALLAGIKAGKKUTF LAGFYALMRSVPDPSTRALLLLALLILLILLILLITALLISLIGGSRAGGAL EBRAVKGLEROVELIRRGSSIGGGSTIRRAVLEDFYTHAGEVG IWAQL BHBAGTOLHRQTGLLLLAMKENOGLIKTIQANLSRGRVEHQCLGS EELKQFFFITHLPRGSVIGGSTIRRAVLEDFYTHAGEVGTUAQL BHBAGTOLHRQTGLLLLAMKENOGLIKTIQANLSRGRVEHQCLGS GUVRDGKVVEINPGLLVYKTSTRSVQARTHTGECYDTALLICH HIYGLPTGEYPGIMKVSYHRIGNADPERGYTATDIGGVQL SSSVRDHLPDLKPERAVIESCMYTHTDEGFTLDRHPKVNILU GAGPSGHGPKTLAPVVGKLIVSTSKYLARDENDLLCH HIYGLPTGEYPGIMKVSYHRIGNADPERGYTATDIGGPUTL SSRVRDHLPDLKPERAVIESCMYTHTDEGFTLDRHPKVNILU GAGPSGHGPKLAPVVGKLIVSTSKYLARDENDLLCH HIYGLPTGEVFTLAVTKALTHTDYGRTS IMPFRYNTPLOC DELERSFYSTYVYCANKERFFFLDPLETKRKKKSEQELKDEE MDLFTKYYSEMKGGRKNTNEFYKT PRYTCPNKKKKSEQELKDEE MDLFTKYYSEMKGGRKNTNEFYKT PRYTCPNKKKKSEQELKDEE EELRYGTATATTUVPLDRVGPCLTYDGEMYTKTUTDLOCHAGNICK REPRALQYNTATHTUVPLDRVGPCCLTYDGEMYTKTUTLDL LEERBELSYGTATHTUVPLDRVG	1	1		HPLSCHGWVLGEHGDSSVPVWSGMNVAGVSLKTLHPDLGTDVDV
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6990 719 258 THASGMASVULLIBETRYTAVISLISPTPATALAVRYASKKSGGSS KNLGKSGGROCIKKWECHYVHAGNI I ATQRHFRWHPGAHVOV GUNKCLYALEGGI VRYTKEVYVPHERNTEAVOLITRID KGAVLY KTFVHVVPAKPEGIT KLVAML 6991 169 451 RESSDFHNIGGI KEWECHYVHERNTEAVOLITRID KGAVLY KTFVHVVPAKPEGIT KLVAML 510 RESSDFHNIGGI KEWECHYVYCGI VRAFTULOGETLITACVEGTGCLF CGRIVH 6992 944 510 ROAPGGSSLALRQVYVGGLVRAPQVQTRPLSSRFVERRGALY RSPHNGENP PYPOGPOTAPYP PYP OGMAPGPMGGPYPPPCGY PYGGYPQYGWGGGPQEP PKTTYVVVEDORRDELGFSTCLTACWT ALCCCLUMMLT 6993 1 374 OWCOTCPGINARGOPAVPPGI QAVGAAPPEDLQVDFTEMSKCRG DRVBI KINNAVASLCPLUKKGPQTVVLSP PTAVKVEGI PAWIHHHH VKPAARETWEARPSPDNP PRVILKKTTSPAPVTDGS GRVBI KINNAVASLCPLUKGPQTVVLSP PTAVKVEGI PAWIHHHH VKPAARETWEARPSPDNP PRVILKKTTSPAPVTDGS SSQVLMAISSAI SVAFFALSGI RAQLLINALGLAGDYLAGGLKLS PGOVOTFILMGCAGLAVVALLISLILIGULALDHALAGGR RDFAPPGQOKERAP LUVTYOTIGSRSVETABHIGHLKUVIF LAGVALMRSVVEDPSTRALLLIALLI LIYALLISRITGSRASGQOL EAKVRGLERQVEELRRRQRAAKGARSVEEB GSVAVISGI INAAQKOLMDATVI GAG GGGFTAYHLAKHRKRIL LLEQFFLPHSRGSSHOGSRI TRKAYLEDFYTRMHECYQI WAQL EBBATGUIRGTGLILLIGUKKENDELKTI TAGPHTNQLL REPLGI EMPLOTILRI RICKWERWIPGS GYOSQAFPCTIMLICH HIYGLIPTCEYPGLMKVSYHHONHADPEEBCCTARTDI GOVQIL SSFVXDHI-POLKPEPAV VERSCHMINTSFYKTI PRYTYELPABERVLIQHH HIYGLIPTCEYPGLMKVSYHHONHADPEEBCCTARTDI GOVQIL SSFVXDHI-POLKPEPAV VERSCHMINTSFYKTI PRYTYELPABERVLIQHE MDLFTKYYSEWKGRRNTNEFYKTI PRYTYELPABERVLIQHE HIYGLIPTCEYPGLMKVSYHHONHADPEEBCCTARTDI GOVQIL SSFVXDHI-POLKPEPAV VERSCHMINTSFYKTI PRYTYELPABERVLIQHE MDLFTKYYSEWKGRRNTNTSFYKTI PRYTYELPABERVLIQHE MDLFTKYYSEWKGRRNTNTSFYKTI PRYTYELPABERVLIQHE MDLFTKYYSEWKGRRNTNTSFYKTI PRYTYELPABERVLIQHE MDLFTKYYSEWKGRRNTNTSFYKTI PRYTYELPABERVLIQHE MDLFTKYYSEWKGRRNTNTSFYKTI PRYTYELPABERVLIQHE MDLFTKYYSEWKGRRNTNTSFYKTI PRYTYELPABERVLIQHE MDLFTKYYSEWKGRRNTNTSFYKTI PRYTYELPABERVLIQH VRRWULHQTTI GLSLYDVAGQCYLRESDLENYLLELIFTLDQL LLELERDELSKESGGTTMFSPABLRVYGQVLLNIDCHINGHNGHLSK EELSRAVTI-QRAKKRELIFSHVOROCHLITAGKKYLDDHINGHNGMIS. EELSRAVTI-QRAKKRELIFSHOLDENDYKTYLDPTULLEN REPAALQYI FKLLDIERNKYLLPFPLYLLINFIGLWSH TVLDPTULALEN REPAALQYI FKLLDIERNKADLOUT AREFERDELDEN TVLI	1	1		RVHPVSTMIKGLYGIKDDVFLSVPCILGONGISDLVKVTLTGFF
THASGMASVULLERTRAVISLISETPATALAGYRASKEGGSS KNLGKSGERGCIKKEGHYVHAGNIIATORHFRWHPGHHVOV GKNKCLYALEGIVRYTKEVYVPHERTRAVDLITRLEKGAVLY KTFYHVVPAKPEGITKLVAML KTSPHVVPAKPEGITKLVAML KRSSDFINDGILSREVSLERNIHHQVICSTKNKERENPKKTAYLL SSLLMTNLHPNESTENQPUDAYWAFTLDQEFLTYACVEGTGCLF CGRRVH G992				EARLKKSADTLWGIOKELOF
RNLAGKSSGRRQIKKMEGHYVHAGNIIATGRHFRMHPGAHVOV GNNKCIVALEEGIVKYTKEVYVPHTRAVDLITRLPKGAVIY KTFVHVVPARPEGTFKLVAML RRSSDFHNPGFLSRFVSLRENIHHQVICSTKMKRRNPKKIAYLL SSLLMTNLAPNESTENQPVDAYMAFTLOQESILTVACVEGTGCLF GGRVH 8992 944 510 RQAPGCSSLALRQVRQVYCGLVRAPQVQTRPLSGRFVERRGALY RSPMNQENPPPYPGPGPTAPYPPYPPPQPMGPPMGGPYPPPGGY PYQGYPQYGMQGGPQPPKTTVTVVEDQRRELGFSTCLTACMT ALCCCCLMMMLT ALCCCLMMMLT 4 00CVTCPQENARQGPAVPPGIQAYGAAPFEDLQVDFTEMSKCRG DRVNIKMWASLCPLWKGPOTVULSPPTAVLVEGIPAWIHHSH VKPAARETMEARPSDDNFFRVTLKKTTSPAPVTPGS 00PKENDFVMAASSISSPWGKHVFKATLWULVALLLGHLAGSR RDPAPPGQCKREAPVDVLTQIGRSVWGTLDAWIGPETMHLVSES SSQVLMAISSAISVAFFALSGLAQLLANLGLAGDYLAGGELKIS PGOVQTFLWGGAGLAVVWHLISLIQUALLGELWIGLKLVIF LAGFVALMRSVPDPSTRALLLALLILVALLGRVALGGLKIS PGOVQTFLWGGAGLAVVWHLISLIQUALLGELWIGLKLVIF LAGFVALMRSVPDPSTRALLLLALLILVALLGRVALGGLKIS PGOVQTFLWGGAGLAVVWHLISLICAUALLGERUKLVIF LAGFVALMRSVPDPSTRALLLLALLILVALLGRVALGGLKIS PGOVQTFLWGGAGLAVVWHLISLICAUALLGERUKLVIF LAGFVALMRSVPDPSTRALLLLALLILVALLGRVALGGLKIS PGOVQTFLWGGAGLAVVWHLISLICAUALLGRILGKLKUIF LAGFVALMRSVPDPSTRALLLLALLILVALLGRVALGGLKIS PGOVQTFLWGGAGLAVVWHLISLICATONLSRGRVEHQCLGLS EELKQRFPNILPGGVGLLDNSGGVIVAYKALRALQDAIRQLG GIVNDESKVPSINPGRVFCANGAKGARSVENGTONLFRGRILAGH REBAGTQHHTQTGLLILGHKENDELTONNESSTVANGLUTAGPWTNQLL RPLGIEMPLQTHRINVCYWRENVPSSTVSQAFPCFLWGLCPH HIYGLPTGEYPGLMKWSYHHGHADPEERDCPTARTDIGDVQIL SSFVRDHHPDLKEPBAVISCNYTHTDEPFTLUTGLCPH HIYGLPTGEYPGLMKWSYHHGHADPEERDCPTARTDIGDVQIL SSFVRDHHPDLKEPBAVISCNYTHDEPGPTLILDRFKKNDLUTGEAMIN YENFLKVGEKAGAKCKOFFTAAVFAKLHTDSYGRSIMQFPNY WRKWMLHQTRIGLSNELDNELQLMPLDLHCRGEMANT YENFLKVGEKAGAKCKOFFTAAVFAKLHTDSYGRSIMQFPNY WRKWMLHQTRIGLSNELDNELQLMPLLARGEDLKYHILDRIPTHLAGSPLING EESRAVPLQRKSRELLDNELQLMPLERDMYTLLDRGEMMIN TENFLKVGEKAGAKCKOFFTAAVFAKLLHTDSYGRSIMGFNY WRKWMLHQTRIGLSHKYOPLALEM REPAALQYIFKLDDLENGKINVPSLMYPFRAIQELMKIHGQD PUSPQDWAEIFDMVKKOPLLIEUGTTAAMPKF PLAGGETTAAMPKSCHAUPSLAUDFSLMWFGGTVATTILIDL NGFWYENRAUVANDSENSADLDDT 1104 RMETTFTILBLATYLTTPILVLINFLGLMSWICKKWFPFFLVRF TVTYNEGGMASKREBLESKLOEPGGGTGAAMPKF	6990	719	258	THASGMASVVLALRTRTAVTSLLSPTPATALAVRYASKKSGGSS
GKNKCLYALEGIVRYTKEVYVPHPRNTEAVDLITRLPKGAVLY KTFVHVVPAKPGSTEKLVAML SSLMTNIHPNGFLSRFVSLRENIHHQVICSTKNKKRNPKKTAYLL SSLMTNIHPNGFLSRFVSLRENIHHQVICSTKNKKRNPKKTAYLL GS92 944 510 RQAPGCSSLALRQVRQVYCGLVRAPQVQTRPLSGRFVSRGALY RSPHNQENPPP PQBGPTAPYPPYPPQPMGGPMGGPYPPGGY PYQGYPQYGWQGGPQEPPKTTVYVVEDQRREDLGPSTCLTACAT ALCCCLMDMLT OWCTTCPQENNANGGPAVPPGIQAYGAAPFEDLQVDFTEMSKCRG DRVWIKNMXVASLCPLWKGPQTVVLSPPTAVKVEGIPAWIHHSH VKPARPARTWEAPPSPDNPFRVTLKKTTSPAPVTPGS 6993 1 374 QWCTTCPQENNANGGPAVPPGIQAYGAAPFEDLQVDFTEMSKCRG DRVWIKNMXVASLCPLWKGPQTVVLSPPTAVKVEGIPAWIHHSH VKPARPARTWEAPPSPDNPFRVTLKKTTSPAPVTPGS RDFAPPGQQKREAPVDVLTQIGRSVRGTIDAMIGPETHHLVSES SSQVLMAISSAISVAFFALSGIAAQLANAGLANDALGAGKLVJES PGQVQTFLLWGAGALVVYWLLSLLLGLVLALLGRILWGLKLVIF LAGFVALMRSVPDPSTRALLLLALLILLALLTRLWGLKLVIF LAGFVALMRSVPDPSTRALLLLALLILLALLTRLWGLKLVIF LAGFVALMRSVPDPSTRALLLLALLILLALLTRLAGRRAGAQL EAKVRGLERQVELKMRQRRAAKGARSVEEE GSVAVGLGGIMAAGKDLWDATVIGAGIGGCTTAHLAKHRKRIL LLEQFPLPHRSGASSHGANGGRAIKRAVLEDFYTRMHECYQIWAQL BHBAGTOLHRQTGLLLLGMKENQEIKTTQANLSRGVBEHQCLSS EELKRFFNIRPREGVGLLDNSGGVIYAYKARARALQDAIRQLG GTVRDGEKVVBINPGLLVTVKTTSSYQAKSLVITAGPTWNGLL RPLGIEMPLQTILRINVCYWREWPGSYGVSQAPPCFLWGLCPH HYGLDFTGEYGGMKVSYHHGHADPEERQCPTARTDIGDVQIL SSFVRDHLPDLKPEBVVBINGSYGVSGAPPCFLWGLCPH HYGLDFTGETSGGMKVSYHHGHADPERGCPTARTDIGDVQIL SSFVRDHLPDLKPEBVVBINGFRHOFFINFTSYDLAPFRISFPSLG KAHL 6996 543 1942 BTANABARAKSAMDWKEVLRRLATPNTCPNKKKSEQELKDEE MDLFTKYYSEWKGGRKNTWFFYKTIPFFYKTPARMEVLLQKRLR EESRAVPLQRKSRELLDNEGLGEAMIN YENFLKVGEKAGAKCKQFFTARVFAKLLHTDSYGRISMQFFNY VRKWWLHQTRIGLSLYDVAGCGYYGADELMYTLLELIPFTLPQL DGLEKSFYSFYVCTAVRKFFFFLDPLRTGKKKJOILACSFLDD LLELRDEELSKESQETNWFSAPSALRVYGGYLNDKDINGGLISK EELSRYGTATMTNVFLDRYFGGEMYNTLDELIPTLPQL DGLEKSFYSFYVCTAVRKFFFFLDPLRTGKKKJOILACSFLDD LLELRDBELSKESQETNWFSAPSALRVYGGYLNDKDINGGLISK EELSRYGTATMTNVFLDRYFRQFKGTTOAMFKF PVSFQDVAGERIPMWKRAPSALLDEVGCGTGAMFKF PVSFQDVAGERIPMWKRAPSKLLEBVGCGTGAMFKF PVSFQDVAGERIPMGASKKEBLEFSKLLEPVGCGTGAMFKF	1	.		KNLGGKSSGRRQGIKKMEGHYVHAGNIIATORHFRWHPGAHVGV
6991 169 451 RRSSDFNPGFLSRPSVSLRRNIHRQVICSTKNKRRNPKKIAYLL SSLLMTNLNPNESTENQPVDAYWAFTLQGEFLTVACVEGTGCLF CGRIVH RQAPGCSSLALRQVRQVYCGLVRAPQVQTRPLSSRFVERRGALY RSPMNQBNPPPYPGPGPTAPYPPYPPQPMGPPMGPPPPGGY PYQGYPQYGMQGPQPPKTTVTVVEDQRBELGFSTCLTACCT ALCCCCLMDMLT 6993 1 374 OWCUTCPQENARQGPAVPPGIQAYGAAPFEDLQVDFTEMSKCRG DRVBIKNWAVASLCLUKKEPDTVLSPPTAVKVEGIPAWIHHH VKPAARETWEARPSPDNPFRVILKKTSPAPVTPGS 6994 346 1100 OWFEKDFVMAASSISSFWGHVPKATLMVLVASLLUHSALAGGR RDFAPPGQQKREAPVDVLTQIGRSVKGTLDAWIGPETHHLVSES SSQVLWAISSAISVAFFALSGLAQLLNALGLAGDYLAGGLKLS PGOVQTFLLWGAGALVVYWLLSLLIGULVALLGRILMGLKLUFF LAGFVALMRSVPDPSTRALLLLALLILLALLGRILMGLKLUFF LAGFVALMRSVPDPSTRALLLLALLILLALLGRILMGLKLUFF LAGFVALMRSVPDPSTRALLLLALLILLALLGRILMGLKLUFF LAGFVALMRSVPDPSTRALLLLALLILLALLGRILMGLKLUFF LAGFVALMRSVPDPSTRALLLLALLILLALLGRILMGLKLUFF LAGFVALMRSVPDPSTRALLLLALLILLALLGRILMGLKLUFF LAGFVALMRSVPDPSTRALLLLALLILLALLGRILMGLKLUFF LAGFVALMRSVPDPSTRALLLLALLILLALLGRILMGLKLUFF LAGFVALMRSVPDPSTRALLLLALLILLALLGRILMGLKLUFF LAGFVALMRSVPDPSTRALLLLALLILLARLLGRAFRAGAGA EARVRCLERQUEELRWRQRRAKGARSVEEE EELKQFFPIRHPPGSGSHGQSRIIRRAVLDFFTRMMHECYQIWAQL EHBAGTQLHRGTGLLLLGHKENQELVTTVKTTSRSYQAKSLVITAGPWTNQLL RPLGIEMPLQTTCTSTREWVFSTRANGHENGELFTTRMHECYQIWGLCLSS EELKQFFPIRHPGTGLLLLGHKENQELVTTVKTTSRSYQAKSLVITAGPWTNQLL RPLGIEMPLQTTCTSTREWVFSTYGASAPCFLWGLCPH HYGLPTCTYBENGKVSYHHGHALDPEERDCPTPARTIOLDVQLL SSFVRDHLPDLKPERAVISCSVYTTTPDEOPTLADRIPKYDNIVI GAGFSSCHGFKLAPVVGKILYELSMKLTPSYDLAPFRISFPSLG KAHL 6996 543 1942 BTANABAARKSAMDWKEVLRRRLATPNTCPNKKKSEQELKDEE MDLFFKYYSENKGGRKNTWEFYKTIPTPTYNLDEAMIN YENPLKVGGKAGAKCRQFFTAKVFAKLLHTDSYGRISIMQFFNY VNRKWWLHQTTIGLSLYDVAGGGYTADELDENTILLELTTLDQL DGLERSFYSFYVCTAVRRFFFFLDPLRGRIKJQDLLACSPLDD LLELEDBELSKSGGTTNTSPSARARVYGQYLNILKGINGMLSK EELSRYGTATMTNVFLDRVFQELGTYTLLDKDINGMLSK EELSRYGTATMTNVFLDRVFQEDDYNTTLIDLNNGGDTVTTILIDL NGFWYENREALVANDSENSADLDDT 40000000000000000000000000000000000	1			GKNKCLYALEEGIVRYTKEVYVPHPRNTEAVDLITRLPKGAVLY
SSLIMTNIAPISSKVSIKENIHHQVICSTKKRRIPKKIAYLL SSLIMTNIAPISSKVSIKENIHHQVICSTKKRRIPKKIAYLL GRRIVH GAPGCSSLALRQVRQVYCGLVRAPQVQTRPLSSRFVERRGALY RQAPGCSSLALRQVRQVYCGLVRAPQVQTRPLSSRFVERRGALY RSPMNGENPPPYPGPQPTAPYPPYPPOGMGGGMGGPYPPPGGY PYQGYPQYGMGGGPQEPPKTTVYVVEDQRRDELGPSTCLTACWT ALCCCLMMDMLT ALCCCLMMDMLT G993 1 374 OWCVTCPGHARAGGPAVPPGIQAYGAAPFEDLQVDPTEMSKCRG DRVWIKNMNVASLCLIMKSPQTVVLISPTAVKUGIPSWIHHGH VKPAARETMEARPSPDNPFRYLIKKTTSPAPVTPGS GDVWIKNMNVASLSCLIMKSPQTVVLISPTAVKUGIPSWIHHGH VKPAARETMEARPSPDNPFRYLIKKTTSPAPVTPGS GPPAPPQQKREAPVDVLTQIGRSVRGTLDAWIGGFTMHIHGHS RDPAPPQQKREAPVDVLTQIGRSVRGTLDAWIGGFTMHIHGHS SSQVLMAISSAISVAFFALSGIAAQLLNALGLAGDYLAGGIKLS PGOVQTFLIMGAGALVVYWLLSLLIGLIVLALLGRILWGIKLVIF LAGFVALMRSVYPDSTRALLLIALLILIVALLSRILMGIKLVIF EAKVRGLERQVEELBHRGRRAAKGARSVEEE GSVAVGLSGIMAAQKDLWDATVIGAGIGGGFTAYHLAKHRKRIL LLEQFFLPHSRGSSIGGSRIIRKAYLEDFYTRMHECYQIMAQL BHBAGTQLHRQTGLLLLGMKENQBLKTIQANLSRGRVEHQCLSS EELKKRFPNIRLPRGEVGLLDINSGGVIYAYKALRALQDAIRQIG GIVRDGEKVVEINPGLUVTKYTTSRSYQAKSLVITAGGWTNQLL RPLGIEMPLQTILRINVCYWREMVPGSYGYAFCPLMIGLCPH HYGLJPTCEYPCIMKNSYHGMIADPEBROCPTARTDIGDVQIL SSFVRDHLPDLKPERAVIESCMYTNTPDEQPILDRHPKYDNIVI GAGPFSGGFKLAPVVGKILYELSMKLTPSYDLAPRRISHTDIGLCH HYGLJPTCYFYCHKWSYHGMIKADPEBROCPTARTDIGDVQIL SSFVRDHLPDLKPERAVIESCMYTNTPDEQPILDRHPKYDNIVI GAGPGGFGFKLAPVVGKILYELSMKLTPSYDLAPRRISHMOPPNY VRKWULHQTTIGISLJVDVAGGYUTLERSDLENYILLLIPTLDQL DGLEKSFYSFYCTAVKRFFFILDPLRTGKIKIQDILACSFLDD LLELRDEELSKESQETNWFSAPSALRVGQVILNDKOHNGMLSK EELSRAYGIATMTNYFLDRVQECLTYDGEMDYKTYLDFVLALEN RKEPAALQYIFKLLDIENKSYLNVFSLWFFRAIQELMKHGQD PUSFGDVADEIFFRALDIENGVEKKWFPYFILVRF PUSFGDVADEIFFRALDIENGVEKKWFPYFILVRF TVIYNEQMASKRELLSINDGERAGSKILLEWGCCTGANPWF	-			KTFVHVVPAKPEGTFKLVAML
SSLLMTMLNPNESTENQPVDAYWAFTLDQEFLTYACVEGTGCLF CGRWH 879AW 879MCRNPPPYPGOPTAPYPPUSPRFVERRGALY RSPMNGENPPPYPGOPTAPYPPYPYPOPMGGGPYPPPGGY PYGGYPYGWGGGPOEPPRTTTYVYVEDQRRDELGPSTCLTACWT ALCCCLUMMLT ALCCCLUMMLT ALCCCLUMMLT ALCCCLUMMLT ALCCCLUMMLT 6993 1 374 0WCVTCPQHNARGGPAVPPGIQAYGAAPPEDLQVDFTEMSKCRG DRWMIKNWAVASLCELWKSPQTVVLSPPTAVKVEGTPAWHHSH VKPAARETWEARPSPDNPPRVTLKKTTSPAPVTPGS 6994 346 1100 0WPEKDPVMAASSISSFWGKWFKAILWLVVALILLHSALAQSR RDFAPPGQKREAPVDVLTQIGRSVRGTLDAWIGPSTMHLVSES SSQVLWAISSAISVAFFALISGIAAQLLNALGLAGDVLAGGIKLS FGQVOTFILWGAGALVVYWLLSLGULJULALLGRILWGLKLVIF LAGFVALMRSVPDPSTRALLLALLILYALLSRITGSRASGQL EAKVRGLERQVEELRWRGRRAAKGARSVEE 6995 144 1346 6SYAVASLSGIMAQROLMDADIVIGAGTGGCFTAYHLAKHRKRIL LLEQFFLPHISRGSSIGQSRITRKAYLEDFYTRMMHECYQIWAQL BHEAGTQLHRQTGLLLIGMKENGELKTIQANLSRGRVEHQCLSS EELKQRFPNIRLPRGEVUELIDNSGGVYYAYKALRALQODAIRQL GGYVADGEKVVEINPGLLUTVKTTSRSYQAKSLVITTAGPWTNQLL RPLGIBMPLOTURINVCYWREMVPGSYGVSQAFPCFLWLGCLCPH HIYGLPTGEYPGLIKVSYHRGNIRADPERRCCPTARTDIGDVQIL SSFVRDHLPDLKPERVUEINVEKTHONSGVYIYAYKALRALAGOAIRQL GAGFSGHGFKLAPVVGKILVELSMKLTPSYDLAPFRISRFPSLG KAHL 6996 543 1942 BTANABAAARKSAMDWKEVLRRRLATFNTCPKKKKSEQELKDEE MDLFTKYYSEWKGGRKNTNEFYKTIPFKYRLDAENEVLLQKLR EESRAVFLQRKSRELLDNEELQNLWFLLDKHQTPPMIGEEAMIN YENPLKVGEKAGAKCKQFFTAKVPSKIKIQDILACSFLDD DGLEKSFYSFYVCTAVRKFFFFLDPLRTGKIKIQDILACSFLDD DGLEKSFYSFYVCTAVRKFFFFLDPLRTGKIKIQDILACSFLDD LLELEDBELSKESQETNWFSAPSALRVYGQYLNLDKDHINGMLSK EELSRYGTATMTNVFLDRVYGCCLTYDGEMDYKTYLDFVLALEN REPAALQYIFKLLDIENKGYLNVESLMYFFRATQELMKINGLSK EELSRYGTATMTNVFLDRVYGCCLTYDGEMDYKTYLDFVLALEN REPAALQYIFKLLDIENKGYLNVESLMYFFRATQELMKINGD PVSGQDVKDEIFFMVKKVKPKDPLLIXDLINNGGDTVTTILIDL NOFWYERRBALVANDSENSADLDDT 6997 370 1104 AMEUTIFILBLATYILTFPLYLLNFLIGUNGCKKWFPYFLVRF	6991	169	451	RRSSDFHNPGFLSRPVSLRENIHHQVICSTKNKRRNPKKIAYLL
GSRIVH GAPGECSSLALRQVRQVYCGLVRAPQVQTRPLSSRFVERRGALY RSPMNQENPPPYPGPQPTAPYPPPYPQCMGGFMGGPYPPPGGY PYQGYPQYGWGGGPQEPPKTTVYVVEDQRRDELGPSTCLTACWT ALCCCCLMMULT G993 1 374	J.	i		SSLLMTNLNPNESTENQPVDAYWAFTLDQEFLTYACVEGTGCLF
ROMARGESSLALRQURQYCGLVRAPQQVTRPLSSRPVERRGALY RSPRINGENPPPYPORGFTAPYPYPPQMGYGAMGPTGPYPPPPQGY PYQGYPQYGMGGGPQEPPKTTYYVVEDQRRDELGPSTCLTACWT ALCCCLMDMLT ALCCCLMDMLT OWCVTCPGHHARGGPAVPPGIQAYGAAPYEDLQVDFTEMSKCRG DRVWIKMINASLCPLWKGPCTVVLSPPTAVKVEGIPAWIHHSH VKPAARSTWEARPSPDNPFRVILKKTTSPAPVTPGS OWPEKDPVMAASSISSPMGKHVFKATLMVLVALILLHSSLAGGR RDFAPPGQQKREAPVDVLTQIGRSVRGTLDAWIGPETMHLVSES SQVLWAISSAISVAFFALISGLAAQLLNALGLAGDYLAAGGKKS PGQVQTFLLWGAGALVYWHLSLLLGLVLALLGRTLMGLKLVJF LAGFVALMRSVPDPSTRALLLLALLILYALLSRLTGSRASGAQL EAKWRGLERQVEELRWRQVRAKGARSVEEE LEQFFLPHSRGSSHGGSIIRKAYLEDFYTRMMHECYQIWAQL EAKWRGLERQVEELRWRQVRGAKARSVEEE BHBAGTQLHRGTGLLLLGMKCARASVEED HEAGTQLHRGTGLLLLGMKCDLKTTQAMLASRQRVHQCLSS EELKQRFPNIRLPRGEVGLLDVSGSVIYYAYKALRALQDAIRQLG GIVROGEKVVEINPGLLVTVKTTSRSYGAKSLVITAGGWTHQLL RPLGIEMPLQTIKINVCWMERVPGSYGVSQAFPCFLUGLCPH HIYGLPTGSYPGLMKVSYHHGNHADPEERDCPTARTDIGDVQIL SSFVRDHLPDLKPEPAVIESCMYTNTPDEQFILDRHFKYDNIVI GAGFSGHGFKLAPVVGKLLYELSMKLTPSYDLAPFRISRFPSLG KAHL 6996 543 1942 ETAMABAAARKSAMDWKEVLRRRLATPNTCPNKKKSEQELKDEE MDLFTKYYSEWKGGRKNTNEFYKIPRFYYALPAENEVLLQKLR EESRAVPIQRKSRELLDMEELQNLWFLLDKHQTPPMIGERAMIN YENFLKVGEKSGAKKCKPFTAPKAFKLLHTDSYGRISIMGFFNY VMRKWWLHQTRIGLSLYDVAGQGYLRESDLENYILLEILPTLPQL DGLEKSFYSFYCTAVRKFFFFLDPLKFRKIKIQDILACSFLDD LLELDBELSKSSQSTNWFSAPSALRVYGQYLNLDKDHNGMLSK EELSRYGTATMTNVFLDRVFGCCLTYDGEMDYKTYLDFVLALEN RKEPAALQYIFKLLDIENKGYLNVFSLNYFFRAIQELMKTHGQD PVSFQDVKDEITFDWYKPGDLYSLQDLINSNQGDTVTTILIDL NGFWYERRRALVANDSENSADLDDT 4MELTIFILERATYILTFPLYLINNFGLGLSWICKKWFFYFYLVFF	2000			CGRHVH
RSPMNGBNPPYPG0GPTAPYPPYPGPGPMGPMGBYPPPQGY PYG9YPQYGNGGGPQEPHKTTVYVEDQRRDELGPSTCLTACWT ALCCCCLMDMLT OWCVTCPGHNARGGPAVPPG1QAYGAAPFEDLQVDFTEMSKCRG DRVM:KNMNVASLCPMKGPDQTVVLSPPTAVKVEGIPAWIHHSH VKPAARETWEARPSPDNPFRVTLKKTTSPAPVPGS 8994 346 1100 OWEKENDVAASSISSPNGKHVEKAILMVLVALILLHSALAQGR RDFAPPGQQKREAPVDVLTJGSVRGTLDAWIGPETMHLVSES SSQVLWAISSAISVAFFALSGIAAQLLNALGLAGTLLNGLKLVIF LAGFVALMRSVPDPSTRALLLALLLYLALLGRILWGLKLVIF LAGFVALMRSVPDPSTRALLLALLLYLVALLGRILWGLKLVIF LAGFVALMRSVPDPSTRALLLALLLYLVALLGRILWGLKLVIF LAGFVALMRSVPDPSTRALLLALLLYLVALLGRILWGLKLVIF EAKVRGLERQVEELRWRQRRAAKGARSVEEE 6595 144 1346 GSVAVGLSGIMAAQKOLWDATVIGAGIGGCFTAYHALKHRKRIL LLEQFLPHSRGSSHGOSRI IRRAYLEDFYTRMMECYQ IWAQL BHEAGTQLHRQTGLLLLGMKENQELKTIQANLSRQRVEHQCLSS EELKQRFFNIRLPRGEVGLLDNSGGVIYAYKALRALQDAIRQLG GIVRDDEKVVEINFGLLVTVXTSSYQAKSLVTTAGWHTNQLL RPLGIEMPLQTLRINVCYWREMVPGSYGVSQAFPCFLWLGLCPH HYGLDFTGEYPGLMRVYSHGMHADPERDCPTARTDIGDVQIL SSFVRDHLPDLAFPEAVIESCHYTNTPDGOPTLDRHPKYDNIVI GAGFSGHGFKLAPVVGKILYBESKLTTAGNTDRIVI GAGFSGHGFKLAPVVGKILYBESKLTTPSYDLAPFRISRFPSLG KAHL 6996 543 1942 ETANNBEARARKSAMDWKEVLRRRLATPWTCPNKKKSEQELKDEE MDLFTKYYSEWKGGRKNTNEFYKTIPRFYYRLPAENEVLLQKLR EESRAVGTAMTMOTELDSELONDHFLLDKHQTPPMIGEERAMIN YENPLKVGEKAGAKCKQFTKAPKALLHTDSYGRISIMQFFNY VWRKWWLHQTRIGLSLYDVAGQGYLRESDLENYILELIPTLPQL DGLEKSFYSFYVCTAVRKFFFFLDPLRFKKKIQDILACSFLDD LLELEDELSKSSGETNWFSAPSALRVYGGYLNLDKOHNGMLSK EELSRYGTATMTNVFLDRVPGCCTTYDGEMDYKTYLDFVLALEN RKEPAALQYIFKLLDIENKGYLNJFSRIJMFRAIQEDTVTTILIDL NGFWYERRBALVANDSENSADLDDT TVIYNEGMASKKRELDSHLOPGFAGPSGKLSLLENGCCTGANPEP	6992	944	510	RQAPGCSSLALRQVRQVYCGLVRAPQVQTRPLSSRFVERRGALY
ALCCCCMMIT 6993 1 374				RSPMNQENPPPYPGPGPTAPYPPYPPOPMGPGPMGGPYPPPOGY
ALCCCCMMMIT OWCVTCPOHNARGGPAVPPGIQAYGAAPFEDLQVDFTEMSKCRG DRVWIKNWNVASLCPLWKGPCTVVLSPPTAVKVEGIPAWIHHSH VKPAARETWEARPSPDNPFRVTLKKTTSPAPVTPGS OWPEKDPVMAASSISSPMGKHVFKAILMVLVALILLHSALAGSR RDFAPPGQQKREAPVDVLTQIGRSVRGTLDAWIGPETMHLVSES SSQVLWAISSAISVAFFALGGIAAQLINALGLAGDYLAQGLKLS PGQVOTFLUMAGALVYYWLLSLLIGLULALLGRILWGLKLVIF LAGFVALMRSVPPDSTRALLLLALLILYALLSRITGSRASGAQL EAKVRGLERQVEELRWRQRRAAKGARSVEEB GSVAVGLSGIMAAQKDLWDAIVVGAGIQGCFTAYHLAKHRKRIL LLEQFFLPHSRGSSHGGSRIIRKAYLDDFTTRMHECYQIWAQL BHBAGTQLHRQTGLILLIGMKENQBLKTIQANLSRQRVEHQCLSS EELKQRFPNIRLPRGEVGLLDNSGGVIYAYKALRALQDAIRQLG GIVRDEKVVEINPGLLVTVKTTSRSYQARSLVITAGPWINQLL RPLGIEMPLQTLRINVCYWREMVPGSYGVSQAFPCFLWLGLCPH HIYGLPTGEYPGLMKVYSYHGHNADPERDCPTARTDIGDVQIL SSFVRDHLPDLKREPAVIBSCMYTNTPDEQFILDRIFKYNNIVI GAGFSGHGFKLAPVVGKILYELSMKLTPSYDLAPFRISRFPSLG KAHL 6996 543 1942 BTANAEAARKSAMDWKEVLRRRLATPNTCPNKKKSEQELKDEE MDLFTKYYSEWKSGRNTMEFYKTIPRFYYRLPAENEVLLQKLR EESRAVFLQRKSRELLDNEELQNLWFLLDKHGTPPMIGEBAMIN YENPLKVGEKAGAKCKQFFTAKVFAKLLHTDSYGRISIMGFFNY VWRKWLHGTRIGLSLYDVAGGGYLRESDLENYILELIPTLPQL DGLEKSFYSFYVCTAVRKFFFFLDPLRTCKIKIQDLACSFLDD LLELRDEELSKESGETNWFSPSABALRVYGQYLNLDKOHNGMLEK EELSRYGTATMINVELDRVFQECLTYDGEMDYKTYLDFVLALEN RKEPAALQYIFKLLDIENKGYLNVFSLNYFFRAIGELMKHGGD PVSPQDVKDEIFDMVKKPDLKISLQDLINSNGGDTVTTILIDL NGFWYYENRELLVANDSSNSADLDDT AMELTIFILRLAIYILTFPLYLLGIMSWICKKWFPYFLVRF TVIYNEMBASKKRELFSNLOEFAGFSGKKSLLEEVGCGTGANRER				PYQGYPQYGWQGGPQEPPKTTVYVVEDQRRDELGPSTCLTACWT
GRVNIKANNVASLCPLWKGPQTVVLSPPTAVKVEGIPAWIHHSH VKPAARETWEARPSPDNPFRVTLKKTTSPAPVTPGS OWEKKDEVMAASSISSFMGKHVFKAIIMVIVAULLIHSALAQSR RDFAPPGQQKEAPVDVDVITQIGSVRGTIDAWIGPETMHLVSES SQVLWAISSAISVAFFALSGIAQQLINALGHALAQSK PGOVQTFLLWGAGAIVVYWHLSLILGILVLALLGRILWGLKLVIF LAGFVALMRSVPDPSTRALLLALLILYLLALLSRITGSRASGAQL EARVRGLERQVEELRWRQRRAAKGARSVEEE GSVAVGLSGIMAAQKDLWDAIVIGAGIQGCFTAYHLAKHRKRIL LLEQFFLPHSRGSSHQQSRIIKAXTLEDFYTRMHECYQIWAQL EHBAGTQLHRQTGLILLGWKENQELKITQANLSRQRVEHQCLSS EELKQRFPNIRLPRGEVGLLDNSGGVIYAYKALRALQDAIRQLG GIVRDGEKVVEINFGLUVTVKTTSRSYQAKSLVITAGPWINQLL RPPLGIEMPLOTHRINVCYWREMVPGSYGVSQAFPCFLWLGLCPH HIYGLPTGEYPGLMKVSYHHGNHADPEERDCFTARTDIGDVQIL SSFVRDHLPDLKPEPAVIESCMYINTPDEQFILDRIPKYDNIVI GAGFSGHGFKLAPVVGKILYELSMKLTPSYDLAPFRISRFPSLG KAHL 6996 543 1942 ETANABAARKSAMDWKEVLRRRLATPWTCPNKKKSEQELKDEE MDLFTKYYSEWKGGRKNTHEFYKTIPRFYYRLPAENEVLLQKLR EESRAVFLQRKSRELLDNEELQNLWFLLDKHQTPPMIGEBAMIN YENFLKVGEKAGAKCKQFFTAKVPAKLLHTDSYGRISIMQFFNY VMRKVWLHQTRIGLSLYDVAGQGYLREBDLENYILELIPTLPQL DGLEKSFYSFYVCTAVKRFFFLDPLRGKIKIQDILACSFLDD LLELRDEELSKESQETNWFSAPSALRVYGQYLNLDKDHNGMLSK EELSRYGTATMTNVFLDRVPQECLTYDGEMDYKTVLDFVLALEN RKEPAALQYIFKLLDIENKGYLNVFSLNYFPRAIQELMKIHGDD PVSPQDVKDEIPFMWKPKDPLKISLQDLINSNQGDTVTTILDL NGFWYYENRRALVANDSENSADLDDT 7VIYNEQMASKRELFSNLQEFAGPSGKLSLLEVGCGTGANBKF	6993			ALCCCCLWDMLT
OVERARETWEARPSPONDERVILKETTSPAPUTPGS	6,555	_	374	QWCVTCPQHNARQGPAVPPGIQAYGAAPFEDLQVDFTEMSKCRG
1100 QWPEKDPVMAASSISSPWGRIVFKAILMVLVALILLHSALAQSR RDFAPPGQQKREAPVDVLIGESVGRIIDAWIGPETMHLVSES SSQVLWAISSAISVAFFALSGIAAQLLNALGLAGDYLAQGLKLS PGQVQTFLLWGAGALVVYWLLSLLIGLVLALLGRILWGLKLVIF LAGFVALMRSVYDPDSTRALLLLALLILYALLSRITGSRASGAQL EAKVRGLERQVEELRWRQRRAAKGARSVEEE 6995 144 1346 GSVAVGLSGIMAAQKOLWDAIVIGAGIGGCFTAYHLAKHRKRIL LEQFFLPHSRGSSHGQSRIIRKAYLEDFYTRMMHECYQIWAQL EHBAGTQLHRQTGLLLLGMKENQELKTIQANLSRQRVEHQCLSS EELKQRFPNIRLPRGGVLLDNSGGVIYAYKALRALQDAIRQLG GIVRDGEKVVEINPGLLVTVKTTSRSVQAKSLVITAGPWTNQLL RPLGIEMPLOTTLRINVCYWREMVPGSYGVSQAFPCFLWLGLCPH HIYGLPTGEYPGLMKVSYHHGNHADPEERDCPTARTOLDDVQIL SSFVRPHLPDLKPEPAVIESCMYTNTPDEQFLLDRHPKYDNIVI GAGFSGHGFKLAPVVGKILYELSMKLTPSYDLAPFRISRFPSLG KAHL 1942 ETANAEAARKSAMDWKEVLRRRLATPNTCFNKKKSEQELKDEE MDLFTKYYSEWKGGRKNTNEFYKTIPRFYYRLPAENEVLLQKLR EESRAVFLQRKSRELLDNEELQNLWFLLDKHQTPPMIGEEAMIN YENFLKVGGKAGAKCKOFFTAKVFAKLLHTDSYGRISIMQFFMY VMRKVWLHQTRIGLSLTDVAGQGYLRESDLENYILELIPTLPQL DGLEKSFYSFYVCTAVRKFFFFLDPLRTGKIKIQDILACSFLDD LLELRDEELSKESQETMWFAPSALRVYGQYLNLDKDHNGMLSK EELSRYGTATMTNVFLDRVFGECLTTDGEMDYKTYLDPVIALEN RKEPAALQVIFKLLDIENKGYLNVSSLNYFFRAIQELMKHGQD PVSPQDVKDEIFDMVKPKDPLKISLQDLINNSQGDTVTTILTDL NGFWTYENREALVANDSENSADLDDT TVIYNEQMASKRELISPSLOEFAGFSGKLSLLEVGCGTGANFKF				DRVWIKNWNVASLCPLWKGPQTVVLSPPTAVKVEGIPAWIHHSH
RDFAPPGQQKERAPUPVLTQIGRSVRGTLDAWIGPETMHLVSES SQVLWAISSAISVAFFALSGIAAQLLMALGLAGDYLAQGIKLS PGOVOTFILWGAGALVYVHLISLLIGULALIGILWGLKLVIF LAGFVALMRSVPDPSTTALLLLALILIALISRITGSRASGAQL EARVRGLERQVEELRWRQRRAKGARSVEEE GSVAVGLSGIMAAQKDLWDAIVIGAGIQGCFTAYHLAKHRKRIL LLQFFLPHSRGSSIGQSRIIRKAYLDDFYTRMMHECYQIWAQL EHEAGTQLHRQTGLLLIGMKENQELKTIQANLSRGRVEHQCLSS EELKQRFPNIRLPRGEVGLLDNSGGVIYAYKALRALQDAIRQLG GIVRDGEKVVEINPGLLVTVKTTSRSYQAKSLVITAGPWINQLL RPLGIEMPLOTLRINVCYWREMVPGSYGVSQAFPCFLWLGLCPH HYGLPFGEYPGLMKVSYHGNHADPEERDCPTARTDIGDVQIL SSFVRDHLPDLKPEPAVIESCMYTNTPDEQFILDRHPKXDNIVI GAGPSGHGFKLAPVVGKILYELSMKLTPSYDLAPFRISRFPSLG KAHL 6996 543 1942 BTANAEAAARKSAMDWKEVLRRRLATPNTCPNKKKSEQELKDEE MDLFTKYYSEWKGGRKNINEFYKTIPRFYYRLPAENEVILQKLR EESRAVFLQRKSRELLDNEELQNLWFLLDKHQTPPMIGEEAMIN YENFLKVGEKAGKCKQFFTAKVPAKLLHTDSYGRISIMQFFMY VMRKVWLHQTRIGLSIVDVAGGGYLRESDLENYILELIPTLPQL DGLEKSFYSFYVCTAVRKFFFFLDPLRTGKIKIQDILACSFLDD LLELRDEELSKESQETMWFSAPSALRVYGQYLNLDKOHNGMLSK EELSRYGTATMTNVFLDRYQGCTLARGEDLYTTYLDPVLALEN RKEPAALQVIFKLLDIENKGYLNVPSLNYFFRAIQELMKHGQD PVSPQDVKDEIFDMVKPKDPLKISLQDLINSNGGDTVTTILTDL NGFWYENREALVANDSENSADLDDT TVIYNEQMASKRELFSNLOEFAGPSGKLSLLEVGCGTGANFKF	6994	346	1100	VKPAARETWEARPSPDNPFRVTLKKTTSPAPVTPGS
SSQVLWAISSAISVAFFALGITAQLINALGLAGDYLAQGIKLS PGQVQTFILWGAGALVVYWLLSLLIGIVLALIGITLYGLKLVIF LAGFVALMRSVPDPSTRALLLIALLITALISRITGSRASGAQL EAKVRGLERQVEELRWRQRRAAKGARSVEEE 6995 144 1346 GSVNVGLSGIMAAQKDLWDAIVIGAGIGCFTAYHLAKHRKRIL LLEQFFLPHSRGSSHQGSRIIRKAYLEDFYTRMHHECYQIWAQL BHEAGTQLHRQTGLLLIGMKENQELKTIQANLSRQRVEHQCLSS EELKQRFPNIRLPRGEVGLLDNSGGVIYAYKALRALQDAIROLG GIVRDGEKVVEINPGLLVTVKTTSRSYOAKSLVITAGPWTNQLL RPLGIEMPLQTTRINVCYWREMVPGSYGVSQAFPCFLWIGCLCPH HYGLPTGEYPGLMKVSYHHGHADPEERDCPTARTDIGDVQIL SSFVRDHLPDLKPEPAVIESCMYTNTPDEQFILDRHPKYDNIVI GAGFSCHGFKLAPVVGKILYELSMKLTPSYDLAPFRISRFPSLG KAHL BTANAEAAARKSAMDWKEVLRRRLATFWTCPNKKKSEQELKDEE MDLFTKYYSEWKGGRKNTNEFYKTIPRFYYRLPAENEVLLQKLR EESRAVFLQRKSRELLDNEELQNLWFLLDKHQTPPMIGEEAMIN YENPLKVGEKAGAKCKQFFTAKVPAKLLHTDSYGRISIMQFFNY VMRKVWLHQTTIGLSLYDVAGQGYLRESDLENYILELIPTLPQL DGLEKSFYSFYVCTAVRKFFFFLDPLRTGKIKIQDILACSFLDD LLELRDEELSKESGETNWFSAPSALRVVGQYLNLDKDHNGMLSK EELSRYGTATMTNVFLDRVFQECLTYDGEMDYKTYLDFVLALEN RKEPAALQYIFKLLDIENGYLNVFSLNYFFRAIQELMKIHGQD PVSFQDVKDEIFDMVKPKDPLKISLQDLINSNQGDTVTTILIDL NGFWYYENREALVANDSSNSADLDDT 6997 370 1104 AMELTIFILRLAIYILTPFLYLLNFLGLWSWICKKWFPYFLVRF TVIYNEQMASKKRELFSNLQEFGGSGKISLLEVGCCTGAWRKF	1	310	1100	QWPEKDPVMAASSISSPWGKHVFKAILMVLVALILLHSALAQSR
FGOVOTFLIMGAGALVYWILLSLLIGIVLALLGRILWGLKLVIF LAGFVALMRSVPDPSTRALLLLALLILYALLSRITGSRASGAQL EARVRGLERQVEELRWRQRRAAKGARSVEEE GSVAVGLSGIMAAQKDLWDAIVIGAGIQGCFTAYHLAKHRKRIL LLEQFFLPHSRGSSHGQSRIIRKAYLEDFYTRMHECYQIWAQL BHEAGTQLHRQTGILLLGMKENQELKTIQANLSRQRVEHQCLSS EELKQRFPNIRLPRGEVGLLDNSGGVIYAYKALRALQDAIRQIG GIVRDGEKVVELNPGLLVTVKTTSRSYQAKSLVITAGFWTNQLL RPLGIEMPLQTLRINVCYWREMVPGSYGVSQAFPCFLWLGLCPH HYGLPTGEYPGLMKVSYHHGNHADPERDCPTARTDIGDVQIL SSFVRDHLPDLKPPEAVUTISCMYTNTPDEQFILDRHFKYDNIVI GAGFSGHGFKLAPVVGKILYELSMKLTPSYDLAPFRISRFPSLG KAHL 6996 543 1942 BTANAEAAARKSAMDWKEVLRRRLATPNTCPNKKKSEQELKDEE MDLFTKYYSEWKGGRNTNEFYKTIPFFYYNLPAENEVLLQKLR EESRAVPLQRKSRELLDNEELQNLWFLLDKHQTPPMIGEEAMIN YENFLKVGEKAGAKCKQFFTAKVFAKLLHTDSYGRISIMQFFNY VMRKVWLHQTRIGLSLYDVAGQGYLRESDLENYILELIPTIPQL DGLEKSFYSFYVCTAVKKFFFFLDPLRTGKIKIQDILACSFLDD LLELRDELSKESQETNWFSAPSALRVYGQYLNLDKDHNGKLSK EELSRYGTATMTNVFLDRVFGECLTYDGEMDYKTYLDFVLALEN RKEPAALQYIFKLLDIENKGYLNVFSLNYFFRAIQELMKHGOD PVSFQDVKDEIFDMVKPKDPLKISLQDLINSNQGDTVTTILIDL NGFWTYENREALVANDESBRSADLDDT 6997 370 1104 AMELTIFILRIAIYILTFPLYLLNFLGLWSWICKKWFFYFLVRF TVIYMEQMASKKRELFSNLQEFAGFSGKLSLLEVGGGTGANPKF			•	RDFAPPGQQKREAPVDVLTQIGRSVRGTLDAWIGPETMHLVSES
EAKVRGLERQVEELRWRQRRAAKGARSVEEE 6995 144 1346 GSVAVGLEGIMAQQKDLWDAIVIGAGIQGCFTAYHLAKHRKRIL LLEQFFLPHSRGSSHGQSRIIRKAYLEDFYTRMHECYQIWAQL BHEAGTQLHRQTGLLLLGMKENQELKTIQANLSRQRVEHQCLSS EELKQFFPNIRLPRGESVGLLDNSGGVIYAYKALRALQDAIRQLG GIVRDGEKVVEINPGLLVTVKTTSRSYQAKSLVITAGPWTNQLL RPLGIEMPLQTLRINVCYWREMVPGSYGVSQAFPCFLWLGLCPH H1YGLPTGEYPGLMKVSYHHGNHADPEERDCPTARTDIGDVQIL SSFVRDHLPDLKPEPAVIESCMYTNTPDEQPILDRHPKYDNIVI GAGFSGHGFKLAPVVGKILYELSMKLTPSYDLAPFRISRFPSLG KAHL 6996 543 1942 ETANAEAAARKSAMDWKEVLRRRLATPNTCPNKKKSEQELKDEE MDLFTKYYSEWKGGRKNTNEFYKTIPRFYYRLPAENEVLLQKLR EESRAVFLQRKSRELLDNEELQNLWFLLDKHQTPPMIGEEAMIN YENFLKVGEKAGAKCKQFFTAKVPAKLLHTDSYGRISIMQFFNY VMRKVWLHQTRIGLSLYDVAGQGYLRESDLENYILELIPTIPQL DGLEKSFYSFYYCTAVRKFFFFLDPLRTGKIKIQDILACSFLDD LLELRDEELSKESQETNWFSAFSALRVYGQYLNLDKDHNGMLSK EELSRYGTATMTNVFLDRVFQECLTYDGEMDYKTYLDFVLALEN RKEPAALQYIFKLLDIENKGYLNVFSLNYFFRAIQELMKIHGOD PVSFQDVKDEIFDMVKPKDPLKISLQDLINSNQGDTVTTILIDL NGFWTYENRRALVANDSENSADLDDT 5997 370 1104 AMELTIFILRLAIYILTFPLYLINFLGLWSWICKKWFPYFLVRF TVIYMEQMASKRELFSNLOGFAGPSGKLSLLEVGCGTGANEKF				BCOVOTEL HOLDS THE STATE OF THE
6995 144 1346 GSVNVGLSGIMAAQKDLWDATVIGAGIQGCFTAYHLAKHRKRIL LLEQFFLPHSRGSSHGQSRIIRKAYLEDFYTRMHECYQIWAQL BHEAGTQLHRQTGLLLLGMKENQELKTIQANLSRQRVEHQCLSS EELKQRFPNIRLPRGEVGLLDNSGGVIYAYKALRALQDAIRQIG GIVRDGEKVVEINPGLLVTVKTTSRSYQAKSLVITAGPWTNQLL RPLGIEMPLQTLRINVCYWREMVPGSYGVSQAFPCFLWIGLCPH H1YGLPTGEYPGLMKVSYHHGNHADPERRDCPTARTDIGDVQIL SSFVRDHLPDLKPEPAVIESCMYTNTPDEQFILDRHPKYDNIVI GAGFSGHGFKLAPVVGKILYELSMKLTPSYDLAPFRISRFPSLG KAHL ETANAEAAARKSAMDWKEVLRRRLATPNTCPNKKKSEQELKDEE MDLFTKYYSEWKGGRKNTNEFYKTIPRFYYRLPAENEVLLQKLR EESRAVFLQRKSRELLDNEELQNLWFLLDKHQTPPMIGEEAMIN YENPLKVGEKAGAKCKQFFTAKVPAKLLHTDSYGRISIMQFFNY VMRKWALHQTRIGLSLTDVAGQGYLRESDLENYILELIPTLPQL DGLEKSFYSFYVCTAVRKFFFTLDPLRTGKIKIQDILACSFLDD LLELRDEELSKESQETNWFSAPSALRVYGQYLNLDKDHNGMLSK EELSRYGTATMTNVFLDRVFQECLTYDGEMDYKTYLDFVLALEN RKEPAALQYIFKLLDIENKGYLNVFSLNYFFRAIQELMKIHGQD PVSFQDVKDEIFDMVRPKDPLKISLQDLINSNQGDTVTTILIDL NGFWTYENRBALVANDSENSADLDDT TVIYMEQMASKRELFSNLOGFRAGPSGKLSLLEVGCGTGANEKE TVIYMEQMASKKRELFSNLOGFRAGPSGKLSLLEVGCGTGANEKE				LAGEVALME SUDDECTE AND THE STATE OF THE STAT
GSVÄVGLSGIMÄÄÄÖKDLWDAIVIGÄÄGIQGCFTÄYHLÄKHRKIL LLEQFFLPHSRGSSHGQSRIIRKÄYLEDFYTRMMECYQIWÄQL BHEAGTQLHRQTGLLLIGMKENQELKTIQANLSRQRVEHQCLSS EELKQRFPNIRLPRGEVGLLDNSGGVIYÄYKÄLRÄLQDAIRQIG GIVRDGEKVVEINPGLLVTVKTTSRSYOÄKSLVITÄGPWTNQLL RPLGIEMPLQTLRINVCYWREMVPGSYGVSQAFPCFLWLGLCPH HIYGLPTGEYPGLMKVSYHHGNHADPEERDCPTÄRTDIGDVQIL SSFVRDHLPDLKPEPAVIESCMYTNTPDEQFILDRHPKYDNIVI GÄGFSGHGFKLAPVVGKILYELSMKLTPSYDLAPFRISRFPSLG KÄHL 6996 543 1942 BTÄNAEAAARKSÄMDWKEVLRRLATPNTCPNKKKSEQELKDEE MDLFTKYYSEWKGGRKNTNEFYKTIPRFYYRLPAENEVLLQKIR EESRÄVFLQRKSRELLDNEELQNLWFLLDKHQTPPMIGEEAMIN YENFLKVGEKÄGAKCKQFFTÄKVPÄKLLHTDSYGRISIMQFFNY VMRKVWLHQTRIGLSLYDVÄGQGYLRESDLENYILELIPTLPQL DGLEKSFYSFYVCTÄVRKFFFFLDPLRTGKIKIQDILACSFLOD LLELRDEELSKESQETNWFSAPSALRVYGQVLNLDKDHNGMLSK EELSRYGTÄTMTNVFLDRVFQECLTYDGEMDYKTYLDFVLALEN RKEPAALQYIFKLLDIENKGYLNVFSLNYFFRAIQELMKIHGQD PVSFQDVKDEIFDMVKPKDPLKISLQDLINSNQGDTVTTILIDL NGFWTYENREALVANDSENSADLDDT 6997 370 1104 AMELTIFILLAIYILTPPLYLLNFLGLWSWICKKWFPYFLVRF TVIYMEQMASKKRELFSNLQEFSGKLSLLEVGCGTGANPKF	1 1			FAKUPGI PROVERI BURODERA KGAROKERE
LLEQFFLPHSRGSSHGQSRIIRKAYLEDFYTRMMHECYQIWAQL BHEAGTQLHRQTGLLLIGMKENQBLKTIQANLSRQRVEHQCLGS EELKQRFPNIRLPRGEVGLLDNSGGVIYAYKALRALQDAIRQIG GIVRDGEKVVEINPGLLVTVKTTSRSYQAKSLVITAGPWTNQLL RPLGIEMPLQTLRINVCYWREMVPGSYGVSQAFPCFLWLGLCPH H1YGLPTGEYPGLMKVSYHHGNHADPEERDCPTARTDIGDVQIL SSFVRDHLPDLKPEPAVIESCMYTNTPDEQFILDRHPKYDNIVI GAGFSGHGFKLAPVVGKILYELSMKLTPSYDLAPFRISRFPSLG KAHL 6996 543 1942 ETANABAAARKSAMDWKEVLRRRLATPNTCPNKKKSEQELKDEE MDLFTKYYSEWKGGRKNTNEFYKTIPRFYYRLPAENEVLLQKLR EESRAVFLQRKSRELLDNEELQNLWFLLDKHQTPPMIGEEAMIN YENFLKVGEKAGAKCKQFFTAKVPAKLLHTDSYGRISIMQFFNY VMRKVWLHQTRIGLSLYDVAGQGYLRESDLENYILELITTLPQL DGLEKSFYSFYVCTAVRKFFFFLDPLRTGKIKIQDILACSFLDD LLELRDEELSKESQETNWFSAPSALRVYGQYLNLDKDHNGMLSK EELSRYGTATMTNVFLDRVFQECLTYDGEMDYKTYLDPVLALEN RKEPAALQYIFKLLDIENKGYLNVFSLNYFFRAIQELMKIHGQD PVSFQDVKDEIFDMVKPKDPLKISLQDLINSNQGDTVTTILIDL NGFWTYENRBALVANDSENSADLDDT AMELTIFILRLAIYILTFPLYLINFLGLWSWICKKWFFYFLVRF TVIYMEQMASKRELFSNLOEFAGPSGKLSILEVGCGTGANFKF	6995	144	1346	GSVAVGLSCIMA ACKRI MDA TUTCA GIOGGE
BHEAGTQLHRQTGLLLLGMKENQELKTIQANLSRQRVEHQCLSS EELKQRFPNIRLPRGEVGLLDNSGGVIYAYKALRALQDAIRQLG GIVRDGEKVVEINPGLLVTVKTTSRSYQAKSLVITAGPWTNQLL RPLGIEMPLQTLRINVCYWREMVPGSYGVSQAFPCFTWLGLCPH HIYGLPTGEYPGLMKVSYHHGNHADPEERDCPTARTDIGDVQIL SSFVRDHLPDLKPEPAVIESCMYTNTPDEQFILDRHPKYDNIVI GAGFSGHGFKLAPVVGKILYELSMKLTPSYDLAPFRISRFPSLG KAHL ETANAEAAARKSAMDWKEVLRRRLATPNTCPNKKKSEQELKDEE MDLFTKYYSEWKGGRKNTNEFYKTIPRFYYRLPAENEVLLQKLR EESRAVFLQRKSRELLDNEELQNLWFLLDKHQTPPMIGEEAMIN YENFLKVGEKAGAKCKQFFTAKVPAKLLHTDSYGRISIMQFFNY VMRKVWLHQTRIGLSLYDVAGQGYLRESDLENYILELIFTLPQL DGLEKSFYSFYVCTAVRKFFFFLDPLRTGKIKIQDILACSFLDD LLELRDEELSKESQETNWFSAPSALRVYGQYLNLDKDHNGMLSK EELSRYGTATMTNVFLDRVFQECLTYDGEMDYKTYLDPVLALEN RKEPAALQYIFKLLDIENKGYLNVFSLNYFFRAIQELMKIHGQD PVSFQDVKDEIFDMVKPKDPLKISLQDLINSNQGDTVTTILIDL NGFWTYENREALVANDSENSADLDDT AMELTIFILRLAIYILTFPLYLINFLGLWSWICKKWFFYFLVRF TVIYMEQMASKRELFSNLOEFAGPSGKLSLLEVGCGTGANFKF	1 1			LLEOFFLPUSPGGGUCOGETTEVAVI PROVIDENCIA
EELKQRFPNIRLPRGEVGLLDNSGGVIYAYKALRALQDAIRQIG GIVRDGEKVVEINPGLLVTVKTTSRSYQAKSLVITAGPWINQLL RPLGIEMPLQTLRINVCYWREMVPGSYGVQAFPCFLWLGLCPH HIYGLPTGEYPGLMKVSYHHGNHADPEERDCPTARTDIGDVQIL SSFVRDHLPDLKPEPAVIESCMYTNTPDEQFILDRHPKYDNIVI GAGFSGHGFKLAPVVGKILYELSMKLTPSYDLAPFRISRFPSLG KAHL ETANAEAAARKSAMDWKEVLRRRLATPNTCPNKKKSEQELKDEE MDLFTKYYSEWKGGRKNTNEFYKTIPRFYYRLPAENEVLLQKLR EESRAVFLQRKSRELLDNEELQNLWFLLDKHQTPPMIGEEAMIN YENFLKVGEKAGAKCKQFFTAKVFAKLLHTDSYGRISIMQFFNY VMRKVWLHQTRIGLSLYDVAGCGYLRESDLENYILELIPTLPQL DGLEKSFYSFYVCTAVRKFFFFLDPLRTGKIKIQDILACSFLDD LLELRDEELSKESQETNWFSAPSALRVYGQYLNLDKDHNGMLSK EELSRYGTATMTNVFLDRVFQECLTYDGEMDYKTYLDFVLALEN RKEPAALQYIFKLLDIENKGYLNVFSLNYFFRAIQELMKIHGQD PVSFQDVKDEIFPMVKPKDPLKISLQDLINSNQGDTVTTILIDL NGFWTYENREALVANDSENSADLDDT AMELTIFILRLAIYILTFPLYLINFLGLWSWICKKWFPYFLVRF TVIYNEQMASKKRELFSNLOEFAGPSGKLSLLEVGCGTGANFKF	1 1			RHEAGTOLUPOTGILLIGMYENORI METONAY GROPETTO OF THE
GIVROGEKVVEINPGLLVTVKTTSRSYQAKSLVITAGPWTNQLL RPLGIEMPLQTLRINVCYWREMVPGSYGVSQAFPCFLWLGLCPH HIYGLPTGEYPGLMKVSYHHGNHADPEERDCPTARTDIGDVQIL SSFVRDHLPDLKPEPAVIESCMYTNTPDEQPILDRHPKYDNIVI GAGFSGHGFKLAPVVGKILYELSMKLTPSYDLAPFRISRFPSLG KAHL ETANAEAAARKSAMDWKEVLRRRLATPNTCPNKKKSEQELKDEE MDLFTKYYSEWKGGRKNTNEFYKTIPRFYYRLPAENEVLLQKLR EESRAVPLQRKSRELLDNEELQNLWFLLDKHQTPPMIGEEAMIN YENFLKVGEKAGAKCKQFFTAKVFAKLLHTDSYGRISIMQFFNY VMRKVWLHQTRIGLSLYDVAGQGYLRESDLENYILELIPTLPQL DGLEKSFYSFYVCTAVRKFFFFILDPLRTGKIKIQDILACSFLDD LLELRDEELSKESQETNWFSAPSALRVYGQYLNLDKDHNGMLSK EELSRYGTATMTNVFLDRVFQECLTYDGEMDYKTYLDFVLALEN RKEPAALQYIFKLLDIENKGYLNVFSLNYFFRAIQELMKIHGQD PVSFQDVKDEIFPMVKPKDPLKISLQDLINSNQGDTVTTILIDL NGFWTYENREALVANDSENSADLDDT 370 1104 AMELTIFILRLAIYILTFPLYLINFLGLWSWICKKWFPYFLVRF TVIYMEQMASKKRELFSNLOEFAGPSGKLSILEVGCGTGANFKF	1 1	-		EELKOREPNIPLEDGEVGLUDNGCGULVAVKALDAL GOALAGE
RPLGIEMPLOTLRINVCYWREMVPGSYGVSQAFPCFLWLGLCPH HIYGLPTGEYPGLMKVSYHHGNHADPEERDCPTARTDIGDVQIL SSFVRDHLPDLKPEPAVIESCMYTNTPDEQFILDRHPKYDNIVI GAGFSGHGFKLAPVVGKILYELSMKLTPSYDLAPFRISRFPSLG KAHL ETANAEAAARKSAMDWKEVLRRRLATPNTCPNKKKSEQELKDEE MDLFTKYYSEWKGGRKNTNEFYKTIPRFYYRLPAENEVLLQKLR EESRAVFLQRKSRELLDNEELQNLWFLLDKHQTPPMIGEEAMIN YENFLKVGEKAGAKCKQFFTAKVFAKLLHTDSYGRISIMQFFNY VMRKVWLHQTRIGLSLYDVAGQGYLRESDLENYILELIPTLPQL DGLEKSFYSFYVCTAVRKFFFFLDPLRTGKIKIQDILACSFLDD LLELRDEELSKESQETNWFSAPSALRVYGGYLNLDKDHNGMLSK EELSRYGTATMTNVFLDRVFQECLTYDGEMDYKTYLDFVLALEN RKEPAALQYIFKLLDIENKGYLNVFSLNYFFRAIQELMKIHGQD PVSFQDVKDEIFDMVKPKDPLKISLQDLINSNQGDTVTTILIDL NGFWTYENREALVANDSENSADLDDT 370 1104 AMELTIFILRLAIYILTFPLYLINFLGLWSWICKKWFFYFLVRF TVIYMEQMASKKRELFSNLQEFAGPSGKLSILEVGCGTGANFKF	ľ		•	GIVRDGEKVVEINPGLI.VTVKTTSPSVONVOI VITTNONVITVOT
HIYGLPTGEYPGLMKVSYHHGNHADPEERDCPTARTDIGDVQIL SSFVRDHLPDLKPEPAVIESCMYTNTPDEQFILDRHPKYDNIVI GAGFSGHGFKLAPVVGKILYELSMKLTPSYDLAPFRISRFPSLG KAHL ETANAEAAARKSAMDWKEVLRRRLATPNTCPNKKKSEQELKDEE MDLFTKYYSEWKGGRKNTNEFYKTIPRFYYRLPAENEVLLQKLR EESRAVFLQRKSRELLDNEELQNLWFLLDKHQTPPMIGEEAMIN YENFLKVGEKAGAKCKQFFTAKVPAKLLHTDSYGRISIMQFFNY VMRKVWLHQTRIGLSLYDVAGQGYLRESDLENYILELIPTLPQL DGLEKSFYSFYVCTAVRKFFFFLDPLRTGKIKIQDILACSFLDD LLELRDEELSKESQETNWFSAPSALRVYGGYLNLDKCHNGMLSK EELSRYGTATMTNVFLDRVFQECLTYDGEMDYKTYLDPVLALEN RKEPAALQYIFKLLDIENKGYLNVFSLNYFFRAIQELMKIHGQD PVSFQDVKDEIFFMVKPKDPLKISLQDLINSNQGDTVTTILIDL NGFWTYENREALVANDSENSADLDDT AMELTIFILRLAIYILTFPLYLINFLGLWSWICKKWFFYFLVRF TVIYMEQMASKRELFSNLOEFAGPSGKLSILEVGCGTGANFKF	i i			RPLGIEMPLOTLRINVCYWREMVPGSVGVSOAFDCFTWT GLODV
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7002 1043 498 PMPSSTRWTTS*TYTDTSSAWACRPTTGTCT*TAAPGPTVRWWP TPCSRHQSRRRLTCWCSTSRPCGR*GGLCVRTAPTRPTTSASSS SWTSAGTSWPAGRRTGTATSGTATTTSVWPGCGTRWWSTQWSSV PRSRSCCSRPATTPPSKPGAPHAPCASSRHLAHGLAPSSPGLPA RGAEVC 7003 818 61 QGRFRAFCWQRDFLQPPGMRLSALLALASKVTLPPHYRYGMSPP GSVADKRKNPPWIRRRPVVVEPISDEDWYLFCGDTVEILEGKDA GKQGKVVQVIRQRNWVVVGGLNTHYRYIGKTMDYRGTMIPSEAP LLHRQVKLVDPMDRKPTEIEWRFTEAGERVRVSTRSGRIIPKPE FPRADGIVPETWIDGPKDTSVEDALERTYVPCLKTLQEEVMEAM GIKETR\NTRRSIGIEPGABQLLPMPCPSLEG 7004 121 2285 FLLPVLTSRSLRQPAVPHARLGGVEPAAMKSARAKTPRKPTVKK G\PKRTLKTQLG/YYCRVRPLGFPDQECCIEVINNTTVQLHTPE GYRLNRNGDYKETQYSFKQVFGTHTTQKELFDVVANPLVNDLIH GKNGLLFTYGVTGSGKTHTMTGSPGEGGLLPRCLDMIFNSIGSF QAKRYVFKSNDRNSMDIQCEVDALLERQKREAMPNPKTSSSKRQ VDPEFADMITVQEFCKABEVDEDSVYGVFVSYIEIYNNYIYDLL EEVPFDPINPNLHNLNCFVKIKNHMYVAGCTEVEVKSTEEAFE		.		
TPCSRHQSRRLTCWCSTSRPCGR*GGLCVRTAPTRPTTSASSS SWTSAGTSWPAGRRTGTATSGTATTTSVWPGCGTRMWSTQWSSV PRSRSCCSRPATTPPSKPGAPHAPCASSRHLAHGLAPSSPGLPA RGAEVC 7003 818 61 QGRFRAFCWQRDFLQPPGMRLSALLALASKVTLPPHYRYGMSPP GSVADKRKNPPWIRRRPVVVEPISDEDWYLFCGDTVEILEGKDA GKQGKVVQVIRQRNWVVVGGLNTHYRYIGKTMDYRGTMIPSEAP LLHRQVKLVDPMDRKPTEIBWRFTEAGERVRVSTRSGRIIPKPE FPRADGIVPETWIDGPKDTSVEDALERTYVPCLKTLQEEVMEAM GIKETR\NTRRSIGIEPGABQLLPNFCPSLEG 7004 121 2285 FLLPVLTSRSLRQPAVPHARLGGVEPAAMKSARAKTPRKPTVKK G\PKRTLKTQLG\/YYCRVRPLGFPDQBCCIEVINNTTVQLHTPE GYRLNRNGDYKETQYSFKQVFGTHTTQKELFDVVANPLVNDLIH GKNGLLFTYGVTGSGKTHTMTGSPGEGGLLPRCLDMIFNSIGSF QAKRYVFKSNDRNSMDIQCEVDALLERQKREAMPNPKTSSSKRQ VDPEFADMITVQBFCKABEVDEDSVYGVFVSYIBIYNNYIYDLL EEVPFDPINPNLHNLNCFVKIKNHMYVAGCTEVEVKSTEEAFE	7002	1043	400	1_i
SWTSAGTSWPAGRRTGTATTSVWPGCGTRMWSTQWSSV PRSRSCCSRPATTPPSKPGAPHAPCASSRHLAHGLAPSSPGLPA RGAEVC 7003 818 61 QGRFRAFCWQRDFLQPPGMRLSALLALASKVTLPPHYRYGMSPP GSVADKRKNPPWIRRRPVVVEPISDEDWYLFCGDTVEILEGKDA GKQGKVVQVIRQRNWVVVGGLNTHYRYIGKTMDYRGTMIPSEAP LLHRQVKLVDPMDRKPTEIEWRFTEAGERVRVSTRSGRIIPKPE FPRADGIVPETWIDGPKDTSVEDALERTYVPCLKTLQEEVMEAM GIKETR\NTRRSIGIEPGABQLLPNFCPSLEG 7004 121 2285 FLLPVLTSRSLRQPAVPHARLGGVEPAAMKSARAKTPRKPTVKK G\PKRTLKTQLG\/YYCRVRPLGFPDQECCIEVINNTTVQLHTPE GYRLNRNGDYKETQYSFKQVFGTHTTQKELFDVVANPLVNDLIH GKNGLLFTYGVTGSGKTHTMTGSPGEGGLLPRCLDMIFNSIGSF QAKRYVFKSDRNSMDIQCEVDALLERQKREAMPNPKTSSSKRQ VDPEFADMITVQBFCKABEVDEDSVYGVFVSYIBIYNNYIYDLL EEVPFDPINPNLHNLNCFVKIKNHMYVAGCTEVEVKSTEEAFE		1033	770	
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GSVADKRKNPPWIRRRPVVVEPISDEDWYLFCODTVEILEGKDA GKQGKVVQVIRQRNWVVVGGLNTHYRYIGKTMDYRGTMIPSEAP LLHRQVKLVDPMDRKPTEIEWRFTEAGERVRVSTRSGRIIPKPE FPRADGIVPETWIDGPKDTSVEDALERTYVPCLKTLQEEVMEAM GIKETR\NTRRSIGIEPGABQLLPNPCPSLEG 7004 121 2285 FLLPVLTSRSLRQPAVPHARLGGVEPAAMKSARAKTPRKPTVKK G\PKRTLKTQLG\TYCRVRPLGFPDQBCCIEVINNTTVQLHTPE GYRLNRNGDYKETQYSFKQVFGTHTTQKELFDVVANPLVNDLIH GKNGLLFTYGVTGSGKTHTMTGSPGEGGLLPRCLDMIFNSIGSF QAKRYVFKSNDRNSMDIQCEVDALLERQKREAMPNPKTSSSKRQ VDPEFADMITVQBFCKABEVDEDSVYGVFVSYIEIYNNYIYDLL EEVPFDPINPNLHNLNCFVKIKNHMYVAGCTEVEVKSTEEAFE	7003	818	61	
GKQGKVVQVIRQRNWVVVGGLNTHYRYIGKTMDYRGTMIPSEAP LLHRQVKLVDPMDRKPTEIBWRFTEAGERVRVSTRSGRIIPKPE FPRADGIVPETWIDGPKDTSVEDALERTYVPCLKTLQEEVMEAM GIKETR\NTRRSIGIEPGABQLLPNPCPSLEG 7004 121 2285 FLLPVLTSRSLRQPAVPHARLGGVEPAAMKSARAKTPRKPTVKK G\PKRTLKTQLG\TYCRVRPLGFPDQBCCIEVINNTTVQLHTPE GYRLNRNGDYKETQYSFKQVFGTHTTQKELFDVVANPLVNDLH GKNGLLFTYGVTGSGKTHTMTGSPGEGGLLPRCLDMIFNSIGSF QAKRYVFKSNDRNSMDIQCEVDALLERQKREAMPNPKTSSSKRQ VDPEFADMITVQBFCKABEVDEDSVYGVFVSYIBIYNNYIYDLL EEVPFDPINPNLHNLNCFVKIKNHMYVAGCTEVEVKSTEEAFE		0.10	91	
LLHRQVKLVDPMDRKPTEIEWRFTEAGERVRVSTRSGRIIPKPE FPRADGIVPETWIDGPKDTSVEDALERTYVPCLKTLQEEVMEAM GIKETR\NTRRSIGIEPGABQLLPNPCPSLEG 7004 121 2285 FLLPVLTSRSLRQPAVPHARLGGVEPAAMKSARAKTPRKPTVKK G\PKRTLKTQLG\TYCRVRPLGFPDQBCCIEVINNTTVQLHTPE GYRLNRNGDYKETQYSFKQVFGTHTTQKELFDVVANPLVNDLIH GKNGLLFTYQVTGSGKTHTMTGSPGEGGLLPRCLDMIFNSIGSF QAKRYVFKSNDRNSMDIQCEVDALLERQKREAMPNPKTSSSKRQ VDPEFADMITVQBFCKABEVDEDSVYGVFVSYIBIYNNYIYDLL EEVPFDPINPNLHNLNCFVKIKNHMYVAGCTEVEVKSTEEAFE				
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G\PKRTLKTQLG\/YYCRVRPLGFPDQBCCIEVINNTTVQLHTPE GYRLNRNGDYKETQYSFKQVFGTHTTQKELFDVVANPLVNDLIH GKNGLLFTYGVTGSGKTHTMTGSPGEGGLLPRCLDMIFNSIGSF QAKRYVFKSNDRNSMDIQCEVDALLERQKREAMPNPKTSSSKRQ VDPEFADMITVQBFCKABEVDEDSVYGVFVSYIBIYNNYIYDLL EEVPFDPINPNLHNLNCPVKIKNHMYVAGCTEVEVKSTEBAFE	7004	721	2205	
GYRLNRNGDYKETQYSFKQVFGTHTTQKELFDVVANPLVNDLIH GKNGLLFTYGVTGSGKTHTMTGSPGEGGLLPRCLDMIFNSIGSF QAKRYVFKSNDRNSMDIQCEVDALLERQKREAMPNPKTSSSKRQ VDPEFADMITVQBFCKABEVDEDSVYGVFVSYIBIYNNYIYDLL EEVPFDPINPNLHNLNCFVKIKNHMYVAGCTEVEVKSTEBAFE	/004	141	2285	
GKNGLLFTYGVTGSGKTHTMTGSPGEGGLLPRCLDMIFNSIGSF QAKRYVFKSNDRNSMDIQCEVDALLERQKREAMPNPKTSSSKRQ VDPEFADMITVQBFCKABEVDEDSVYGVFVSYIBIYNNYIYDLL EEVPFDPINPNLHNLNCFVKIKNHNMYVAGCTEVEVKSTEBAFE		1		
QAKRYVFKSNDRNSMDIQCEVDALLERQKREAMPNPKTSSSKRQ VDPEFADMITVQEFCKABEVDEDSVYGVFVSYIEIYNNYIYDLL EEVPFDPINPNLHNLNCFVKIKNHNMYVAGCTEVEVKSTEEAFE		ļ		
VDPEFADMITVQEFCKABEVDEDSVYGVFVSYIEIYNNYIYDLL EEVPFDPINPNLHNLNCFVKIKNHNMYVAGCTEVEVKSTEEAFE				
EEVPFDPINPNLHNLNCPVKIKNHNMYVAGCTEVEVKSTEEAFE		ł		
		Ì		
VFWRGQKKRRIANTHLNRESSRSHSVFNIKLVQAPLDADGDNVL	j	Į		
			~	VFWKGQKKRRIANTHLNRESSRSHSVFNIKLVQAPLDADGDNVL

SEQ	Predicted	Predicted end	Amino agid coment containing
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
!	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
İ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
J	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion.
	sequence		\=possible nucleotide insertion)
1			QEKEQITISQLSLVDLAGSERTNRTRAEGNRLREAGNINQSLMT
	1		LRTCMDVLRENOMYGTNKMVPYRDSKLTHLFKNYFDGEGKVRMI
1	i		VCVNPKAEDYEENLQVMRFAEVTQEVEVARPVDKAICGLTPGRR
Ì		1	YRNQPRGP\IGNEPLVTDVVLQSFPPLPSCEILDINDEQTLPRL
]			IEALEKRHNLRQMMIDEFNKQSNAFKALLQEFDNAVLSKENHMQ
i	İ		GKLNEKEKMISGQKLBIERLEKKNKTLBYKIEILEKTTTIYEED
1			KRNLQQELETQNQKLQRQFSDKRRLEARLQGMVTETTMKWEKEC ERRVAAKQLEMQNKLWVKDEKLKQLKAIVTEPKTEKPERPSRBR
ì		•	DREKVTQRSVSPSPVPVSYL
7005	63	876	RNMALYQRWRCLRLQGLQACRLHTAVVSTPPRWLAERLGLFEEL
		- · -	WAAQVKRLASMAQKEPRTIKISLPGGQKIDAVAWNTTPYQLARQ
1			ISSTLADTAVAAQVNGEPYDLERPLETDSDLRFLTFDSPEGKAV
			FWHSSTHVLGAAAEQFLGAVLCRGPSTEYGFYHDFFLGKERTIR
			GSELPVLERICQELTAAARPFRRLEASRDQLRQLFKDNPFKLHL
			IEEKVTGPTATVYGCGTLVDLCQGPHLRHTGQIGGLKLLSNSSS
nc			LWRSSG
7006	22	898	NAFGRHSTAVKMAAAAWLQVLPVILLLLGAHPSPLSFFSAGPAT
1			VAAADRSKWHIPIPSGKNYFSFGKILFRNTTIFLKFDGEPCDLS
1			LNITWYLKSADCYNEIYNFKAREVELYLEKLKEKRGLSGKYQTS
1		•	SKLFQNCSELFKTQTFSGDFMHRLPLLGEKQEAKENGTNLTFIG
			DKTAMHEPLQTWQDAPYIFIVHIGISSSKESSKENSLSNLFTMT
l			VEVKGPYEYLTLEDYPLMIFFMVMCIVYVLFGVLWLAWSACYWR DLLRIQFWIGAVIFLGMLEKAVFYAGFQ
7007	2	1001	AMTVSGPGTPEPRPATPGASSVEQLRKEGNELFKCGDYGGALAA
1			YTQALGLDATPQDQAVLHRNRAACHLKLEDYDKAETEASKAIEK
ì			DGGDVKALYRRSQALEKLGRLDQAVLDLQRCVSLEPKNKVFQEA
			LRNIGGQIQEKVRYMSSTDAKVEQMFQILLDPEEKGTEKKQKAS
	•		QNLVVLAREDAGAEKIFRSNGVQLLQRLLDMGETDLMLAALRTL
			VGICSEHQSRTVATLSILGTRRVVSILGVESQAVSLAACHLLQV
1			MFDALKEGVKKGFRGKEGAIIVGEWKQVWGLLDVTVMEGMGLSQ
7008			PGQFFGDQTCSCRLFGIRFGDIILL
/008	70	1478	CRSALGHERPPPAHLPAGGRRLQTCPRSCRWLGRPPSGLPPGPR
			SPPPLAGPGQKMVQKKPAELQGFHRSFKGQNPFELAFSLDQPDH
			GDSDFGLQCSARPDMPASQPIDIPDAKKRGKKKRGRATDSFSG
			RFEDVYQLQEDVLGEGAHARVQTCINLITSQEYAVKIIEKQPGH IRSRVFREVEMLYQCQGHRNVLELIEFFEEEDRFYLVFEKMRGG
)		SILSHIHKRRHFNELEASVVVQDVASALDFLHNKGIAHRDLKPE
			NILCEHPNQVSPVKICDFDLGSGIKLNGDCSPISTPELLTPCGS
	!		AEYMAPEVVEAFSEEASIYDKRCDLWSLGVILYILLSGYPPFVG
	ļ		RCGSDCGWDRGEACPACQNMLFESIQEGKYEFPDKDWAHISCAA
	1		KDLISKLLVRDAKQRLSAAQVLQHPWVQGCAPENTLPTPMVLQR
	· · · · · · · · · · · · · · · · · · ·		WDSHFLLPPHPCRIHVRPGGLVRTVTVNE
7009	1	626	ARQLRNSWVDDFVAAPLIPLSQQIPTGNSLYESYYKQVDPAYTG
			RVGASEAALFLKKSGLSDIILGKIWDLADPEGKGFLDKOGFYVA
1			LRLVACAQSGHEVTLSNLNLSMPPPKFHDTSSPLMVTPPSAEAH
1 1]	İ	WAVRVEEKAKFDGIFESLLPINGLLSGDKVKPVLMNSKLPLDVL
7010	79		GRVWDLSDIDKDGHLVRDEFAVAMHLVYRALE
'**	13	571	SHTRRAVVPETLLSPLCPLLGGGTAMSGGEQKPERYYVGVDVGT
	Ì		GSVRAALVDQSGVLLAFADQPIKNWEPQFNHHEQSSEDIWAACC
			VVTKKVVQGIDLNQIRGLGFDATCSLVVLDKQFHPLPVNQEGDS
7011	3	994	HRNVIMWLDHRAVSQVNRINETKHSVLQYVGG
	-	224	RIQTLPNQNQSQTQPLLKTPPAVLQPIAPQTTFGVQTQPQPQSL
	İ		LQAQISAASITPLLQTQPQPLLQQPQQKAGLLQPPVRIVSQPQP ARRLDPPSRFSGRNDRGDQVPNRKDDRSRERERERRRSRERSPQ
	Ì		RKRSRERSPRERERSPRRVRRVVPRYTVQFSKFSLDCPSCDMM
			ELRRRYQNLYIPSDFFDAQFTWVDAFPLSRPFQLGNYCNFYVMH
		 	

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
- 1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
Ì	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
- }	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
- 1	residue of	amino acid	W-Tomtonban V Tomos vivi
l	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	Sequence	Codon, /=possible nucleotide deletion,
<u> </u>	1 1 1		\-possible nucleotide insertion)
i			REVESLEKNMAILDPPDADHLYSAKVMLMASPSMEDLYHKSCAL
i			AEDPQELRDGFQHPARLVKFLVGMKGKDEAMAIGGHWSPSLDGP
7012	1	2661	DPEKDPSVLIKT\AIRCCKALTG
/	1 -	2001	RRAGSVKRGEARLFGPTERQSERPLRPSAARRPEMLSGKKAAAA
			AAAAAAATGTEAGPGTAGGSENGSEVAAQPAGLSGPAEVGPGA
ì	1		VGERTPRKKEPPRASPPGGLAEPPGSAGPQAGPTVVPGSATPME
ĺ	į.	ĺ	TGIAETPEG\RRTSRRKRAKVEYREMDESLANLSEDEYYSEEER
ı	1	i	NAKAEKEKKLPPPPPQAPPEEENESEPEEPSGVEGAAFQSRLPH
1	1		DRMTSQEAACFPDIISGPQQTQKVFLFIRNRTLOLWLDNPKIOL
	l		TFEATLQQLEAPYNSDTVLVHRVHSYLERHGLINFGIYKRIKPI.
1 .		}	PTKKTGKVIIIGSGVSGLAAARQLQSFGMDVTLLEARDRVGGRV
1			ATFRKGNYVADLGAMVVTGLGGNPMAVVSKOVNMELAKIKOKCP
			LYEANGQAVPKEKDEMVEQEFNRLLEATSYLSHOLDFNVLNNKP
[1		VSLGQALEVVIQLQEKHVKDEQIEHWKKIVKTOEELKELLNKMV
į.	[NLKEKIKBLHQQYKEASEVKPPRDITAEFLVKSKHRDLTALCKE
ľ			YDELAETQGKLEEKLQELEANPPSDVYLSSRDROILDWHFANLR
	!		FANATPLSTLSLKHWDQDDDFRFTGSHLTVRNGYSCVPVALAEG
1			LDIKLNTAVRQVRYTASGCEVIAVNTRSTSOTFIYKCDAVLCTT
ı			PLGVLKQQPPAVQFVPPLPEWKTSAVQRMGFGNLNKVVLCFDRV
	<u> </u>		FWDPSVNLFGHVGSTTASRGELPLFWNLYKAPILLALVAGEAAG
1			IMENISDDVIVGRCLAILKGIFGSSAVPQPKETVVSRWRADPWA
1			RGSYSYVAAGSSGNDYDLMAQPITPGPSIPGAPOPTPRIFFAGE
}	. 1		HTIRNYPATVHGALLSGLREAGRIADQFLGAMYTLPRQATPGVP
7013			AQQSPSM
/013	1	2661	RRAGSVKRGEARLFGPTERQSERPLRPSAARRPEMLSGKKAAAA
	l .		AAAAAAATGTEAGPGTAGGSENGSEVAAOPAGLSGPAFVGDGA
}			VGERTPRKKEPPRASPPGGLAEPPGSAGPQAGPTVVPGSATPME
1 :	,		TGIAETPEG\RRTSRRKRAKVEYREMDESLANLSEDEYYSEEER
			NAKAEKEKKLPPPPPQAPPEEENESEPEEPSGVEGAAFQSRLPH
1			DRMTSQEAACFPDIISGPQQTQKVFLFIRNRTLQLWLDNPKIQL
1 1			TFEATLQQLEAPYNSDTVLVHRVHSYLERHGLINFGIYKRIKPL
1 1			PTKKTGKVIIIGSGVSGLAAARQLQSFGMDVTLLEARDRVGGRV
1 1			ATFRKGNYVADLGAMVVTGLGGNPMAVVSKQVNMELAKIKQKCP
1			LYEANGQAVPKEKDEMVEQEFNRLLEATSYLSHQLDFNVLNNKP
1 1			VSLGQALEVVIQLQEKHVKDEQIEHWKKIVKTQEELKELLNKMV
			NLKEKIKELHQQYKEASEVKPPRDITAEFLVKSKHRDLTALCKE
1 1	i		YDELAETQGKLEEKLQELEANPPSDVYLSSRDRQILDWHFANLE
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1 1			LDIKLNTAVRQVRYTASGCEVIAVNTRSTSQTFIYKCDAVLCTL
1 1			PLGVLKQQPPAVQFVPPLPEWKTSAVQRMGFGNLNKVVLCFDRV
1		•	FWDPSVNLFGHVGSTTASRGELFLFWNLYKAPILLALVAGEAAG
1 1		1	IMENISDDVIVGRCLAILKGIFGSSAVPQPKETVVSRWRADPWA
	ļ	.1	RGSYSYVAAGSSGNDYDLMAQPITPGPSIPGAPQPIPRLFFAGE
1 1	1		HTIRNYPATVHGALLSGLREAGRIADQFLGAMYTLPRQATPGVP
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	1	Į.	ETMALPQEGSLARIPETSLDCLENTLGVEEQRHETSDHEAEEPD
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[[l	}	PLATDSPTSDPTEVVNGISSQPQVPFHPNLOKSOYYSTVGGSHP
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		1	SVSASRVVKPRQSSPQLHNLASYTKKHHTSSVYSISERLEMKPG
] [1	PQAQGLVMEAATHSQGDGSTDLDSKLTQQLIEFEKSLAGPGTEP
1		į.	DKILRHFSIMDFNSEKDIVRGSSKLITEOELPERRKALRPPDDD
		- 1	PCTPVSTSPHLLVDQNLKPAPPLVVRPSRPAPLPPSAOORTNAV
1 1		i	SPKLLSRHRPTCETLEKEGPGHMGRSLDOTSPCPLVLVRIERME
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TOTAPO INDEVPETERINFRMOERLIKESTIRDISLIKLOHIRES ACVEVVANAVEMBUNDELGEPERUNTELOSPTINKER TERLVISSIMOLISMITOPHKLUORREPOKLLDFYNCTERREKLK DEKTLEELOSARUNYBALMAQLLDELPKEHOYAQCEPTUCHGY ARHCOFYHOALEQUKPULDELKVAGREGORLTAITHEBERSVLQ UCQVETFFPESLEATKKFFERKTIRGSARKELIGLISVANLOSE ELRASLLARYPERKFFERKTIRGSARKELIGLISVANLOSE ELRASLLARYPERKFFERKTIRGSARKELIGLISVANLOSE ELRASLLARYPERKFFERKTIRGSARKELIGLISVANLOSE ELRASLLARYPERKFFERKTIRGSARKELIGLISVANLOSE ELRASLLARYPERKFFERKTIRGSARKELIGLISVANLOSE ELRASLLARYPERKFFERKTIRGSARKELIGLISVANLOSE DPMSSQNRWILDDGVIKGFYVSSFIKEYNPRRSHBDANSVERSSES TESSENGSSSPFPRORGOSTILTNIN)\S\AMVASTIGSGCOKOPQ DASPPREMOGOTLASAINDSNESSPSCFSDPDSTSGCOKOPQ CARTAQAPEDRSTEPDGSEAEGROVYPAVTTKRANDRIELSVSA NOKKILLEFRAVORTOTERWILSVANKKOVOPAVATKRASPENDLISVSA NOKKILLEFRAVORTOTERWILSVANKKOVOPAVATKRASPENDELSVSA NOKKILLEFRAVORTOTERWILSVANKKOVOPAVATKRASPEDS SVITCVPAVSHMINDEQUVILVHHPDMENSRYLRVILVAGAPRAG KSTISNOLLORKVFVSRKVHTTRCOALGVITEKSTOVILLDITP GIISPGKRKHHLEISLLEDPHENKENSBALUVVILDVISDKWTRN OLSPOLLRCITKYSOIPSVLVMNKVOLCKKKSVILLELTAALTEG VVNKKLMERGAPHSHEGTICSPAVEDNYRONGOIGHENDE FKEIPMLSALSQEDVKTIKGYLLTDAQDGFBEYHSAVLTISOTPE BICANTISRKLEHLDSVEDPHYNOKOMEORIGHENTSV LUVRESYVKLLIGPKGHVISQIAQEAGHDIMDIFLCOVDIRLSV KLLK 7016 167 2513 TIANSPFPPPBBSVERVANAKRDTGGGSKGTGNDVSGOETDWEST AFROKLUSGIADAMRKAGVAHSKSKNDMESHYFIKKANTEGVILE LVARLITHREDHINKKSGASVSDPMNALOSILTGGPAAGAAGIGM PPROPOGSLGGMGSLGANGQAPSLGGOPPOTSKGMAPHMAVVS TATTGTOLOLQOQUADAAAAATRASSSSSERREXYSSSSSSSNSK GOQAQSAMQO\GFOA\VVQQQQQQQQQQULIKILHINNQ QIQQQQATAOTAQAAQAMAPGVOVSQSSLPMLSSPSFSGOQVOTP QOXOQTAVOTAQAAQAMAPGVOVSQSSLPMLSSPSFSGOQVOTP QOXOQTAVOTAQAAQAMAPGVOVSQSSLPMLSSPSFSGOQVOTP QOXOQTAVOTAQAAQAMAPGVOVSQSSLPMLSSPSFSGOQVOTP QOXOQTAVOTAQAAQAMAPGVOVSQSSLPMLSSPSFSGOQVOTP QOXOQTAVOTAQAAQAMAPGVOVSQSLPMLSSPSFLESPSDOPP SKRCDLKTLCKKESTAAREKKOLLARYPSPYPTTRAQOCSSVACLARYPSTYCKKOLD. KLDDKOLFSVPFIELSVPADPTPAGSPGLANDGCSSVLRKICHL KLDDKOLFSVPFIELSVPADPTPAGSPGLANDGCSSVLRKICHL KLDDKOLFSVPFIELSVPADPTPAGSPGLANDGCSSVLRKICHL KLDDKOLFSVPFIELSVPADPTPAGSGOCSSTLPFLIDTD SKRCDLKKICHTHANGSVAGARATOLISLARPPS YSLEWISCPOCSSSS		!		
ACVEVVAAVSWEDVCMERGHEDLEGPERVHRYTSDOLETNIKEER TERLVISPINGLISMITEGPHKLVQKREDIDFNICTEERREKLK DEKTLEELQSARNNYEALNAGLLDELPKFHQYAGGLFTNCVHGY AEAHCDFVEQALEGLEKPLISLEKVAGREGNILTIFTEERSKYLGE GLOVFIFTPESIPATKER PERKTITERGSARKPLIGJESVILGE ELRASILARYSPEKLEGAERNFNAADDLDVSLLEGDLVGVIKKS DPMGSQNRAILDNGVIKGVYSSILKEYNERSHODAVGSHSS TESSHGSSSPEPPRQNSGSTLTPHFN\S\MAVSTSGSCOKOPO DASPPEKEMDGOTLSASLANDSNISSSSSPEDPSTSGORDIJVKG CARTAQAPEDSSTEPIOSEBERGNOVYFAVYTFKARPNELSVAS ADVARDVKQPTATPRSYNDYEHEETVGYSVPGGNGGSGOLVKG CARTAQAPEDSSTEPIOSEBERGNOVYFAVYTFKARPNELSVAS AQKLKILEFKDVTGNTEWLLEVNGKGVVPSNYIRKTEYT 7015 1842 513 RQAMER\VAAPSHRGARLVGSVLKVWGVOPHVAAERSYT GGGRCVSCVGAGSAFSGPEALSARSRGNGGSALDHFLGSSQDS SVTTCVPAVSHNINDEGOVLLVHHEDMENSKVLKVVLLGADNAG KSTLSNGLLGKKVFPVSRKYHTTRCOALDSKHTFFSSLL GISPOKKGRHHLELSLLSDPMKSMSADLVVVLVDDSKWTRN QLSFOLLBGLTKYSOIPSVLVANNVCUCKGVSLLELTAATTEG VVNGKKLKMGQAFHSHGTHCCSSDAVEDDNTQSVGBRGIGWPH FKEIFMLSALGGBOVTLKKYQDIPSVLVANNVCUCKGVLLELTAATTEG VVNGKKLKMGQAFHSHGTHCCSSDAVEDDNTQSVGBRGIGWPH FKEIFMLSALGGBOVTLKGVYLDVANVCUCKGVLLEUTAATTEG VVNGKKLKMGQAFHSHGTHCCSSDAVENDSTGGGEDIVGGKL LVFRESYVELLIGFKGHVISQIAQEAGHDLMDIFLCVDVIRLSV VNGKKLKMGQAFHSHGTHCCSSGAVGTMMVSGGETDWRST KLLK 7016 167 2513 ILMAPKPPPPERDSVEAVAAKRDTIGGSMGTGMDVSGGETDWRST KLLK FROKLVSSGIBDAMRRAGVARSKSSKOMBSHVFLKAKTRBEYLS LVARLI HIFRDIINKKSGASVSDPMRALGSLTGGAAAGAGIGM PPRGGGGGGLGGMGGLGAMGAMSHSKSKOMSHVFLKAKTRBEYLS LVARLI HIFRDIINKKSGASVSDPMRALGSLTGGAAAAGAGIGM PPRGGGGGGLGGMGGLGAMGAMSHSKSKOMSHVFLKAKTRBEYLS LVARLI HIFRDIINKKSGASVSDPMAALGSLTGGAAAAGAGIGM PPRGGOGGGLGGMGGLGAMGAAAAAATARSSSSSSRNKK POAQQSAMQQQQCAQQQCALQAGPFTQGP PMQQPGPPSGAALGOQCQQQQQQQQQQCALQAGPFTQGP PMQQPGPPSGAALGOQCACQQQCQQQQQQQCALQAGPFTQGP PMQQPGPPSGAALGOQCACQQCQQQQQQQQQCALQAGPFTQGP PMQQPGPPSGAALGORALTTGPILKFYARMVVQQPPVQ QVQQQCTAVOTAQAAAAAAATARSSSSSSRNKKSLLDLITD SKCCPLKTLQKCSLALEKLXDDMAYFTPPAPPPVQCTRK RLEDDERGSTFSVTGCFSVAFGAGATATHLLICFTTTTAAF RLEDDERGSTFSVTGCFSVAFGAGACASAA THESDERGSTPSVTGCFSVAFGAGACASAA THERCHTSRLLGLPKHAFTATHAAATTHABPITAAPPVCTTRK RLEDDERGSTFSVTGCFSVAFGAGAGAGCQCC GGGCTGSVTGVTULLTTTAAFTGGAGAAAAATTHA	1	}		
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LLDAVLANIRSPVFNHSLYRTFVPAMTAIHGPPITAPVVCTRKR RLEDDERQSIPSVLQGEVARLDPKFLVNLDPSHCSNNGTVHLIC KLDDKDLPSVPPLELSVPADYPAQSPLWIDRQWQYDANPFLQSV HRCMTSRLLQLPDKHSVTALLNTWAQSVHQACLSAA 7017 1 1785 INLGNTCYMNSVI*ALFMATDFRRQVLSLNLNGCNSLMKKLQHL FAPLAHTQREAYAPRIFFEASRPPWFTPRSQQDCSEYLRFLLDR LHEEEKILKVQASHKPSEILECSETSLQEVASKAAVLTETPRTS DGEKTLIEKNFGGKLRTHIRCLNCRSTSQKAEAFTDLSLAFWPS YSLEYMSCPDCSQSPSIQDGGLMQASVPGPSEEFVVYNPTTAAF ICDSLVNEKTIGSPPNEFYCSENTSVPNESNKILVNKDVPQKPG GETTPSVTDLLNYPLAPEILTGDNQYYCENCASLQNAEKTMQIT		İ		
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LHEEEKILKVQASHKPSEILECSETSLQEVASKAAVLTETPRTS DGEKTLIEKMFGGKLRTHIRCLNCRSTSQKAEAFTDLSLAFWPS YSLEYMSCPDCSQSPSIQDGGLMQASVPGPSEEFVVYNPTTAAF ICDSLVNEKTIGSPPNEFYCSENTSVPNESNKILVNKDVPQKPG GETTPSVTDLLNYPLAPEILTGDNQYYCENCASLQNAEKTMQIT	1011	1	1785	_
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The state of the s	L			EEPEYLILTLLRFSYDQKYHVRRKILDNVSLPLVLELPVKRITS

SEQ	Predicted	Predicted end	Amino not?
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
- 1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ĺ	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	1	\=possible nucleotide insertion)
1		······································	FSSLSESWSVDVDFTDLSENLAKKLKPSGTDEASCTKLVPYLLS
[1	SVVVHSGISSESGHYYSYARNITSTDSSYQMYHQSEALALASSQ
ļ		İ	SHLLGRDSPSAVFEQDLENKEMSKEWFLFNDSRVTFTSFQSVQK
		}	ITSRFPKDTAYVLLYKKQHSTNGLSGNNPTSGLWINGDPPLQKE
1			LMDAITKDNKLYLQEQELNARARALQAASASCSFRPNGFDDNDP
<u> </u>	<u> </u>		PGSCGPTGGGGGGFNTVGRLVF
7018	484	1066	SLVFRGNTWSGEAGHHCSALFNLAAYHOLFVGTERTRAPETTFO
1			PSLIGEEQAGIAETLQYILDRYPKDVOEMLVONVFLTGGNTMYP
1	1		GMKARMEKELLEMRPFRSSFQVQLASNPVLDAWYGARDWALNHI.
i			DDNEVWITRKEYEEKGGEYLKEHCASNIYVPIRLPKQASRSSDA
7019			QASSKGSAAGGGGAGEQA
1019	1048	335	APGGFLVTMVFPAPSPPWMLGCCSHEVTAGPPTLCKDMSALVAA
1			RMRHIPLAPGSDWRDLPNIEVRLSDGTMARKLRYTHHDRKNGRS
			SSGALRGVCSCVEAGKACDPAAROFNTLIPWCLPHTGNRHNHWA
1	i i		GLYGRLEWDGFFSTTVTNPEPMGKQGRVLHPEQHRVVSVRECAR
1			SQGFPDTYRLFGNILDKHRQVGNAVPPPLAKAIGLBIKLCMLAK
7020	1	2154	ARESASAKIKEEEAAKD
1		2134	FADSKRKSVLLDKIKNLQVALTSKQQSLETAMSFVARNTFKRVR
1			NGFLMRKVAVFFSNTPTRASPQLREAVLKLSDAGITPLFLTRQE
1			DRQLINALQINNTAVGHALVLPAGRDLTDFLENVLTCHVCLDIC
1	}	•	NIDPSCGFGSWRPSFRDRRAAGSDVDIDMAFILDSAETTTLFQF
			NEMKKYIAYLVRQLDMSPDPKASQHFARVAVVQHAPSESVDNAS MPPVKVEFSLTDYGSKEKLVDFLSRGMTQLQGTRALGSAIEYTI
			ENVFESAPNPROLKIVVLMLTGEVPEQQLEBAQRVILQAKCKGY
1 1			FFVVLGIGRKVNIKEVYTFASBPNDVFFKLVDKSTELNEEPLMR
1			FGRLLPSFVSSENAFYLSPDIRKQCDWFQGDQPTKNLVKFGHKQ
			VNVPNNVTSSPTSNPVTTTKPVTTTKPVTTTTKPVTTTTKPVTI
1 1			INOPSVKPAAAKPAPAKPVAAKPVATKTATVRPPVAVKPATAAK
1 .	1		PVAAKPAAVRPPAAAAAKPVATKPEVPRPQAAKPAATKPATTKP
} !			MVKMSREVQVFEITENSAKLHWERPEPPGPYFYDLTVTSAHDQS
1			LVLKQNLTVTDRVIGGLLAGQTYHVAVVCYLRSOVRATYHGSFS
))	J		TKKSQPPPPQPARSASSSTINLMVSTEPLALTETDICKLPKDEG
1. 1			TCRDFILKWYYDPNTKSCARFWYGGCGGNENKFGSQKECEKVCA
7021			PVLAKPGVISVMGT
,021	2	338	VNAVSFFPNGYAFATGSDDATCRLFDLRADQELLLYSHDNIICG
	1		ITSVAFSKSGRLLLAGYDDFNCNVWDTLKGDRAGVLAGHDNRVS
7022	2	000	CLGVTDDGMAVATGSWDSFLRIWN
	~	856	VYIGSFWSHPLLIPDNRKLFEAEEQDLFRDIQSLPRNAALRKLN
	.]		DLIKRARLAKVHAYIISSLKKEMPSVFGKDNRKKELVNNLAEIY
	ļ		GRIEREHQISPGDFPNLKRMQDQLQAQDFSKFQPLKSKLLEVVD
] . []	j	DMLAHDIAQLMVLVRQEESQRPIQMVKGGAFEGTLHGPFGHGYG
]	. 1	}	EGAGEGIDDAEWVVARDKPMYDEIFYTLSPVDGKITGANAKKEM
]].			VRSKLPNSVLGKIWKLADIDKDGMLDDDEFALANHLIKVKLEGH ELPNELPAHLLPPSKRKVAE
7023	2	748	AMVFGGVVPYVPQYRDIRRTQNADGFSTYVCLVLLVANILRILF
		· = -	WFGRRFESPLLWQSAIMILTMLLMLKLCTEVRVANELNARRRSF
	1		TAADSKDEEVKVAPRRSFLDFDPHHFWQWSSFSDYVQCVLAFTG
]	ĺ	VAGYITYLSIDSALFVETLGFLAVLTEAMLGVPQLYRNHRHQST
l			EGMS I KMVLMWTSGDAFKTAYFLLKGAPLQFSVCGLLQVLVDLA
			ILGQAYAFARHPQKPAPHAVHPTGTKAL
7024	1207	190	RTGVTGVVAQVWMFGGGGVLSSGEQLQMPVKPERGLGPSDGWLV
			SSRRGSPGTVLGLPFWLLTPVLVSRSIRSMLLLTRSPTAWHRLS
1			QLKPPVLPGTLGGQALHLRSWLLSRQGPABTGGQGQPQGPGLRT
		j	RLLITGLFGAGLGGAWLALRAEKERLQQQKRTEALRQAAVGQGD
 	•	1	FHLLDHRGRARCKADFRGQWVLMYFGFTHCPDICPDELEKLVQV
		ł	VRQLEAEPGLPPVQPVFITVDPERDDVEAMARYVQDFHPRLLGL
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SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	Hahistidine, IaIsoleucine, Kabysine,
İ	corresponding	to first	LaLeucine, Mamethionine, Nasparagine,
ĺ	to first	amino acid	PeProline, Q=Glutamine, R=Arginine,
ŀ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
<u> </u>	sequence		\=possible nucleotide insertion)
			TGSTKQVAQASHSYRVYYNAGPKDEDQDYIVDHSIAIYLLNPDG
<u></u>	L		LFTDYYGRSRSAEQISDSVRRHMAAFRSVLS
7025	232	832	ERNSPIGNNENL*K\HSLDCLCFRGDWEGNTQFQTLQDNQBECF
1			KQVIRTCEKRPTFNQHTVFNLHQRLNTGDKLNEFKELGKAPISG
}			SDHTQHQLIHTSEKFCGDKECGNTFLPDSEVIQYQTVHTVKKTY
1			ECKECGKSFSLRSSLTGHKRIHTGEKPFKCKDCGKAFRFHSQLS
<u> </u>			VHKRIHTGEKSYECKECGKAFSCG
7026	328	1146	NPNPSIGDIKDIKKAAKSMLDPAHKSHFHPVTPSLVFLCFIFDG
	[LHQALLSVGVSKRSNTVVGNENEERGTPYASRFKDMPNFIALEK
			SSVLRHCCDLLIGVAAGSSDKICTSSLQVQRRFKAMMASIGRLS
			HGESADLLISCNAESAIGWISSRPWVGELMFTFLFGDFESPLHK
ſ			LRKSS*LPRKHR*QPINAVRMFLDQCMDGSIALRAIVSEIPVFE
i			BKKNNG*KGIGEIF*VWGCTLPPHYWGAVTTNVPKLSNSGKLLG
			QDEQPHIFG
7027.	43	954	GRRLQQQQRPEDAEDGAEGGGKRGEAGWEGGYPEIVKENKLPEH
			YYQELKIVPEGEWGQFMDALREPLPATLRITGYKSHAKEILHCL
1			KNKYFKELEDLEMDGQKVEVPQPLSWYPEELAWHTNLSRKILRK
1			SPHLEKFHQFLVSETESGNISRQEAVSMIPPLLLNVRPHHKILD
1			MCAAPGSKTTQLIEMLHADMNVPFPEGFVIANDVDNKRCYLLVH
		•	QAKRLSSPCIMVVNHDASSIPRLQIDVDGRKEILFYDRILCDVP
7000			CSGDGTMRKNIDVWKKWTTLNSLQLHGLOLRIATRGAEOL
7028	189	608	SRPPPEPEPGTMVEKGSDSSSEKGGVPGTPSTQSLGSKNFIRNS
1 J			KKMQSWYSMLSPTYKQRNEDFRKLFSKLPEAERLIVDYSCALOR
	1		EILLQGRLYLSENWICFYSNIFRWETTISIQLKEVTCLKKEKTA
7029			KLIPNAIQ
1029	1343	40	VLESNTEAKQATGTSSKLRHGTGQEKGREGPRCPSGLAQLRLWG
	1		/PCPHAGRETGPRASAPIPGS*GHGWHW*RKDGRGERSEGPSAL
1			SPHSPSLLNMQQAPTHVGPGMGSQRPRSSVVPEQVGVGSQLSRE
1 1			RWRA*RSLPGAAASERTEMTKERSP/RPCQGYDSSNWFTQPGKK
1 1			TRKRNSRRNTMVSRGGGCLLYPLQSIMPE*QLR*GAHASPPTQG
1 1	1		R*GKGGPRSPLTKASGTTHIPTPFFGSIP/RPTRDSGPGTDNS\
i 1	• [AAPGQKRGHREA*QGPEPV/WGRVTTHLQGPAG*TKPLGS\RNW
1 1	}		VPGPAEGEQGEGAGLEGRP*PLKGCRSTLTFSPQLSIPMVGKKP
1			PEGTTASFFF\RSCHSE*RKPPPSCPHAPALSLPHPLPLPLPL
1 1			PLPLPGAGT*HSARSGRPGQSETGSLCHNCHHCPPHCPKCSPGG T
7030	2	521	1 -
i l	- ,		FVCFSAPGSGGGKRRVNMELSAVGERVFAAEALLKRRIRKGRM
	·		EYLVKWKGWSQKYSTWEPEENILDARLLAAFEEREREMELYGPK KRGPKPKTFLLKAQAKAKAKTYEFRSDSARGIRIPYPGRSPQDL
1	· 1		ASTSRAREGLRN\RVCPRQRAAPAPAP\PRRGPSGFGPRPG*G
j l			PGLHFPGPGGPSKHGFVPASEQHQHQQHLPRRGPSGPGPRPG
7031	960	59	HCSVPGAEWPRKPPAQICPQLTSRPHLSSPRSLSPGCGHSPGPG
]	1		/CKPS/RHCDELHEGPSRTAALPCGKPQPKHGVEECG/PCPCLA
[[ľ		PRRLTEPPALTVSPVGRAAPSGAL*PSGRACSACSHRLAPEAAL
] [SAAAPRPSLGSGQNASGLPAASLPPQDSSQPHKTVPSPARSVPP
[]	1	ļ	LGAQARAAPPRLWCPRALVSG*EASPEAVSVAAGPPVPGGTTPST
'	1		SGSTASHSRRGC*SPR*TPAPPRRDHGRSAAFEVLTAAASAQPC
L I	1		ASQGGPRPTGAGRTPSPLGLPFSRGPPAASARPFCRHPSL
7032	1393	2104	RRPGRTEPVEPPPVPPPPRASNSKSRCR*RNLHLAPL*QSPLRK
	1	· · · · · · · ·	SRQIGTSSLPFGRSAGERPRPAATFCLSRGGSSPVFL*PSSSSL
	J		EPWMKRQFGRLHSLFWKSWQKMNSPLLTPKLDTSLMSGWRYRQR
		[LPRLHTFLKKSLQMASELAPPLPTPAPLASSLPPPPGPPPLLPV
			PLA+LSRSGILVPPNSGFSLSC\PLGDH+GSSGEVRGSCGSPPP
		1	HHCWVLPPPP*LLLPPR
7033	689	815	RSRDCLSSSATSNRARRSKCSGPKRATPLDSGPGP*APPGPSSA
	······································		TOTAL CONTROL ROAT FEB 3 GF GF APPGPSSA

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ŀ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
İ	sequence	1 3	\=possible nucleotide insertion)
	 		LMMPSSCPWRTGALGPSPAGSRALGRCTSSVGPGSRWLTRTSSP
1		ŀ	GCATRIWRTMRMEPRPLRSRMGESAPGIPAELPSAAPSGPSAPS
1	ļ		AAAPSAPTTPAAAGPNTL*SRRTAEWCWPPSCSCCWGWC*SWSA
			WDWRRPPLQVSPAPSSSCRASCCWCLESIT*SSSTARSRATGAS
1			SSSTCPTSRSDRGAAWTP\SPMGAPLLPCSVPLISREEALQDPR
	j		NPSP*GVCSGSSGHAGLALGKPPVACSVP
7034	92	1942	EDTSSMPFRLLIPLGLLCALLPQHHGAPGPDGSAPDPAHYRERV
	1	17.2	KAMFYHAYDSYLENAFPFDELRPLTCDGHDTWGSFSLTLIDALD
			TLL\TLFYFQILGNVSEFQRVVEVLQDSVDFDIDVNASVFETNI
1	Ì		RVVGGLLSAHLLSKKAGVEVEAGWPCSGPLLRMAEEAARKLLPA
}			FQTPTGMPYGTVNLLHGVNPGETPVTCTAGIGTFIVEFATLSSL
į.			TGDPVFEDVARVALMRLWESRSDIGLVGNHIDVLTGKWVAQDAG
ì			IGAGVDSYFEYLVKGAILLQDKKLMAMFLEYNKAIRNYTRFDDW
l			YLWVQMYKGTVSMPVFQSLEAYWPGLQSLIGDIDNAMRTFLNYY
1		!	TVWKQFGGLPEFYNIPQGYTVEKREGYPLRPBLIESAMYLYRAT
1			CODTILEI CODAVECTRA CAMEGORA MINDERS DE COMPANIO
1			GDPTLLELGRDAVESIEKISKVECGFATIKDLRDHKLDNRMESF
			FLAETVKYLYLLFDPTNFIHNNGSTFDAVITPYGECILGAGGYI FNTEAHPIDPAALHCCQRLKEEQWEVEDLMREFYSLKRSRSKFQ
1			KNTVSSGPWEPPARPGTLPSPENHDQARERKPAKQKVPLLSCPS
			QPFTSKLALLGQVFLDSS*PLDNFFIFIFLRLNYNKLLLAIIKK
			K K
7035	92	1942	EDTSSMPFRLLIPLGLLCALLPQHHGAPGPDGSAPDPAHYRERV
			KAMFYHAYDSYLENAFPFDELRPLTCDGHDTWGSFSLTLIDALD
			TLL\TLFYFQILGNVSEFQRVVEVLQDSVDFDIDVNASVFETNI
	ĺ		RVVGGLLSAHLLSKKAGVEVEAGWPCSGPLLRMAEEAARKLLPA
1			FQTPTGMPYGTVNLLHGVNPGETPVTCTAGIGTFIVEFATLSSL
			TGDPVFEDVARVALMRLWESRSDIGLVGNHIDVLTGKWVAQDAG
1			IGAGVDSYFEYLVKGAILLQDKKLMAMFLEYNKAIRNYTRFDDW.
1 ' 1		,	YLWVQMYKGTVSMPVFQSLEAYWPGLQSLIGDIDNAMRTFLNYY
1			TVWKQFGGLPEFYNIPQGYTVEKREGYPLRPELIESAMYLYRAT
1			GDFTLLELGRDAVESIEKISKVECGFATIKDLRDHKLDNRMESF
) .			FLABTVKYLYLLFDPTNFIHNNGSTFDAVITPYGECILGAGGYI
			FNTEAHPIDPAALHCCQRLKEEQWEVEDLMREPYSLKRSRSKFQ
	1		KNTVSSGPWEPPARPGTLPSPENHDQARERKPAKQKVPLLSCPS
			QPFTSKLALLGQVFLDSS*PLDNFFIFIFLRLNYNKLLLAIIKK
1	j		K K
7036	442	761	CLAPLFSCFQIINLHLAPSGRLRWAWLRGPGRN*LPGEGPSIPT
1	į	·	RNW*BRKAGCSQPC/PAQQHHGRPPGVSPLPRDPHPTTLRPLPP
1 1	• • [PPPPPPPPPPRRPPRNRRPG
7037	442	761	CLAPLFSCFQIINLHLAPSGRLRWAWLRGPGRN*LPGEGPSIPT
]	-		RNW+ERKAGCSQPC/PAQQHHGRPPGVSPLPRDPHPTTLRPLPP
}	ļ		PPPPPPPPPRRPPRNRRPG
7038	155	891	
, · · · · · · · · · · · · · · · · · · ·		V-1	GAGAASDMSSGLRAADFPRWKRHISEQLRRRDRLQRQAFEEIIL OVNKILLEKSDLEGU ACKLOAEKUDVANDUELORGUDGE
1 1		ļ	QYNKLLEKSDLHSVLAQKLQAEKHDVPNRHEISPGHDGTWNDNQ
	1		LQEMAQLRIKHQEELTELHKKRGELAQ\RVIDLNNQMQRKDREM
		į	QMNEAKIAECLQTISDLETECLDLRTKLCDLERANQTLKDEYDA
ļ [LQITFTALEGKLRKTTEENQELVTRWMAEKAQEANRLNARE*KR
7039	155	891	LQEAASPAAERACRSSKGTSTSRTG
'		031	GAGAASDMSSGLRAADFPRWKRHISEQLRRRDRLQRQAFEEIIL
]			QYNKLLEKSDLHSVLAQKLQAEKHDVPNRHEISPGHDGTWNDNQ
l i			LQEMAQLRIKHQEELTELHKKRGELAQ\RVIDLNNQMQRKDREM
		İ	QMNEAKIAECLQTISDLETECLDLRTKLCDLERANQTLKDEYDA
			LQITFTALEGKLRKTTEENQELVTRWMAEKAQEANRLNARE*KR
7040	34	700	LQEAASPAAERACRSSKGTSTSRTG
,,,,,	34	789	KITPPRRPHRCSSGHGSDNSSVLSGELPPAMGKTALFYHSGGSS
		<u></u> -	GYESVMRDSEATGSASSAQDSTSENSSSVGGRCRSLKTPKKRSN

Doginning location	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Notation Corresponding	1			(A=Alanine, C=Cysteine, D=Aspertic Acid B
corresponding to first and mino acid amino first according to the first according to	NO:		location	Glutamic Acid, F=Phenylalanine, G=Glycine
to first amino acid residue of amino acid residue of amino acid residue of amino acid sequence sequenc	1	l .		H=Histidine, I=Isoleucine, K=Lysine
amino acid residue of amino acid residue of amino acid	1		1	L=Leucine, M=Methionine, N=Asparagine,
xesidue of amino acid sequence	ŀ		1	P=Proline, Q=Glutamine, R=Arginine.
amino acid sequence Codon, /-possible mucleotide deletion, -possible mucleotide insertion)	}		I .	S=Serine, T=Threonine, V=Valine,
Sequence A-possible nucleotide insertion	1			W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
PGGGRRLIPALSLUTSSPVRKPRNSTOVRNUGDFLRSSPRGLG EPFEINVTEIDDVERLORRRGGASKEAMCTMAKLKTLEHROGNE ALVVEALSCUTERLESSKVBCCKHILMMITCFDIT 567 SGRVANGRRRAPAGSGIGRALMRGTORSRSHRHTDSNLHTSEL NDGYDMGKLNLGSVTEGSSLDDFLATAELAGTEFVAKKINTHSEL NDGYDMGKLNLGSVTEGSSLDDFLATAELAGTEFVAKKINTHSEL LKQAEKDHFLENRRGLVALLEERGKLILTPFERNLDFWRQMTTEE LKQAEKDHFLENRRGLVALLEERGKLILTPFERNLDFWRQMTV LERSDITVQTVUA 7 345 PIHMAAALBRDT\SDLFPHIQGYLLLSASHG\ATSLHTKGAL PLETVTMTVIDESKYVULKOPDVYSENLDEFKRLARSAN DDLLMABWAISDVGOKLTLEIREKY ARGMARESDISEEDLVSVGTGLEFLEERGKFKHEIPGDVTVRD EKGRYKRFHGAFSGGFSACYENTVGSKEGHTEFTVSSKORRAD KSYLGPEPHOEGULSSKYTULKOPDVYSENLDEFKRLARSAN DDLLMABWAISDVGOKLTLEIREKY ARGMARESDISEEDLVSVGTGLEFLEERGKFKKFIELDDVTVRD EKGRYKRFHGAFSGGFSACYENTVGSKEGHTEFTVSSKORRAD KSYLGPEPHOEGULSSKYTULKSUGGELLERGKKEGGCOVGF RVKRRPRGEPPHOEGULSSKINGVLLISGGAFVCALEEGDDTVLDTWTA APKDVTPVDTTRONVGLAVKGLSGVGELTVSSKORRAD KSYLGPEPHOEGULSSKINGVLLISGGAFVCALEEGDDDTVLATETI-S APKDVTPVDTFRONVGLAVKGLOFFGSSSGSEGDDDTVLDDWTATETI-S APKDVTPVDTFRONVGLAVKGLOFFGSSGSEGEDDDTVLATETI-S KYDTVLKDEERGODLVAVTARGYNGKGESKOLTSEIFHLESGG SERAGDLOEIGINKGRKLISGGAFVCALEEEDDDTVATETI-S KYDTVLKDEERGOOLVAVTARGYNGKGESKOLTSGATSVLEF LSCKKERIKEKKOATDLKAAQLKARSI-AQNACSSRAOPSPAA AGICKSKNNALIGGTATTLKASNEFFYAKDELGEFTPLOGSATSVLEF LSCKKERIKEKKOATDLKAAQLKARSI-AQNACSSRAOPSPAA AGICKSKNNALIGGTATTLKASNEFFYAKDERGEKVEPT-VINEKA GOXDALERCLDPSWTEKREGEERDFRAAALLYASSHETLSDTFOR HPDKLLFO/ALVGLPEVKRBUKTSVFNFLITTPETASLFTTOASSE KVSQNGPBEKSREFSKROTSKHEKKEDSISEFFIRLARSKAEPPY QOSSPLIVKEEHAPLISAN FORTHER AND AND AND AND AND AND AND AND AND AND	1	l	sequence	Codon, /=possible nucleotide deletion,
REPETENVELIDUVERLOGRREGGASKEAMCTNAKLKILLERROGRI AEUVRAKYEMIKELEATROYLUMLDNIKULSELGWYELDSILED TUEALECVTERLESRUNDCKAHLMAITTEFDIT TO 567 SERVAMORRARPAGGGLGRAKHMAITTEFDIT NOGDMORLINLOSVTEQSLDDPLATAELAGTEPVASKLINLEV PARARTIGLISESSESORIKKHENHENKOPLOT PRERVINCATTPEE LKOAEKOWFLENBROGLVERLERSORIKKHENENGPLOT PRERVINCATTPEE LKOAEKOWFLENBROGLVERLERSORIKHENENGPLOT PRERVINCATTPEE LKOAEKOWFLENBROGLVERLENDENGLERV TERSDIVVOLUDA 7042 7 345 PIEMAAALERDIVTSPLFPHIQGYLLESASHQVATSLHTKGAL PLETVTMITVIRKSVULVEDPTOTYPSERLDEFKRLASNASAN DDLLARAFASIDSDSEDLVSTGTGLEFLEEGERFKKEIPLODOTYRD EKRYKRFRORFSGGFSAGYTNIVOSKEWOTPSTYVSSRONRAD KSVLGBEPFMEEDLSSFGIFAKAIVITDDRASKTKORIRSKRA QLAAATAPIPBATLUDLITTRAKJSVOFFLLERKAN KSVLGBEPFMEEDLSSFGIFAKAIVITDDRASKTKORIRSKRA QLAAATAPIPBATLUDLITTRAKJSVOFFLLERKSKR VERRORROKEDDGVKITGCALPPOSSEGSBGEDDDYLDFWIT APKDOVTPVDTFKDNVIGLAYKIJOLPHQALFTSGSHIFNLESGG SERAGLJCEIGINKGRKLGISGGAFGVGALEEEDDDIVATTATTLS KYDVILKDERBEGGIJVANTAPKSJOFFLLERKSKREVAVGKILDGG SLASKELSSKKIYPPPELPRDVRYNGKSEKEDRYVGKILDGG SLASKELSSKKIYPPPELPRDVRYNGKSEKEDRYVGKILDGG SLASKELSSKKIYPPPELPRDVRYNGKSEKEDRYVGKILDGG SLASKELSSKKIYPPPELPRDVRYNGKSEKENDRYVGKILDGG GOKDALERCLDPSMTEWERGRERDEFARALLVASSHSTLESRY THAKEEDDSDOVEVPROCHNOROMONOSAVUKNEULTDTFEN LSOKDKER IKEMKOATDLKAAGUKASSLAQNAGSSRAOPSBAA AGHCSWINALGGATALKANSVPPARDERGKYLTDTFTANSE KVÖGRGPDUSSKREPSBTOTSKHEKKEDDSISFFLUTARKASLPPK QOSSPLVINKEEHRAPELSN THAKEEDDSDOVEVPROCHNOROMONOSAVUKNEULTDTFTANSE KVÖGRGPDUSSKREPSBTOTSKHEKKEDDSISFFLUTARKASLPPK QOSSPLVINKEEHRAPELSN THAKEEDDSDOVEVPROCHNOROMONOSAVUKNEULTDTFTANSE KVÖGRGPDUSSKREPSBTOTSKHEKKEDDSISFFLUTARKASLPPK QOSSPLVINKEEHRAPELSN THAKEEDDSDOVEVPROCHNOROMONOSAVUKNEULTDTFTANSE KVÖGRGPDUSSKREPSBTOTSKHEKKEDDSISFFLUTARKASLPPK QOSSPLVINKEEHRAPELSN THAKEEDDSDOVEVPROCHNOROMONOSAVUKNEULTDTFTANSE FERROGLATIONOSAVERSPROTOSHKIKKEELDSISFFLUTARKASLPPK THAKEEDDSDOVEVPROCHNOROMONOSAVUKNEULTDTFTANSE THAKEEDDSDOVEVPROCHNOROMONOSAVUKNEULTDTFTANSE THAKEEDDSDOVEVPROCHNOROMONOSAVUKNEULTDTFTANSE THAKEEDDSDOVEVPROCHNOROMONOSAVUKNENGURTURDVEVPR FORSTOTTONOSAVUKNENGURTURDVEVPR PROCHOROMONOSAVUKNE				PGSOPPRITAL CIPTOCOURAGE Insertion)
TO41 1 567 SGRVANGRERAPAGGSLGRALMMITCEPET VERLESSENER STORMENT OF STORMANGERERAPAGGSLGRALMMITCEST STORMANGERERAPAGGSLGRALMMITCES STORMANGERERAPAGGSLGRALMMITCH SERICITIVE PARAPTICLLS PERSOR INKLHERNOLP LIPE PROMINGNIT PER LIKOPEUM PARAPTICLLS PERSOR INKLHERNOLP LIPE PROMINGNIT PER LIKOPEUM LIKEPET PARAPTICLLS PERSOR INKLHERNOLP LIPE PROMINGNIT PER LIKOPEUM LIKEPET PARAPTICLLS PERSOR INKLHERNOLP LIPE PROMINGNIT PER LIKOPEUM LIKEPET PARAPTICLE PERSOR PARAPTICLE PERSOR PARAPTICLE PERSOR PARAPTICIS PERSOR PARAPTICIS PERSON PARAPTICI	Į.			EPFELKYVELDDVERLOBBEGACKEAMSERIANI VALENDOBE
Total	ŀ			AEVRAKYEWI MKELEATKOVI MI DDNIKHI CERDI POLINET DOLE
1 567 SCRVANGRERAPAGGSLGRALMRHOTORGESISHRTIDGHTTSEL NOGYDMGRIANGSYTQGSSLDDFLATEALGGTSEYAPKINIKEY PARAPTGLLSSESGORIKKHEENKOJPLCT PREPNINGNTTPEE LKOAEUNPLEWROLLVRLEEDKILLTPEERKIDIKUMITTEE LKOAEUNPLEWROLLVRLEEDKILLTPEERKIDIKUMITTEE LKOAEUNPLEWROLLVRLEEDKILLTPEERKIDIKUMITTEE LKOAEUNPLEWROLLVRUEEDKILLTPEERKIDIKUMITTEE TOTAL 7042 7 345 PIEMAAALEADT\SPLFFHIGGYLLLSASHG\ATSLHTKGAL PLETVIMITYIPESKYULVKPDTQYPYSEHLDEFKRLARNSAEN DDLLAABVAISDYGKLITELBERKY RAGMARANDSEEDLVSYGTGLEFHEBGERPKKFIPLQDGTVRD EKGRYKRFHGAFSGOFSAGYFITVOSSKOWTPSTFYSSKQNRAD KSVLGEDPIPDEBLDSEGTIAFKIUTVSKOWTPSTFYSSKQNRAD KSVLGEDPIPDEBLDSEGTIAFKIUTVSKOWTPSTFYSSKQNRAD KSVLGEDPIPDEBLDSEGTIAFKIUTVSKOWTPSTFYSSKQNRAD KSVLGEDPIPDEBLDSEGTIAFKIUTVSKOWTPSTFYSSKQNRAD KSVLGEDPIPDEBLDSEGTIAFKIUTVSKOWTPSTFYSSKQNRAD KSVLGEDPIPDEBLDSEGTIAFKIUTVSKOWTPSTFYSSKQNRAD KSVLGEDPIPDEBLDSEGTIAFKIUTVSKOWTPSTFYSSKQNRAD KSVLGEDPIPDEBLDSEGTIAFKIUTVSKOWTPSTFYSSKQNRAD KSVLGEDPIPDEBLDSEGTIAFKIUTVSKOWTPSTFYSSKQNRAD KSVLGEDPIPDEBLDSEGTIAFKIUTVSKOWTPSTFYSSKQNRAD KSVLGEDDIJVATTLAS APKOVTPVDFTYDKDNVIGLAYKGLDYPGLITAFKOWTPSTG RAGMARDSTALLANG SEERGLEINKGRICHARKIUTTSTFAGTIAFKIUTVSKOWTPSTFY LASKELDSBOUGVATAFROYNTOWTPSTFY THAKKEDDSBOUGVATAFROYNTOWTPSTFY THAKKEDDSBOUGVATAFROYNTOWTPSTFY HDKLLIPO/KLUGLBFRYKROKSYSTFILLPETASLPTTQASSE KVSQRRGDENSKRYSROTTSKHKKKEDISSFYTDGISATSVLESSFY THAKKEDDSBOUGVATAFROKORGKATAVKHRGKLTUTDTFFST HDKLLIPO/KLUGLBFRYKROKSYSTFILLPETASLPTTQASSE KVSQRRGDENSKRYSROTTSKHKKKEDISSFYTLLDETASLPTTQASSE KVSQRRGDENSKRYSROTTSKHKKKEDISSFYTLLDETASLPTTQASSE KVSQRRGDENSKRYSROTTSKHKKKEDISSFYTLLDETASLPTTQASSE KVSQRRGDENSKRYSROTTSKHKKKEDISSFYTLLDETASLPTTQASSE KVSQRRGDENSKRYSROTTSKHKKKEDISSFYTLLDETASLPTTOWTWKS FPOSKKOLLKDLVMKCRGVGHELRGLFLENVLLQCTRRILLDDG PETPESTGGI ISBNOPVLLINPARANILLVARMOHOHOHOHOHOHOHOHOHOHOHOHOHOHOHOHOHOHOH				YLEALECVTERLESRVNFCKAHLMMITCFDIT
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PARARTGLISTESSQRIKKLHEENKGFLCIPRRPNNONTTPEE LKQAEKDNFLEWRRGL\UVBLEEGKLILIPFERNLDFWRQLWRV TERSDIVVQIVDA 7042 7 345 PIHMAABLARDIYISDLFPHYQGYLLLSASHG\ATSLHTKGAL PLETVTWYTVIPKSKYVLVKPDTQYPYSENLDEFKRLENSASN DDLLMAEVAISUTGONLITLBLREKY ARGWARDSDSEEDLWSYSTGLEPLEEGERFKKPIPLQOYTVRD EKGRYKRFHGAFSGGFSAGYNTVTGSKEGWTPSTFVSSRQNRAD KSVLGEDPHOBEBLLEGTENPKLIVTDDDASKTKDRIERKAR QLAAATAPIPGATLLDDLITATALSGVFFLLRKMGKKSGGCVGF RVKRRPRRGKSDFSGYSAGYNTVGSKEGWTPSTFVSSRQNRAD KSVLGEDPHOBEBLLEGTENPKLIVTDDASKTKDRIERKAR QLAAATAPIPGATLLDDLITATALSGVFFLLRKMGKKSGCOVGF RVKRRPRRGKSDFDGVILOALPGSSESGEDDDYLPDNVTT APKOVTPVDFTPKDNVHGLAYKGLDPHQALFGTSGEHTNLFSGG SERAGDLGEIGLNKGRKLGISGGAFOVGALEEEDDITATELTS KYDTVLKDEERGGGIJGMTARRQYKNQKESKDLRYVCKLLOGF SLASKELSKLIVPPFLDGTNSRVHYPRFRWVANTSENSHLLQV LSSAGKATPDOTTHSKUGLNASKRABLEGKROPSFLOGNATSVLEP LSOKKERIKGMKOATDLKAAGLKARSLAQNAGSSRAOPSPAAA AGHCSNNNALGGSTATLKANSKPENALGKYDEFTUGSATSVLEP LSOKKERIKGMKOATDLKAAGLKARSLAQNAGSSRAOPSPAAA AGHCSNNNALGGSTATLKANSKPENALDEFIGGSATSVLEP LSOKKERIKGMKOATDLKAAGLKARSLAQNAGSSRAOPSPAAA AGHCSNNNALGGSTATLKANSKPENALDEFIGGSATSVLEP LSOKKERIKGMKOATDLKAAGLKARSLAQNAGSSRAOPSPAAA AGHCSNNNALGGSTATLKANSKPENALDEFIGGSATSVLEP LSOKKERIKGMKOATDLKAAGLKARSLAQNAGSSRAOPSPAAA AGHCSNNNALGGSTATLKANSKPENALDFIGGSSELFLARKKEEP TAKEEDDSDOVEVPDQEDENVOKOGSAVHYGKTURTDFEWRA FOSKROLLKULFOKOVENOCHVOKOGAVHYGGLTRTDIPDEG EPTDEETTGDISDSNDFVLLINFAENKLWVRMOHQGHSRDREKR FOSKROLLKULFUNIVLIKIGV FOSKROLLKULFUNIVLIKIGV TOA4 276 734 EVYLLTDEFAKGRKVABDLYELNOYAGNITPELVLLYTVGVVVVS FOSKROLLKULFOKOPHPLRGLEFIRHVLLQCTRNILLPDEG EPTDEETTGDISDSNDFVLLINFAENKLWVRMOHQGGHSRDREKR ERROGLERIUVTUNIVLIKIGV TOA4 276 734 EVYLLTDEFAKGRKVABDLYELNOYAGNITPELVLLYTVGVVVVYVS FOSKROLLKULFOKOPHPLRGLEFIRHVLLQCTRNILLPDEG EPTDESTGDISDSNDFVLLINFARSISTYLLQCTRNILLPDEG EPTDESTGDISDSNDFVLLINFARSISTYLLQCTRNILLPDEG FOSKROLLKULFUNIVLIKIGV LGFKWEALSBRAGGEMSLAALKORDPYTTSIADLTGQVALLYTFCP KANQMEKTDISTONLERULFUNIVLIKIGV DLEFQLHEPPLLYNNALSISTYSIMPYDNOCHRIAKMANDEVEE ETRASGOA/RSGGTSTSOPGGMUQRPOAHRHODASGGGO NANGHKTOLSGGTSTIKONCHEPTTA	1	ļ		NDGYDWGRLNLQSVTEQSSLDDFLATAELAGTEFVAEKINIKFV
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APKDVTPVDFTPRDNVHGLAYKGLDPHQALPGTSGSHFNLFSG SERAGDLGSIGLNKGRKLGISGQAFGVGALEEDDDIYATETLS KYDTVLKDEEPGDGIYGNTAFRQYKNQKBESKDLRYVGKILDGF SLASKELSSKKIYPPPELPRDYRPYHYPRPWAATSENSHLLQV LSESAGKATPDFOTRISKHQLNASKRABLLGETPJGGSATSVLEF LSQXDKERIKEMKQATDLKAAQLKARSLAQNAQSSRAQPSPAAA AGHCSWNMALGGGTATLKASNFKPFAKDPBKQKRYDEFLVHHKQ GQXDALERCLDPSMTEWBRGRERPEFRAALLVASHSTLSGRF THAKEEDDSDQVEVPRDQENDVGDKQSAVKMKMFGKLTRDTFEW HPDKLLFQ/RLVGLPRVKRDKYSVFNFLILTBETASLPTTQASSE KVSQHRGPPKSRKYSRWDTSKHEKKEDSISEFLRLARSKAEPPK QQSSPLVNKEEHAPELSAN 7044 276 734 EVYLTDEFAKGRKVADLYELVQYAGNIIFRLYLLITVGVVYVKS FPQSRKDILKDLVEMCROVOHPLRGLELRNYLLIQCTRNILPDEG EPTDEETTGDISDSMDFVLINFABMNKLWVRMQHQGHSRDREKR FPQSRKDILKDLVEMCROVOHPLRGLELRNYLLIQCTRNILPDEG EPTDEETTUSISDSMDFVLINFABMNKLWVRMQHQGHSRDREKR ERERQELRILWGTNLVKLSQV KANQWEKTDISGTLYVKRSASPYHGFTIVNRLINMINLVEPVNK DLEFQLHEPFLLYRNASLSIYSIWFYDKNDCHRIAKLMADVVEE ETRRSQQA/RSGQTESQPGWLQRPQAHRHPDDAECSQC 7046 3 513 LGFKWEALSRAGGEMSLAALKQHDPYITSIADLTGQVALYTFCP KANQWEKTDISTLFVVRRSASPYHGFTIVNRLINMINLVEPVNK DLEFQLHEPFLLYRNASLSIYSIWFYDKNDCHRIAKLMADVVEE ETRRSQQA/RSGQTESQPGWLQRPQAHRHPDDAECSQC 7047 103 486 QKKIEKCCWSSGLTFVVRRSASPYHGFTIVNRLINMINLVEPVNK DLEFQLHEPFLLYRNASLSIYSIWFYDKNDCHRIAKLMADVVEE ETRRSQQA/RSGQTESQPGWLQRPQAHRHPDAECSQC 7048 92 627 FFCLITLSWMPYRHTYATISKDVTYKELKNLLNSKN IMLIDVREIWEILEYQKIPESINVPLDEVGRALQMNPRDFKEKY NEVKPSKSBS/IVFSYLAGVRSKKALDTAISLGFHSYYER 7048 92 627 FFCLITLSSWMPYRHATRRYVSSPYMEDSKKTFSEEEEANY WKDLAMTYKQRAENTQEELREFQEGSREYEAELETQLQQIETRN RDLLSENNRIRMELETIKEKFEVQHSEGYRGISALEDDLAQTKA RDLLSENNRIRMELETIKEKFEVQHSEGYRGISALEDDLAQTKA RDLLSENNRIRMELETIKEKFEVQHSEGYRGISALEDDLAQTKA RDLLSENNRIRMELETIKEKFEVQHSEGYRGISALEDDLAQTKA RDLLSENNRIRMELETIKEKFEVQHSEGYRGISALEDDLAQTKA RDLLSENNRIRMELETIKEKFEVQHSEGYRGISALEDDLAQTKA RDLLSENNRIRMELETIKEKFEVQHSEGYRGISALEDDLAQTKA RDLLSENNRIRMELETIKEKFEVQHSEGYRGISALEDLAQTKA RDLLSENNRIRMELETIKEKFEVQHSEGYRGISALEDLLAQTKA RDLLSENNRIRMELETIKEKFEVGHSEGYRGISALEDLLAQTKA RCKWASSLWG S933 938 KRTGSASYGGPFRIKAGRAVREL NYSELRGGRIYAVASAADKMKNRGLRLRGVREPFRGCHWLGRKLIAWX ASSLWG	1			RVKRRPRRQKPDPGVKIYGCALPPGSSRGSEGEDDDVLDDNUTTE
SERAGDIGIGIANGRIKLGIISGGAFGVGALEEEDDDIYATETLS KYDTVLKDEEPGGDLYGWTAGYKSEKDLRYVGKILDGF 9LASKPLSSKKIYPPPELPRDYRPVHYFRPMVAATSENSHLLQV LSESAGKATDDGTHSKHQLINASKRAELLGETPIGGSATSVLEF LSQXDKERIKEMKQATDLKAGNASSKAQAPSPAAA AGHCSNINMALGGGTATLKASNPKPFAKDPEKQKRYDEFLVHMKQ GQKDALERCLDPSMTEWERGRERDEFARAALLYASSHSTLSSRF THAKEEDDSDQVEVPRDQENDVODKQGAVMKMFGKLTRDTHFEW HPDKLLFQ/RLVGJPEVKRDKGSVPNFJTLPETASLPTTOASSE KVSGHROPDKSRKPSRWDTSKHEKKEDSISEFLRLARKAEPPK QQSSPLVNREEHAPELSAN 7044 276 734 EVYLTDEFAKGRKVADLIYELVQYAGNITERLYLLITVGVVVVKS FPQSRKDILKDLVEMCGGVOHPLRGLFLRNYLLQCTRNILPDEG EPTDEETTGDISDSMDFVLLNFAENNKLWVRMQHGGHSRDREKR FPQSRKDILKDLVEMCGGVOHPLRGLFLRNYLLQCTRNILPDEG EPTDEETTGDISDSMDFVLLNFAENNKLWVRMQHGGHSRDREKR ERERGELRILVGTNLVTLSQV 7045 3 513 LGFKMEALSFAGGEMSLAALKQHDPYITSIADLTGQVALYTFCP KANOMEKTDIEGTLFVYRRSASPYHGFTIVNRLNMHNLVEPVNK DLEFQLHEPFLLYRNASLSIYSIWFYDNDCHRIAKKMADVVEE ETTRRSQQA/RSGQTESQCQMLQRPQARRHPGDAEOSGC 7046 3 513 LGFKMEALSFAGGEMSLAALKQHDPYITSIADLTGQVALYTFCP KANOMEKTDIEGTLFVYRRSASPYHGFTIVNRLNMHNLVEPVNK DLEFQLHEPFLLYRNASLSIYSIWFYDNDCHRIAKKMADVVEE ETTRRSQQA/RSGQTESQCQMLQRPQARRHPGDAEOSGC 7047 103 486 QMKIEKCGWSEGLTSIKGNCHNFYTAISKDVTYKELKNLINSKN INLIDVRBIWBILEEVGKIPESINVPLDEVGEALQMNPROFKEKY NEVKPSKSDS/IVFSYLAGVSKKALDTAISLGFHSYYER 7048 92 627 FFCLTLLSSWDYHHHATRVISSPYFTMEDGGKTFGSEEEANY WKDLAMTYKQRAENTQEELREFQEGSREYEAELETQLQQIETRN RDLLSENNRLRMELETIKEKFEVQHSEGYRQISALEDDLAQTKA IKDQLQKYIRELEQANDDLERAKRATDHGLSKTFFSQEEEANY WKDLAMTYKQRAENTQEELREFGEGSREYFGAELETQLQQIETRN RDLLSENNRLRMELETIKEKFEVQHSEGSVGKIPARRCYEDEL VPVFEAVGRIVELRIMMDFOGKNRGYAFVMYCHKHEAKRAVREL NNYBIRPGRALGVCCSVDNCRLFIGGIPKMKKREEILEBIAKVT EGYLDVIVYASAADKMKNRGLRLRGVKEPPRGCHWLGRKLLIAMX ASSLWG	1.			APKDVTPVDFTPKDNVHGLAYKGLDPHOALFGTSGEHFNLFSGG
KYDTVLKDEPGIOLYGWTAPRQYINGKESEKDLRYVGKILIGG GLASKLISKKIYPPPELPRYYPYYFRPMVARTSENSHLLQV LSESAGKATPDPGTHSKHQLINASKRAELIGETPIGGSATSVLEF LSQXDKERIKEMKQATDLKAAQLKARSLAQNAQSSRAQPSPAAA AGHCSMMALGGGTATLKASKPFAKDPEKQKRYDEFLVHMKQ GQKDALERCLDPSMTEWERGRERDEFARAALLYASSHSTLSSRF THAKEEDDSDQVEVPRDQENDVCDKQSAVKMKMFGKLTRDTFEW HPDKLFG/RLVGJEVYKENKYSYFNFILIPETASLPTTQASSE KVSQHRGPDKSRKPSRWDTSKHEKKEDSISEFLRLARSKAEPPK QQSSPLVNKEEHAPELSAN 7044 276 734 EVYLTDEFAKGRKVADLYSLVQYAGNITPRLYLLXTVGVVYVKS FPQSRKDILKDLVEMCRGVQHPLRGLFLRNYLLQCTRNILEDEG EPTDEETTGDISDSMDFVLLNFAENNKLWVRMQHQGHSRDREKR FPQSRKDILKDLVEMCRGVQHPLRGLFLRNYLLQCTRNILEDEG EPTDEETTGDISDSMDFVLLNFAENNKLWVRMQHQGHSRDREKR FPQSRKDILKDLVEMCRGVQHPLRGLFTLNYLLMVRNHNLVEPVNK LGFKMEALSEAGQEMSLAALKQHDPYITSIADLTGQVALYTFCP KANQWEKTDISGTLFVYRRSASPYHGFTIVNRLMMHNLVEPVNK DLEFQLHEPFLLYRNAASLISISIYSIWFYDKNDCHRIAKLMADVVEE ETRRSQQA/RSQGTESQPGQMLQRPQAHRHPGDAEQSQG 7046 3 513 LGFKMEALSRAGGMSLAALKQHDPYITSIADLTGQVALYTFCP KANQWEKTDISGTLFVYRRSASPYHGFTIVNRLMMHNLVEPVNK DLEFQLHEPFLLYRNAASLISIYSIWFYDKNDCHRIAKLMADVVEE ETRRSQQA/RSQGTESQPGQMLQRPQAHRHPGDAEQSQG 7047 103 486 QMKIEKCGWSEGLTSIKONCHNFYTAISKDYTKELKNLLNSKN INLIDVRSIWSILESTJKNYLDSVGRAHRPGDAEQSQG 7048 92 627 FFCLTLLSSWDYRHHATRVIYTSIADLTGQVALYTFCLW NEVKPSKSDS/IVFSYLAGVRSKKALDTAISLGFHSYYER 7048 92 627 FFCLTLLSSWDYRHATRVIYTSIADLTGGLACHTN RDLLSENNRLRMELETIKBKFEVQHSBGYRGISALEDDLAQTKA IKDQLQKYIRELEQANDDLERAKRATDHGLSKTFE\QRINGYTKN RDLLSENNRLRMELETIKBKFEVQHSBGYRGISALEDDLAQTKA RDLLSENNRLRMELETIKBKFEVQHSBGYRGISALEDDLAQTKA RTDLSENNRLRMELETIKBKFEVQHSBGYRGISALEDDLAQTKA RTDLSENNRLRMELETIKBKFEVGHSBGYRGISALEDDLAQTKA RTDLSENNRLRMELETIKBKFEVGHSBGYRGISALEDDLAQTKA RTDLSENNRLRMELETIKBKFEVGHSBGYRGISALEDDLAQTKA RTDLSENNRLRMELETIKBKFEVGHSBGYRGISALEDDLAQTKA RTDLSENNRLRMELETIKBKFEVGHSBGYRGYFSGEEEEANY WKDLAMTYKQRAEMTPGELRRFTQGGIPKMKKREEILEBIAKVT EGYLDVIVYASAADKMKNRGLRLRGVREPPRGCHWLGRKLLIAWX ASSLWG	!			SERAGDLGEIGLNKGRKLGISGOAFGVGALEEEDDDIYATETLS
SLASKEJSKKIYPPPELPRDYRPHYPRPMWAATSENSHLLQV LSSAGKATPDPGTHSKQLMASKRABLLGETPIQGSATSVLEF LSQXDKERIKEMKQATDLKAAQLKARSLAQNAQSSRAQPSPAAA AGHCSMMALGGTATLKAAQLKARSLAQNAQSSRAQPSPAAA AGHCSMMALGGTATLKAAQLKARSLAQNAQSSRAQPSPAAA AGHCSMMALGGTATLKAANPKPFAKDPEKQKRYDEFLVHMKQ GQKDALERCLDPSMTEWERGREDEFARAALLYASSHSTLSERF THAKEEDDSQVEVPRQDQENDVGDKQSAVKMKMFGKLTRDTFEW HPDKLLFQ/RLVGLPRVKRDKYSVFNFLTLETASLPTTQASSE KVSQHROPDKSRKPSRYDTSKHEKKEDSISEFLRLARSKAEPPK QQSSPLVNKEEHAPELSAN 7044 276 734 EVYLTDEFAKGRKVADLYELVQYAGNITPRLYLLQTVGUVVKS FPQSRKDILKDLVEMCRGVQHPLRGLFFLRNYLLQTRNILDEG EPTDETTGDISDSMDFVLLNFARMNKLWRMQHQGHSRDREKR FPQSRKDILKDLVEMCRGVQHPLRGLFFLRNYLLQTRNILDEG EPTDETTGDISDSMDFVLLNFARMNKLWRMQHQGHSRDREKR ERERQELRILVGTNLVRLSQV ANAQMEKTDIEGTLFYVRRSASPYHGFTIVNRLMMHNLVEPVNK DLEFQLHEPFLLYRNASLSIYSLWFYDKNDCHRIAKLMADVVEE ETRRSQQA/RSQQTESQPGQWLQRPQAHRHGDAEGSQG 7046 3 513 LGFKMEALSRAGGEMSLAALKQHDPYITSIADLTGQVALYTFCP KANQMEKTDIEGTLFYVRRSASPYHGFTIVNRLMMHNLVEPVNK DLEFQLHEPFLLYRNASLSIYSLWFYDKNDCHRIAKLMADVVEE ETRRSQQA/RSQGTESQPGGWLQRPQAHRHGDAEGSQG 7047 103 486 QMKIEKCGWSEGLTSIKGNCHNFYTAISKDVTYKELKNLLNSKN INLIDVREIWEILEVQKIPESINVPILDEVGEALQMBPDPFKEKY NEVKPSKSDS/TYFSYLAGKKKALDTAISLGFHSYYER 7048 92 627 FFCLTLLSSWDYRHHATRRVISSPVFTMEDSGKTFSSEEEEANY WKDLAMTYKQRAENTQEELREFQEGSREYEAELETQLQQIETRN RDLLLSENNRIHRELETIKEKFEVQHSEGYRQISALEDDLAQTKA IKDQLQKYIRELEQANDDLERAKRATDHGLSKTFE\QRLN\QAI EKKW 7049 393 938 KRTGSASYGGPPFGLGGPATXASVAGRCSSVGKIPARRCYEDEL NNYBIRPGRLLGVCCSVDNCRLFIGGIPKMKKREEILEBIAKVT EGYLDUVIVASAADKMKNRGLRLRGVREPPRGCHWLGRKLLIAMX ASSLMG				KYDTVLKDEEPGDGLYGWTAPROYKNOKESEKDLRYVGKILDGF
LSOXDERIKEMKOATDLKAAQLKARSILAQNAQSSRAQPSPAAA AGHCSMIMALGGGTATLKASNIKPIPAKOPEKOKRYDEFLVIHKKO GQKDALERCLDPSMTEWERGRERDEFARALLYASSHSTLSSRF THAKEEDDSDQVEVPROQENDVGDKQSAVKKKMFGKLTRDTFEW HPDKLLFQ/RLVGLPRVKRDKYSVFNFLTLPETASLPTTQASSE KVSQHROPDKSRKPSRWDTSKHEKKEDSISEFLRLARSKAEPPK QGSSPLVNKEEHAPELSAN 7044 276 734 EVYLTDEFAKGRKVADLYELVQYAGNITPRLYLLITVGVVVVKS FPOSRKDILKDLVEMCRGVOHPLRGLEFLRNYLLQCTRNILEDEG EPTDEETTGDISDSMDFVLLNFAEMNKLWVRMQHQGHSRDREKR FROSRIDILKDLVEMCRGVOHPLRGLEFLRNYLLQCTRNILEDEG EPTDEETTGDISDSMDFVLLNFAEMNKLWVRMQHQGHSRDREKR ERERQELRILVGTINLVRLSQV ANQWEKTDIEGTLFVYRRSASPYHGFTIVNRLMMHNLVEFVNK DLEFQLHEPFLLYRNASLSIYSIWFYDKNDCHRIAKLMADVVEE ETRRSQQA/RSGQTESQFGGWLQRPQAHRHPGDAEQSQG 7046 3 513 LGFKMEALSRAGGEMSLAALKQHDPYTTSIADLTGQVALYTFCP KANQWEKTDIEGTLFVYRRSASPYHGFTIVNRLMMHNLVEFVNK DLEFQLHEPFLLYRNASLSIYSIWFYDKNDCHRIAKLMADVVEE ETRRSQQA/RSGQTESQPGQWLQRPQAHRHPGDAEQSQG 7047 103 486 OMKIEKCGWSEGLTSIKGNCHNFYTAISKDVTYKELKNLINSKN IMLIDVREIWEILEYQKIPESINVPIDEVGEALQMBPDFKEKY NEVKPSKSDS/IVFSYLAGVRSKKALDTAISLGMPROPKEKY NEVKPSKSDS/IVFSYLAGVRSKKALDTAISLGMPROPKEKY WKDLAMTYKQRAENTQEELREFQEGSREYEAELETQLQQIETRN RDLLLSENNRIHRELETIKEKFEVQHSEGSREYEAELETQLQQIETRN RDLLLSENNRIHRELETIKEKFEVQHSEGSREYEAELETQLQQIETRN RDLLSENNRIHRELETIKEKFEVGHSEGSREYEAELETQLQQIETRN RDLLSENNRIHRELETIKEKFEVGHSEGYRQISALEDDLAQTKA IKDQLQKYIRELEQANDDLERAKRATDHLISKTFE\QRLN\QAI EKKM 7049 393 938 KRTGSASYGGPPFGLGGPATXASVAGRCSSVGKIFARRCYEDEL NNYBIRPGRLLGVCCSVDNCRLFIGGIPMKKREEILEBIAKVT EGYLDVIVYASAADKMKNRGLRLRGVREPPRGCHWLGRKLLIAWX ASSLWG	1 .			SLASKPLSSKKIYPPPELPRDYRPVHYFRPMVAATSENSHLLOV
AGHCSWAMALGGGTATLKASNFRFFARDPEKQKRYDEFLVEMKQ GQKDALERCLDPSMTEWERGRERDEFARAALLYASSHSTLESRF THAKEEDDSDQVEVPRDQENDVGDKQSAVMKMFGKLTRDTFEW HPDKLLFQ/RLVGDFRVKRDKYSVFNFLTLPETASLPTTQASSE KVSQHRGPDKSRKPSRWDTSKHEKKEDSISEFLRLARSKAEPPK QQSSPLVNKEEBHAPELSAN 7044 276 734 EVYLTDEFAKGRKVADLYELVQYAGNIYPRLYLLITVGVVYVKS FPQSRKDLIKDLVEMCRGVQHEPLGLFLRNYLLQCTRNILPDEG EPTDEETTGDISDSMDFVLLNFAEMNKLWVRMQHQGHSRDREKR ERERQELRILVGTNLVRLSQV 7045 3 513 LGFKMEALSRAGGEMSLAALKQHDPYITSIADLTGQVALYTFCP KANQWEKTDIEGTLFVYRRSASPYHGFTIVNRLMMHNLVEPVNK DLEFQLHEPFLLYRNASLSIYSIWFYDKNDCHRIAKIMADVVEE ETRSQQA/RSGQTESQPGQWLQRPQAHRHPGDAEQSQG 7046 3 513 LGFKMEALSRAGGEMSLAALKQHDPYITSIADLTGQVALYTFCP KANQWEKTDIEGTLFVYRRSASPYHGFTIVNRLMMHNLVEPVNK DLEFQLHEPFLLYRNASLSIYSIWFYDKNDCHRIAKIMADVVEE ETRRSQQA/RSGGTESQPGGWLQRPQAHRHPGDAEQSQG 7047 103 486 QMKIEKCGWSEGLTSIKGNCHNFYTAISKDVTYKELKNLLNSKN LMLIDVREIWEILEFQKIPSINVPLDEVGRALQMMPRDFKEKY NEVKPSKSDS/IVFSYLAGVRSKKALDTAISLGFHSYYER 7048 92 627 FFCLTLLSSWDYKHHATTRYISSPYTWEDSGKTFSSEEEEANY WKDLAMTYKQRAENTQEELEFQEGSREYEAELETQLQGIFTRN RDLLSENNRLRHELETIKEKFEVQHSEGYRGISALEDDLAQTTRA KKWL RDLLSENNRLRHELETIKEKFEVQHSEGYRGISALEDDLAQTTRA IKDQLQKYIRELEQANDDLERAKRATDHGLSKTFFSGEEEANY WKDLAMTYKQRAENTQEELEFFGGGRYEAELETQLQGIFTRN RDLLSENNRLRHELETIKEKFEVQHSEGYRGISALEDDLAQTTRA IKDQLQKYIRELEQANDDLERAKRATDHGLSKTFFSCEEEANY WYFEAVGRIYELRMMDFDGKNRGYAFVMYCHKHEAKRAVKEL NNYSIRPGRILGVCCSVDNCRLFIGGIPKMKREEILEEIAKVT EGVULDVIVYASAADKMKNRGLRLRGVREPPRGCHWLGRKLIAMX ASSLWG				LSESAGKATPDPGTHSKHQLNASKRABLLGETPIQGSATSVLEF
GQKDALERCLDPSMTEWERGRERDEFARAALLVASSHSTLSERF THAKEEDDSDQVEVPRDQENDVGDKQSAVKMKMFGKLTRDTFEW HPDKLEFQ/RLVGLPRVKRDKYSVFNFLTLPETASLETTOASSE KVSQHRGPDKSRKPSRWDTSKHEKKEDSISEFLRLARSKAEPPK QQSSPLVNKEEHAPELSAN 7044 276 734 EVYLTDEFAKGRKVADLYELVQYAGNITPRLYLLITVGVVYVKS FPQSRKDILKDLVEMCRGVQHPLRGLFLRNYLLQCTRNILPDEG EPTDEETTGDISDSMDFVLLMFAENNKLWVRMQHQGHSRDREKR FPQSRKDILKUTNLVSLAGV 7045 3 513 LGFKMEALSRAGQEMSLAALKQHDPYITSIADLTGQVALYTFCP KANQWEKTDIEGTLFVYRRASLYSIWFYDKNDCHRIAKLMADVVEE ETRRSQOA/RSGTESQPGQWLQRPQAHRHPGDAEQSOG 7046 3 513 LGFKMEALSRAGGEMSLAALKQHDPYITSIADLTGQVALYTFCP KANQWEKTDIEGTLFVYRRASLYSIWFYDKNDCKRIAKLMADVVEE ETRRSQOA/RSGTESQPGGWLQRPQAHRHPGDAEQSOG 7047 103 486 QMKIEKCGWSEGITSIKGNCHNFYTAISKDVYYKELKNLINSKN LLEFQLHEPFLLYRNASLSIYSIWFYDKNDCKRIAKLMADVVEE ETRRSQOA/RSGQTESQPGQWLQRPQAHRHPGDAEQSOG 7047 103 486 QMKIEKCGWSEGITSIKGNCHNFYTAISKDVTYKELKNLINSKN LLIDVREIWELLEYQKIPESINVPLDEVGEALQMNPRDFKEKY NEVKPSKSDS/IVFSYLAGVRSKKALDTAISLGFHSYYER 7048 92 627 FFCLTLLSSWDYHHATTRRVISSPVFTMEDSGKTFSSEEEEANY WKDLAMTYKQRAENTQEELEFQGSREYGRISALEDDLAQTKA IKDQLQKYIRELEQANDDLERAKRATDHGLSKTFSQEEEANY WKDLAMTYKQRAENTQEELEFGGSREYEAELETQLQQIETRN RDLLSENNRLRWELETIKEKFEVQHSEGSREYGRISALEDDLAQTKA IKDQLQKYIRELEQANDDLERAKRATDHGLSKTFF\QRLN\QAI EKKW RTGSASYGGPPFGLGGPATXASVAGRCSSVGKIPARRCYEDEL VPVFEAVGRIYELRLMMDFDGKNRGYAFVMYCHKHEAKRAVKEL NNYSIRPGRLLGVCCSVDNCRLFIGGIPKMKREEILEBIAKVT EGVULDVIVYASAADKMKNRGLRLRGVREPPRGCHMLGRKLLIAMX ASSLWG	1 1			LSQKDKERIKEMKQATDLKAAQLKARSLAQNAQSSRAQPSPAAA
THAKEEDSDQVEVPRDQENDVGDKQSAVMKMFGKLTRDTFEW HPDKLLFQ/RLVGLPRVKRDKYSVFNFLTLPETASLPTTQASSE KVSQHROPDKSRKPSRWDTSKHEKKEDSISEFLRLARSKAEPPK QQSSPLVMKEEHAPELSAN 7044 276 734 EVYLTDEFAKGRKVADLYSLLVQYAGNTIPRLYLLITVGVVYVKS FPOSRKDILKDLVEMCRGVQHPLRGLFLRNYLLQCTRNILPDEG EPTDEETTGDISDSMDFVLLNFAEMNKLWVRMQHQGHSRDREKR EERRQELRILVGTNLVRLSQV 7045 3 513 LGFKMEALSRAGQEMSLAALKQHDPYITSIADLTGQVALYTFCP KANQWEKTDIEGTLFVYRRSASPYHGFTIVNRLNMHINLVEPVNK DLEFQLHEPFLLYRNASLSIYSIWFYDKNDCHRIAKLMADDVEE ETRRSQQA/RSGQTESQPGQWHQRPQAHRHEDAEQSQG 7046 3 513 LGFKMEALSRAGQEMSLAALKQHDPYITSIADLTGQVALYTFCP KANQWEKTDIEGTLFVYRRSASPYHGFTIVNRLNMHINLVEPVNK DLEFQLHEPFLLYRNASLSIYSIWFYDKNDCHRIAKLMADDVEE ETRRSQQA/RSGQTESQPGQWLQRPQAHRHEDAEQSQG 7047 103 486 QMKIEKCGWSEGLTSIKGNCHNFYTAISKDVTYKELKNLLNSKN IMLIDVREIWEILEYQKIPESINVPLDEVGEALQMNPRDFKEKY NEVKPSKSDS/IVFSYLAGVRSKKALDTAISLGFHSYYER 7048 92 627 FFCLTLLSSWDYRHHATRRVISSPVFTMEDSGKTFSSEEEEANY WKDLAMTYKQRAENTQELREFQEGSREYEAELETQLQQIETRN RDLLSENNRLRMELETIKEKFEVQHSEGYRQISALEDDLAQTKA IKDQLQKYIRELEQANDDLERAKRATDHGLSKTFE\QRLN\QAI EKKM 7049 393 938 KRTGSASYGGPPFGLGGPATKASVAGRCSSVGKIPARRCYEDEL VPVFEAVGRIYELRLMMDFDGKNRGYAFVMYCHKHEAKRAVREL NNYSIRPGRLLGVCCSVDNCRLFIGGIPKMKKREEILEEIAKVT EGVLDVIVYASAADKMKNRGLRLRGVREPPRGCHWLGRKLIAWX ASSLWG ASSLWG	}			GOKDALERCLDROMTEWERCHERSPERSON
HPDKLEG/RLVGLPRVKRDKYSVFNFLTLPETASLPTTQASSE KVSQHRGPDKSRKPSRWDTSKHEKKEDSISEFLRLARSKAEPPK QQSSPLVNKEEBHAPELSAN EVYLTDEFAKGRKVADLYELVQYAGNIYPRLYLLITVGVVYVKS FPQSRKDILKDLVEMCRGVOHPLRGLFLRNYLLQCTRNILPDEG EPTDEETTGDISDSMDFVLLNFAEMNKLWVRMQHQGHSRDREKR EERRQELRILVGTNLVRLSQV CERRQELRILVGTNLVRLSQV LGFKMEALSRAGQEMSLAALKQHDPYITSIADLTGQVALYTFCP KANQWEKTDIESTLFYVRRSASPYHGFTIVNRLMHNLVEPVNK DLEFQLHEPFLLYRNASLSIYSIWFYDKNDCHRIAKLMADVVEE ETRRSQQA/RSGQTESQPGGWLQRPQAHRHPGDAEQSQG TO46 3 513 LGFKMEALSRAGQEMSLAALKQHDPYITSIADLTGQVALYTFCP KANQWEKTDIESTLFYVRRSASPYHGFTIVNRLMHNLVEPVNK DLEFQLHEPFLLYRNASLSIYSIWFYDKNDCHRIAKLMADVVEE ETRRSQQA/RSGQTESQPGGWLQRPQAHRHPGDAEQSQG TO47 103 486 QMKIEKCGWSEGLTSIKGNCHNFYTAISKDVTYKELKNILNSKN IMLIDVREIWBILEYQKIPESINVPLDEVGEALQMNPRDFKEKY NEVKPSKSDS/IVFSYLGVRSKKALDTAISLGFHSYYER TO48 92 627 FFCLTLLSSMDYRHHATRRVISSPVFTMEDSGKTFSSEEEEANY WKDLAMTYKQRAENTQEELREFQEGSREVEAELETQLQQIETRN RDLLSENNRLRMELETIKEKFEVGHSEGYRQISALEDDLAQTKA IKDQLQKYIRELEQANDDLERAKRATDHGLSKTFE\QRIN\QAI EKKW TO49 393 938 KRTGSASYGGFPPGLGGPATXASVAGRCSSVGKIPARRCYEDEL NNYBIRPGRILGVCCSVDNCRLFIGGIPKMKKREEILEEIAKVT EGYLDVIVVASAADKMKNRGLRLRGVREPPRGCHWLGRKLIAWX ASSLWG	1 1			THAKEEDDSDOVEVPPDOFNDVCDVOCAUVNVMEOVY MDDWCDV
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FPGSRKDILKDLVEMCRGVQHPLRGLFLRNYLLQCTRNILPDEG EPTDEETTGDISDSMDFVLLNFAEMNKLWVRMQHQGHSRDREKR ERERQELRILVGTNLVRLSQV 1045 3 513 LGFKMEALSRAGQEMSLAALKQHDPYITSIADLTGQVALYTFCP KANQWEKTDIEGTLFVYRRSASPYHGFTIVNRLNMHNLVEFVNK DLEFQLHEPFLLYRNASLSIYSIWFYDKNDCHRIAKLMADVVEE ETRRSQQA/RSGQTESQPGQWLQRPQAHRHPGDAEQSQG 1046 3 513 LGFKMEALSRAGGEMSLAALKQHDPYITSIADLTGQVALYTFCP KANQWEKTDIEGTLFVYRRSASPYHGFTIVNRLNMHNLVEFVNK DLEFQLHEPFLLYRNASLSIYSIWFYDKNDCHRIAKLMADVVEE ETRRSQQA/RSGQTESQPGQWLQRPQAHRHPGDAEQSQG 1047 103 486 QMKIEKCGWSEGLTSIKGNCHNFYTAISKDVTYKELKNLINSKN IMLIDVREIWEILLEYQKIPESINVPLDEVGEALQNNPRDFKEKY NEVKPSKSDS/IVFSYLAGVRSKKALDTAISLGFHSYYER 1048 92 627 FFCLTLLSSWDYRHATRRVISSFVFTMEDSGKTFSSEEEEANY WKDLAMTYKQRAENTQEELREFQEGSREYEAELETQLQQIETRN RDLLSENNRLRMELETIKEKFEVQHSEGYRQISALEDDLAQTKA IKDQLQKYIRELEQANDDLERAKRATDHGLSKTFE\QRLN\QAI EKKW 1049 393 938 KRTGSASYGGPPFGLGGPATXASVAGRCSSVGKIPARRCYEDEL VPVFEAVGRIVELLEMMDFDGKNRGYAFVMYCHKHEAKRAVREL NNYBIRFGRLLGVCCSVDNCRLFIGGIPKMKKREEILEEIAKVT EGVLDVIVYASAADKMKNRGLRLRGVREPPRGCHWLGRKLIAWK ASSLWG	I	1		QQSSPLVNKEEEHAPELSAN
FPGSRKDILKDLVEMCRGVQHPLRGLFLRNYLLQCTRNILPDEG EPTDEETTGDISDSMDFVILNFAENNKLWVRMQHQGHSRDREKR EPERQELRILVGTNLVRLSQV 1045 3 513 LGFKMEALSRAGQEMSLAALKQHDPYITSIADLTGQVALYTFCP KANQWEKTDIEGTLFVYRRSASPYHGFTIVNRLNMHNLVEPVNK DLEFQLHEPFLLYRNASLSIYSIWFYDKNDCHRIAKLMADVVEE ETRRSQQA/RSGQTESQPGQWLQRPQAHRHPGDAEGSQG 1046 3 513 LGFKMEALSRAGQEMSLAALKQHDPYITSIADLTGQVALYTFCP KANQWEKTDIEGTLFVYRRSASPYHGFTIVNRLNMHNLVEPVNK DLEFQLHEPFLLYRNASLSIYSIWFYDKNDCHRIAKLMADVVEE ETRRSQQA/RSGQTESQPGQWLQRPQAHRHPGDAEQSQG 1047 103 486 QMKIEKCGWSEGLTSIKGNCHNFYTAISKOVTYKELKNLLNSKN IMLIDVREIWEILEYQKIPESINVPLDEVGEALQMNPRDFKEKY NEVKPSKSDS/IVFSYLAGVRSKKALDTAISLGFHSYYER 1048 92 627 FFCLTLLSSWDYRHHATRRVISSPVFTMEDSGKTFSSEEEEANY WKDLAMTYKQRAENTQEELREFQEGSREYEAELETQLQQIETRN RDLLSENNRLRMELETIKEKFFVQHSEGYRQISALEDDLAQTKA IKDQLQKYIRELEQANDDLERAKRATDHGLSKTFE\QRLN\QAI EKKW 1049 393 938 KRTGSASYGGPPPGLGGPATXASVAGRCSSVGKIPARRCYEDEL VPVFEAVGRIVELRLMMDFDGKNRGYAFVMYCHKHEAKRAVREL NNYEIRPGRLLGVCCSVDNCRLFIGGIPKMKKREEILEEIAKVT EGVLDVIVYASAADKMKNRGLRLRGVREPPRGCHWLGRKLIAWX ASSLWG	7044	276	734	EVYLTDEFAKGRKVADLYELVOYAGNIIPRLYLLITVGVVYVKS
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TOTAMEASKAGGEMSLAALKQHDPYITSIADLTGQVALYTFCP KANQWEKTDIEGTLFVYRRSASPYHGFTIVNRLNMHNLVEPVNK DLEFQLHEPFILIYRNASLSIYSIWFYDKNDCHRIAKLMADVVEE ETRRSQQA/RSGQTESQPGQWLQRPQAHRHPGDAEQSQG TO46 3 513 LGFKMEALSRAGQEMSLAALKQHDPYITSIADLTGQVALYTFCP KANQWEKTDIEGTLFVYRRSASPYHGFTIVNRLNMHNLVEPVNK DLEFQLHEPFLLYRNASLSIYSIWFYDKNDCHRIAKLMADVVEE ETRRSQQA/RSGQTESQPGQWLQRPQAHRHPGDAEQSQG TO47 103 486 QMKIEKCGWSEGLTSIKGNCHNFYTAISKDVTYKELKNLLNSKN IMLIDVREIWEILEYQKIPESINVPLDEVGEALQMNPRDFKEKY NEVKPSKSDS/IVFSYLAGVRSKKALDTAISLGFHSYYER TO48 92 627 FFCLTLLSSWDYRHHATRRVISSPVFTMEDSGKTFSSEEEEANY WKDLAMTYKQRAENTQEELREFQEGSREYEAELETQLQQIETRN RDLLSENNRLRMELETIKEKFEVQHSEGYRQISALEDDLAQTKA IKDQLQKYIRELEQANDDLERAKRATDHGLSKTFE\QRLN\QAI EKKW TO49 393 938 KRTGSASYGGPPPGLGGPATXASVAGRCSSVGKIPARRCYEDEL VPVFEAVGRIYELRLMMDFDGKNRGYAFVMYCHKHEAKRAVREL NNYEIRPGRLLGVCCSVDNCRLFIGGIPKMKKREEILEEIAKVT EGVLDVIVYASAADKMKNRGLRLRGVREPPRGCHWLGRKLIAWK ASSLWG	7045			ERERQELRILVGTNLVRLSQV
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103 166 CANCELLE CONTROL CONTR	1 1			ETERSOON / PSCOTESOROUM OF PONTBURGEN TRACE
KANQWEKTDIEGTLFVYRRSASPYHGFTIVNRLNMHNLVEPVNK DLEFQLHEPFLLYRNASLSIYSIWFYDKNDCHRIAKLMADOVEE ETRRSQQA/RSGQTESQPGQWLQRPQAHRHPGDAEQSQG OMKIEKCGWSEGLTSIKGNCHNFYTAISKDVTYKELKNLLNSKN IMLIDVREIWEILEYQKIPESINVPLDEVGEALQMNPRDFKEKY NEVKPSKSDS/IVFSYLAGVRSKKALDTAISLGFHSYYER OE27 FFCLTLLSSWDYRHHATRRVISSPVFTMEDSGKTFSSEEEEANY WKDLAMTYKQRAENTQEELREFQEGSREYEAELETQLQQIETRN RDLLSENNRLRMELETIKEKFEVQHSEGYRQISALEDDLAQTKA IKDQLQKYIRELEQANDDLERAKRATDHGLSKTFE\QRLN\QAI EKKW OVAFFAVGRIYELELMMDFDGKNRGYAFVMYCHKHEAKRAVREL NNYEIRPGRLLGVCCSVDNCRLFIGGIPKMKKREEILEEIAKVT EGVLDVIVYASAADKMKNRGLRLRGVREPPRGCHWLGRKLIAWK ASSLWG	7046	3	513	LGFKMEALSRACORMST.AAT.KOUDDYTTTCTADT TCCVIA
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7048 92 627 FFCLTLLSSWDYRHATRRVISSPVFTMEDSGKTFSSEEEEANY WKDLAMTYKQRAENTQEELREFQEGSREYEAELETQLQQIETRN RDLLSENNRLRMELETIKEKFEVQHSEGYRQISALEDDLAQTKA IKDQLQKYIRELEQANDDLERAKRATDHGLSKTFE\QRLN\QAI EKKW 7049 393 938 KRTGSASYGGPPPGLGGPATXASVAGRCSSVGKIPARRCYEDEL VPVFEAVGRIYELRIMMDFDGKNRGYAFYMYCHKHEAKRAVREL NNYEIRPGRLLGVCCSVDNCRLFIGGIPKMKKREEILEEIAKVT EGVLDVIVYASAADKMKNRGLRLRGVREPPRGCHWLGRKLIAWK ASSLWG	 	ľ		IMLIDVREIWEILEYQKIPESINVPLDEVGEALOMNPRDFKEKY
WKDLAMTYKQRAENTQEELREFQEGSREYEAELETQLQQIETRN RDLLSENNRLRMELETIKEKFEVQHSEGYRQISALEDDLAQTKA IKDQLQKYIRELEQANDDLERAKRATDHGLSKTFE\QRLN\QAI EKKW 7049 393 938 KRTGSASYGGPPPGLGGPATXASVAGRCSSVGKIPARRCYEDEL VPVFEAVGRIYELRLMMDFDGKNRGYAFYMYCHKHEAKRAVREL NNYEIRPGRLLGVCCSVDNCRLFIGGIPKMKKREEILEEIAKVT EGVLDVIVYASAADKMKNRGLRLRGVREPPRGCHWLGRKLIAWX ASSLWG	7048			NEVKPSKSDS/IVFSYLAGVRSKKALDTAISLGFHSYYER
RDLLSENNRLRMELETIKEKFEVQHSEGYRQISALEDDLAQTKA IKDQLQKYIRELEQANDDLERAKRATDHGLSKTFE\QRLN\QAI EKKW 7049 393 938 KRTGSASYGGPPPGLGGPATXASVAGRCSSVGKIPARRCYEDEL VPVFEAVGRIYELRLMMDFDGKNRGYAFVMYCHKHEAKRAVREL NNYBIRPGRLLGVCCSVDNCRLFIGGIPKMKKREEILEEIAKVT EGVLDVIVYASAADKMKNRGLRLRGVREPPRGCHWLGRKLIAWX ASSLWG	,040	34	627	FFCLTLLSSWDYRHHATRRVISSPVFTMEDSGKTFSSEEEEANY
1KDQLQKYIRELEQANDDLERAKRATDHGLSKTFE\QRLN\QAI EKKW 7049 393 938 KRTGSASYGGPPPGLGGPATXASVAGRCSSVGKIPARRCYEDEL VPVFEAVGRIYELRLMMDFDGKNRGYAFVMYCHKHEAKRAVREL NNYBIRPGRLLGVCCSVDNCRLFIGGIPKMKKREEILEEIAKVT EGVLDVIVYASAADKMKNRGLRLRGVREPPRGCHWLGRKLIAWX ASSLWG	[-	ì	WKDLAMTYKQRAENTQEELREFQEGSREYEAELETQLQQIETRN
7049 393 938 KRTGSASYGGPPPGLGGPATXASVAGRCSSVGKIPARRCYEDEL VPVFEAVGRIYELRLMMDFDGKNRGYAFYMYCHKHEAKRAVREL NNYBIRPGRLLGVCCSVDNCRLFIGGIPKMKKREEILEEIAKVT EGVLDVIVYASAADKMKNRGLRLRGVREPPRGCHWLGRKLIAWX ASSLWG		,	j	TYPOLOGYTHE FOANDALED TAREFUL TO THE TOTAL
7049 393 938 KRTGSASYGGPPPGLGGPATXASVAGRCSSVGKIPARRCYEDEL VPVFEAVGRIYELRLMMDFDGKNRGYAFVMYCHKHEAKRAVREL NNYBIRPGRLLGVCCSVDNCRLFIGGIPKMKKREEILEEIAKVT EGVLDVIVYASAADKMKNRGLRLRGVREPPRGCHWLGRKLIAWX ASSLWG]	i	EKKW
VPVFEAVGRIYELRIMMDFDGKNRGYAFVMYCHKHEAKRAVREL NNYBIRPGRLLGVCCSVDNCRLFIGGIPKMKKREEILEEIAKVT EGVLDVIVYASAADKMKNRGLRLRGVREPPRGCHWLGRKLIAWX ASSLWG	7049	393	938	
NNYEIRPGRLLGVCCSVDNCRLFIGGIPKMKKREEILEEIAKVT EGVLDVIVYASAADKMKNRGLRLRGVREPPRGCHWLGRKLIAWX ASSLWG		·		VPVFEAVGRIVELDI.MMDEDGVADGUS BERVOLUNIA COLOR
EGVLDVIVYASAADKMKNRGLRLRGVREPPRGCHWLGRKLIAWX ASSLWG]	ļ	NNYEIRPGRLIGVCCSVDNCRI, ETCCTDVMVVDEBTI BETTE
ASSLWG			ſ	EGVLDVIVYASAADKMKNRGLRLRGVREDDRGCHWIGDRITAGV
7050 393 938 KRTGSASYGGPPPGLGGPATXASVAGRCSSVGKIPARRCYEDEL				ASSLWG
	7050	393	938	KRTGSASYGGPPPGLGGPATXASVAGRCSSVGKIPARRCYEDEL

SEQ	Predicted	Predicted end	I bring and
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ļ	location	corresponding	HaHistidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ł	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			VPVFEAVGRIYELRIMMDFDGKNRGYAFVMYCHKHEAKRAVREL
ı	1		NNYEIRPGRLLGVCCSVDNCRLFIGGIPKMKKREEILEEIAKVT
			EGVLDVIVYASAADKMKNRGLRLRGVREPPRGCHWLGRKLIAWX
L	1		ASSLWG
7051	119	816	KKMNLABICDNAKKGREYALLGNYDSSMVYYQGVMQQIQRHCQS
	ł		VRDPAIKGKWQQVRQELLEEYEQVKSIVGTLESFKIDKPPDPPV
ł	1		SCQDEPFRDPAVWPPPVPAEHRAPPQIRR/RQSRSKTSEERNGR
}	}		SRSPGTCRPST\PISKSEKPSTSRDKDYRARGRDDKGRKNMQDG
l			ASDGEMPKFDGAGYDKDLVEALERDIVSRNPSIHWDDIADLEEA
			KKLLREAGVLPMWM
7052	467	715	SCPGRGKMSKLLNPEEMTSRDYYFDSYAHFGIHEEMLKDEVRTL
			TYRNSMYHNKHVFKDKVVLDVGSGTGILSMFAARQGPRR
7053	467	715	SCPGRGKMSKLLNPEEMTSRDYYFDSYAHFGIHEEMLKDEVRTL
L			TYRNSMYHNKHVFKDKVVLDVGSGTGILSMFAARQGPRR
7054	1	1036	GTSQRSRETDARRRSAGAEPTARLPWPAALEEWPSCPCEPLGPG
			RRCRWDAMEYDEKLARFRQAHLNPFNKQSGPRQHEQGPGEEVPD
1 1	1		VTPEEALPELPPGEPEFRCPERVMDLGLSEDHFSRPVGLFLASD
1 1			VQQLRQAIEECKQVILELPEQSEKQKDAVVRLIHLRLKLQELKD
ł			PNEDEPNIRVLLEHRFYKEKSKSVKQTCDKCNTIIWGLIQTWYT
i l			CTGCYYRCHSKCLNLISKPCVSSKVSHQAEYELNICPETGLDSQ
1)	ļ		DYRCAECRAPI/CS/DGVVPSEARQCDYTGQYYCSHCHWNDLAV
			IPARVVHNWDFEPRKVSRCSMRYLALMVSRPVLRLREIN
7055	2	527	DSRRVSWRSWLANE/WGKHLCLFIWLSMNVLLEWKTRLLVNGGR
1 1			EYHYLHQMLG/ALCLSRASASVLNLNCSLILLPMCRTLLAVLRC
			SQKVPSRRTRRLLDKSRTFHITCGATICIFSGVHVAAHT.UNALN
1 [ĺ		FSVNYSEDFVELNAARYRDEDPRKLLFTTVPGLTGVCMEVVLFL
7056			M
1.036	2	527	DSRRVSWRSWLANE/WGKHLCLPIWLSMNVLLFWKTFLLYNQGP
1 1	ľ		EYHYLHQMLG/ALCLSRASASVININCSI.TIJ.DMCDTIIAVIDG
1 1	ł		SQKVPSRRTRRLLDKSRTFHITCGATICIFSGVHVAAHI.VNALN
1			FSVNYSEDFVELNAARYRDEDPRKLLFTTVPGLTGVCMEVVI.FI.
7057	- 3260		M
1,037	1368	431	GIYLHVNEKIPRPTCIGDRQENDKENLNLENHRDQELLHASCQA
J. J			SGEVPSQASLRGFFTEDEPGCFGEGENLPEALONIODEGTGEOL
		j	SPQERISEKQLGQHLPNPHSGEMSTMWLEEKRRTSOKGODDADM
]			AQKLPTCRECGKTFYRNSQLIFHORTHTGETYFOCTTCKKAFIB
1 1	[SSDFVKHQRTHTGEKPCKCDYCGKGFSDFSGLRHHEKTHTGEKP
1		•	YKCPICEKSFIQRSNFNRHQRVHTGEKPYKCSHCGKSFSWSSSL
1	1		DKHQRSHLGKKPFQ*PVTKLSFPISISQPSHKNTOLHOEELCLR
7058	1	469	GYPC
1	-	עס צי	FSGFGAVPDALGCRMSDLRITEAFLYMDYLCFRALCCKGPPPAR
}	1	1	PEYDLVCIGLTGSGKTSLLSKLCSESPDNVVSTTGFSIKAVPFQ
1		į	NAILNVKELGGADNIRKYWSRYYQGSQGVIFVLDSASSEDDLEA
7059	1	1178	ARN*SCTQLLQHPQLCTLPFLILA
1	=		WPAFPRQPAAAAMDALLGTGPRRARGCLGAAGPTSSGRAARTPA
j l	ļ	ŀ	APWARPSAWLECVCVVTFDLELGQALELVYPNDFRLTDKEKSSI
] [ŀ	CYLSFPDSHSGCLGDTQFSFRMRQCGGQRSPWHADDRHYNSRAP
[]			VALQREPAHYFGYVYFRQVKDSSVKRGYFQKSLVLVSRLPFVRL
1 1	ł		FQALLSLIAPEYFDKLAPCLEAVCSEIDQWPAPAPGQTLNLPVM
			GVVVQVRIPSRVDKSESSPPKQFDQENLLPAPVVLASVHELDLF
	ł	Į	RCFRPVLTHMOTLWELMLLGEPLLVLAPSPDVSSEMVLALTSCL
l j			QPLRFCCDPRPYFTIHDSEPKEFTTRTQAPPNVVLGVTNPFFIK
7060	90	1670	TLQHWPHILRVGEPKMSGDLPKQVKLKKPFKV*RPWDTKP
		10,0	SVNLPPSLWPNEEAMDSTKSEPLKGSPEAEDGNIEYKKLVNPSQ
			YRFEHLVTQMKWRLQEGRGEAVYQIGVEDNGLLVGLAEEEMRAS

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
}	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ĺ		amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /-possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
	1		LKTLHRMAEKVGADITVLREREVDYDSDMPRKITEVLVRKVPDN
1	ł	ł	QQFLDLRVAVLGNVDSGKSTLLGVLTQGELDNGRGRARLNLFRH
}			LHEIQSGRTSSISFEILGFNSKGEVHGINGTQWGQTLRMGW***
į		}	RT*DGGRVWRLFEIV*MNALRGL*TSSAPLRKSMGNQLN*IKNG
	1	1	VKIKRQGHPGNGLGPGNSEGVGRAGRRH*GPWALGQVVNYSDSR
ļ			TAEEICESSSKMITFIDLAGHHKYLHTTIFGLTSYCPDCALLLV
l.			SANTGIAGTTREHLGLALALKVPFFIVVSKIDLCAKTTVERTVR
1			QLERVLKQPGCHKVPMLVTSEDDAVTAAQQFAQSPNVTPIFTLS
			SVSGESLDLLKVFLNILPPLTNSKEQEELMQQLTEFQVDEIYTV
			PEVGTVVGGTLSR*IDLLATLPTQPSPIYSKTSWPKGGDPGI
7061	364	710	ARMPSPLGPPCLPVMDPETTLEEPETARLRFRGFCYQEVAGPRE
1			ALARLRELCCQWLQPEAHSKEQMLEMLVLEQFLGTLPPEIQAWV
ĺ			RGQRPGSPEEAAALVEGLQHDP*ARMPSPLGPPCLPVMDPETTL
İ			EEPETARLRFRGFCYQEVAGPREALARLRELCCQWLQPEAHSKE
1			QMLEMLVLEQFLGTLPPEIQAWVRGQRPGSPEEAAALVEGLQHD
7062	 		PGQLLG
7002	71	744	AKAGTNLERLHWLSYFFCIPKHKLKSSQKDKVRQFMACTQAGER
			TAIYCLTQNEWRLDEATDSFFQNPDSLHRESMRNAVDKKKLERL
l	1	[YGRYKDPQDENKIGVDGIQQFCDDLSLDPASISVLVIAWKFRAA
l			TQCEFSRKEFLDGMTELGCDSMEKLKALLPRLEQELKDTAKFKD
1			FYQFTFTFAKNPGQKGLDL*MAGAYWKLVLSGRFKFLYLWNTFL
7063	2		менн
/ /003	4	562	LRTVPDLPGRRFRAMRTGQRR*PELPPDMNSLEQAEDLKAFERR
ļ			LTEYIHCLQPATGRWRMLLIVVSVCTATGAWNWLIDPETQKVSF
1	ł		FTSLWNHPFFTISCITLIGLFFAGIHKRVVAPSIIAARCRTVLA
]			EYNMSCDDTGKLILKPRPHVQ*QSSLIVMGLKIAFLRISDTAKS
7064	300	884	HKGFLLRLDM ·
, , , ,	}	004	RDTGSDPSSTRRLCSTCCTGH*PAEPIASPHPSRGTCPPASSAS
	1		SRRTGCWTCPPESGHAQARRSRRASASRWGARGAVRSAVAARGC SSRAGRWLETPGRRRGPPACAAAAGRLRGPAP+AAPPTASVPAR
			CRCPAARTGAPAAATWLRRRLSGLRAPALGRRRSPGPSPKSAAP
)		PLLTPLGAGRAGGSRANS
7065	1	555	
) -	J-33	ATTTHSARRSGRGAAAEAAASAAGGRQKGPDRKAWEGRRTTPGG RSQSEPKAPPPQKRSEAAFASMAHSPVAVQVPGMQNNIADPEEL
	·	,	FTKLERIGKGSFGEVFKGIDNRTQQVVAIKIIDLEEAKDEIEDI
	<i>.</i>		QQEITVLSQCDSSYVTKYYGSYLKGSKLWIIMEYLGGGSALDLL
			RAGPFDEFO
7066	356	676	PGPQRGPWRAREGGHPLDPADHPRAPASLRSNVRAATMMQICDT
		-70	YNQKHSLFNAMNRFIGAVNNMDQTVMVPSLLRDVPLADFGLDND
			VGVEVGGSGGCLEERTPP
7067	152	973	KENITMATEIGSPPRFFHMPRFQHQAPRQLFYKRPDFAQQQAMQ
]	-,-	QLTPDGKRMRKAVNRKTIDYNPSVIKYLENRIWQRDQRDMRAIQ
•	<u> </u>		PDAGYYNDLVPPIGMLNNPMNAVTTKFVRTSTNKVKCPVFVVRW
	·		TPEGRRLVTGASSGEFTLWNGLTFNFETILQAHDSPVRAMTWSH
			NDMWMLTADHGGYVKYWQSNMNNVKMFQAHKEAIREARFIHNIP
			FSVVPIVMVKLPSKCILGAEMHGLCQFLGNFLHPINTIFFFVFT
			HSPFCWAPF
7068	222	816	DTMKEYVLLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDD
			DDDDDDDDDDDDDDDDSLFPTREPRSHFFPFDLFPMCPFGCQCYSRV
	}		VHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLY
			GLILMANKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLMLPKSL
			AELRIHENKVKKIOKOTFKKK
7069	1147	1765	FRDHRRYFYVNEQSGESQWEFPDGEEEEEESQAQENRDETLAKO
	,	2705	TLKDKTGTDSNSTESSETSTGSLCKESFSGQVSSSSLMPLTPFW
J	}		TLLQSNVPVLQPPLPLEMPPPPPPPPESPPPPPPPPPPPPPPPPPPPPPPP
——			

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
Í	corresponding	to first	L-Leucine, M-Methionine, N-Asparagine,
l	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
}	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
	 		EKTKKGRKDKAKKSKTKMPSLVKKWQSIQRELDEEDNSSSSEED
			RVSTAQKRIEEWKQQQLVSGMAERNANFEA
7070	1	547	DGTMEDSEAVQRATALIEQRLAQEEENEKLRGDARQKLPMDLLV
ļ	}		LEDBKHHGAQSAALQKVKGQERVRKTSLDLRREIIDVGGIQNLI
	i		ELRKKRKQKKRDALAASHEPPPEPEEITGPVDEETFLKAAVEGK
1			MKVIEKFLADGGSADTCDQFRRTALHRASLEGHMEILEKLLDNG
L	1		ATVDFQ
7071	2	921	ARGTLRALETAKKVGKVGANGQKAAGPSADSVTENKIGSPPKTP
1	J		VSNVAATSAGPSNVGTELNSVPQKSSPFLTRVPAYPPHSENIQY
			FQDPRTQIPFEVPQYPQTGYYPPPPTVPAGVAPCVPRFVRSNNU
ľ			PESSI, PPASMPYADHYSTFSPRDRMNSSPYOPPPPOPYGPVPPV
			PSGMYAPVYDSRRIWRPPMYQRDDIIRSNSLPPMDVMHSSVYOT
Į.			SLRERYNSLDGYYSVACQPPSEPRTTVPLPREPCGHLKTSCEEO
			IRRKPDQWAQYHTQKAPLVSSTLPVATQSPTPPSTLNRGEGS
7072	2	921	ARGTLRALETAKKVGKVGANGQKAAGPSADSVTENKIGSPPKTP
1	1		VSNVAATSAGPSNVGTELNSVPQKSSPFLTRVPAYPPHSENIOY
	i		FODPRTQIPFEVPQYPQTGYYPPPPTVPAGVAPCVPRFVRSNNV
1	•		PESSLPPASMPYADHYSTFSPRDRMNSSPYQPPPPQPYGPVPPV
1	'		PSGMYAPVYDSRRIWRPPMYQRDDIIRSNSLPPMDVMHSSVYQT
4.			SLRERYNSLDGYYSVACQPPSEPRTTVPLPREPCGHLKTSCEEQ
7073	50		IRRKPDQWAQYHTQKAPLVSSTLPVATQSPTPPSTLNRGEGS
'''	50	504	LAHGSFGVSDFPAPAAAPAHTLTSFSGSLSPQFRKPLGRAPAMP
1 1	·		LVRYRKVVILGYRCVGKTSLAHQFVEGEFSEGYDPTVENTYSKI
1 1	•		VTLGKDEFHLHLVDTAGQDEYSILPYSFIIGVHGYVLVYSVTSL
7074	263	1003	HSFQVIESLYQKLHEGHGK
		2005	VCPVLCSTRQEPGHSSLVTYFGKPTRRKEFLLGHCIAAGKMNIS VDLETNYAELVLDVGRVTLGENSRKKMKDCKLRKKQNERVSRAM
			CALLNSGGGVIKAEIENEDYSYTKDGIGLDLENSFSNILLFVPE
1	1		YLDFMQNGNYFLIFVKSWSLNTSGLRITTLSSNLYKRDITSAKV
			MNATAALEFLKDMKKTRGRLYLRPELLAKRPRVDIQEENNMKAL
	ı		AGVFFDRTELDRKEKLTFTESTHVEI
7075	598	1005	NYINFFFRKEYPPHVQKVEINPVRLSRLQGVERIMKKTEESESQ
1 1	j		VEPEIKRKVQQKRHCSTYQPTPPLSPASKKCLTHLBDLQRNCRQ
	i	•	AITLNESTGPLLRTSIHQNSGGQKSQNTGLTTKKFYGNNVEKVP
		•	IDII
7076	279	1049	LOSESSNAAEGNEORHEDEORSKRGGWSKGRKRKKPLRDSNAPK
			SPLTGYVRFMNERREQLRAKRPEVPFPEITRMLGNEWSKLPPEE
			KQRYLDEADRDKERYMKELEQYQKTEAYKVFSRKTQDRQKGKSH
l 1			RQDAARQATHDHEKETEVKERSVFDIPIFTEEFLNHSKAREAEL
1 1			RQLRKSNMEFEERNAALQKHVESMRTAVEKLEVDVIQERSRNTV
2000			LQQHLETLRQVLTSSFASMPLPEXGETPTVDTIDSYM
7077	3	1119	SSMGSNSEINGLALRKTDKYGFLGGSQYSGSLKSSIPVDVARQR
1			ELKWLDMFSNWDKWLSRRFQKVKLRCRKGIPSSLRAKAWQYLSN
Į į	1		SKELLEQNPRKFEBLERAPGDPKNLDVIEKDLHROFPFHEMFAA
1 1	1		RGGHGQQDLYRILKAYTIYRPDEGYCQAQAPVAAVLLMHMPAEQ
	1	ľ	AFWCLVQICDKYLPGYYSAGLEAIQLDGBIFFALLRRASPLAHR
}		• 1	HLRRQRIDPVLYMTEWFMCIFARTLPWASVLRVWDMFFCEGVKI
1		ł	IFRVALVLLRHTLGSVEKLRSCQGMYETMEQLRNLPQQCMQEDF
	.		LVHEVTNLPVTEALIERENAAQLKKWRETRGELQYRPSRRLHGS
7078	483	767	RAIHEERRRQQPPLGPSSS
	103	767	FQGQRMAGEQKPSSNLLEQFILLAKGTSGSALTALISQVLEAPG
1	1	ł	VYVFGELLELANVQELAEGANAAYLQLLNLFAYGTYPDYIANKE
7079	2	376	SLPELY
	-	٥,٠	SVVEPKRPKEPSGSDGESDGPIDVGQEGQLSQMARPLSTPSSSQ
	·		MQARKKRRGIIEKRRRDRINSSLSELRRLVPTAFEKQGSSKLEK

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	Hatistidine, ImIsoleucine, Kalysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	Securing T. Theread W. M. A.
1	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ļ	sequence	sequence	Codon, /=possible nucleotide deletion, -possible nucleotide insertion)
	-54-5		/=possible nucleotide insertion)
7080	200	595	ABVLQMTVDHLKMLHATGGTGTHALLFQASFIQQIF
1	""] 333	VQLPLEAPCLSLLSCRDHSGGNRDLSRRHRDCRVYGSPQDGIPY
		İ	LTHPLCHQDVVSVGRLQIRALATPGHTQGHLVYLLDGEPYKGPS
7081	213	506	CLFSGDLLFLSGCGEFPRKRBELGEEGETEVRAATVPWRALKP
''		500	AVTEEEMILNSLSLCYHNKLILAPMVRVGTLPMRLLALDYGADI
1			VYCEELIDLKMIQCKRVVNEVLSTVDFVAPDDRVVFRTCEREQN RVVFOMGTS
7082	3	1137	
/ / / / /	1	1137	APSRNTMLMAWCRGPVLLCLRQGLGTNSFLHGLGQEPFEGARSL
	1		CCRSSPRDLRDGEREHEAAQRKAPGAESCPSLPLSISDIGTGCL
			SSLENLRLPTLREESSPRELEDSSGDQGRCGPTHQGSEDPSMLS
I		}	QAQSATEVEERHVSPSCSTSRBRPFQAGELILAETGEGETKFKK
ı			LFRLNNFGLLNSNWGAVPFGKIVGKFPGQILRSSFGKQYMLRRP
ĺ			ALEDYVVLMKRGTAITFPKDINMILSMMDINPGDTVLEAGSGSG
i			GMSLFLSKAVGSQGRVISFEVRKDHHDLAKKNYKHWRDSWKLSH
			VEEWPDNVDFIHKDISGATEDIKSLTFDAVALDMLNPHVTLPVF
7083	115	541	YPHLKHGGVCPVYVVNITQVIELLD
		347	RSNAVQLTRMEYAMKSLSLLYPKSLSRHVSVRTSVVTQQLLSEP
			SPKAPRARPCRVSTADRSVRKGIMAYSLEDLLLKVRDTLMLADK
1			PFFLVLEEDGTTVETEEYFQALAGDTVFMVLQKGQKWQPPSEQG TRHPLSLSHK
7084	3	522	NSVSVSSQSRFLASVPGTGVQRSAAADMAASTAAGKQRIPKVAK
1		344	WOWN DREWOTTHEOUT BEAKENING BY A BRESCHATTER
· .			VKNKAPAEVQITAEQLLREAKERELELLPPPPPQQKITDEEELND YKLRKRKTFEDNIRKNRTVISNWIKYAQWEESLKEIQRARSIYE
1 1			RALDVDYRNITLWLKYAEMEMKNRQVNHARNIWDRAITTL
7085	243	1499	RQLARLRRRGWRSPFGGAPMAHITINQYLQQVYEAIDSRDGASC
ł I			ABLVSFKHPHVANPRLQMASPEEKCQQVLEPPYDEMFAAHLRCT
1 1			YAVGNHDFIEAYKCQTVIVQSFLRAFQAHKEENWALPVMYAVAL
			DLRVFANNADQQLVKKGKSKVGDMLEKAABLLMSCFRVCASDTR
			AGIEDSKKWGMLFLVNQLFKIYFKINKLHLCKPLIRAIDSSNLK
ł ł	1		DDYSTAQRVTYKYYVGRKAMFDSDFKQAEEYLSFAFEHCHRSSQ
			KNKRMILIYLLPVKMLLGHMPTVELLKKYHLMQFAEVTRAVSEG
i i			NLLLHEALAKHEAFFIRCGIFLILEKLKIITYRNLFKKVYLLL
1 1			KTHQLSLDAFLVALKFMQVEDVDIDEVQCILANLIYMGHVKGYI
			SHQHQKLVVSKQNPPPPLSTGC
7086	256	525	ILAARMGKQNSKLRPEVMQDLLESTDFTEHEIQEWYKGPLRDCP
			SGHLSMEEFKKIYGNPPPYGDASKFAEHVFRTFDANGDGTIDFR
			EF
7087	166	723	LSGSSAGKVAAPCVPPSNHELVPITTENAPKNVVDKGEGASRGG
j			NTRKSLEDNGSTRVTPSVQPHLQPIRNMSVSRTMEDSCELDLVY
[1		VTERIIAVSFPSTANEENFRSNLREVAQMLKSKHGGNYLLFNLS
] [*	ERRPDITKLHAKVLEFGWPDLHTPALEKICSICKAMDTWLNAHP
			HRCRVLHNKG
7088	104	759	GTSAASPSSLLEMAGEITETGELYSSYVGLVYMFNLIVGTGALT
[]			MPKAFATAGWLVSLVLLVFLGFMSFMTTTFVIEAMAAANAQLHW
	!		KRMENLKEEEDDDSSTASDSDVLIRDNYERAEKRPILSVORRGS
	ļ	.]	PNPFEITDRVEMGQMASMFFNKVGVNLFYFCIIVYLYGDLAIYA
			AAVPFSLMQVTCSATGNDSCGVEADTKYNDTDRCWGPLRRVD
7089	33	1775	SVCWEDRYLKARMEESPLSRAPSRGGVNFLNVARTYIPNTKVEC
			HYTLPPGTMPSASDWIGIFKVEAACVRDYHTFVWSSVPESTTDG
		į	SPIHTSVQFQASYLPKPGAQLYQFRYVNRQGQVCGOSPPFOFRE
			PRPMDELVTLEEADGGSDILLVVPKATVLQNQLDESQQERNDLM
1			QLKLQLEGQVTELRSRVQELERALATARQEHTELMEQYKGISRS
	j	•	HGEITEERDILSRQQGDHVARILELEDDIQTISEKVLTKEVELD
1	Ī		RLRDTVKALTREQEKLLGQLKEVQADKEQSEAELQVAQQENHHL
<u> </u>		İ	NLDLKEAKSWQEEQSAQAQRLKDKVAQMKDTLGQAQQRVAELEP

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F-Phenylalanine, G-Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1 1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
] }	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
•	amino acid	sequence	Codon, /=possible nucleotide deletion,
1 1	sequence	004	\=possible nucleotide insertion)
		· · · · · · · · · · · · · · · · · · ·	LKEQLRGAQELAASSQQKATLLGEELASAAAARDRTIAELHRSR
1 1			LEVAEVNGKLAELGLHLKEEKCQWSKERAGLLQSVEAEKDKILK
			LSAEILRLEKAVQEERTQNQVFKTELAREKDSSLVQLSESKREB
1			TELRSALRVLQKEKEQLQEEKQELLEYMRKLEARLEKVADEKWN
1			EDATTEDEBAAVGLSCPAALTDSEDESPEDMRLHPMAFVSVETQ
1 1			ASLLIGLE
7090	33	1775	SVCWEDRYLKARMEESPLSRAPSRGGVNFLNVARTYIPNTKVEC
1 ,050	33	1773	
1 1			HYTLPPGTMPSASDWIGIFKVEAACVRDYHTFVWSSVPESTTDG
1			SPIHTSVQFQASYLPKPGAQLYQFRYVNRQGQVCGQSPPFQFRE
			PRPMDELVTLBEADGGSDILLVVPKATVLQNQLDESQQERNDLM
]]	•		QLKLQLEGQVTELRSRVQELERALATARQEHTELMEQYKGISRS HGEITEERDILSRQQGDHVARILELEDDIQTISEKVLTKEVELD
1	•		
1			RLRDTVKALTREQEKLLGQLKEVQADKEQSEAELQVAQQENHHL NLDLKEAKSWQEEQSAQAQRLKDKVAQMKDTLGQAQQRVAELEP
1 [
1 1			LEVA FUNCYLARICH HIVE FOR COME YEAR OF THE PROPERTY OF THE PRO
1			LEVAEVNGKLAELGLHLKEEKCOWSKERAGLLOSVEAEKDKILK
1 1			LSAEILRLEKAVQEERTQNQVFKTELAREKDSSLVQLSESKREL
1 1			TELRSALRVLQKEKEQLQEEKQELLEYMRKLEARLEKVADEKWN
1			EDATTEDEEAAVGLSCPAALTDSEDESPEDMRLHPMAFVSVETQ ASLLLGLE
7091	186	1076	
1 .05	100	1076,	EGMLTREHRCGRSEEQELEPWPSPKKARSGRWLRNGFKRKMEEP
1 1			EEPADSGQSLVPVYIYSPEYVSMCDSLAKIPKRASMVHSLIEAY
1 1			ALHKQMRIVKPKVASMEEMATFHTDAYLQHLQKVSQEGDDDHPD SIEYGLGYDCPATEGIFDYAAAIGGATITAAQCLIDGMCKVAIN
]]			WSGGWHHAKKDEASGFCYLNDAVLGILRLRRKFERILYVDLDLH
1 1			HGDGVEDAFSFTSKVMTVSLHKFSPGFFPGTGDVSDVGLGKGRY
]]			YSVNVPIQDGIQDEKYYQICERYEPPAPNPGL
7092	522	809	KQGINEDQEESQKPRIGEGCEPISKRQMKKLIKQKQWEEQRELR
	1	00,	KQKRKEKRKKLERQCQMEPNSDGHDRKRVRRDVVHSTLRLII
1			DCSFDXLM
7093	454	655	NFGVSGVELAQQASMVRMSFVIAACQLVLGLLMTSLTESSIQNS
	•••	033	ECPQLCVCEIRPWFTPQSTYREA
7094		508	
''''	•	306	FVRSMHWGVGFASSRPCVVDLSWNQSISFFGWWAGSEBPFSFYG
[[i i		DIIAFPLODYGGIMAGLGSDPWWKKTLYLTGGALLAAAAYLLHE
] }			LLVIRKQQEIDSKDAIILHQFARPNNGVPSLSPFCLKMETYLRM
7095	1	411	ADLPYQNYFGGKLSAQGKMPWIEYNHEKVSGTEFII
	*	447	IASSLPKMASLLQSDRVLYLVQGEKKVRAPLSQLYFCRYCSELR SLECVSHEVDSHYCPSCLENMPSABAKLKKNRCANCFDCPGCMH
, I			
1 1			TLSTRATSISTQLPDDPAKTTMKKAYYLACGFCRWTSRDVGMAD KSVGE
7096	224	2067	I
''''	244	2007	ETRSLAVQEKPSQAGRRRSSRISFAGALFLTRFLLQELLLNNFC
1	,		SAMSPAPDAAPAPASISLFDLSADAPVFQGLSLVSHAPGEALAR
			APRTSCSGSGERESPERKLLQGPMDISEKLFCSTCDQTFQNHQE
	1		QREHYKLDWHRFNLKQRLKDKPLLSALDFEKQSSTGDLSSISGS
[[[EDSDSASEEDLQTLDRERATFEKLSRPPGFYPHRVLFQNAQGQF
1			LYAYRCVLGPHQDPPREAELLLQNLQSKGPRDCVVLMAAAGHFA
[Ĭ		GAIFQGREVVTHKTFHRYTVRAKRGTAQGLRDARGGPSHSAGAN
]]	,	•	LRRYNBATLYKDVRDLLAGPSWAKALEEAGTILLRAPRSGRSLF
] [1		FGGKGAPLQRGDPRLWDIPLATRRPTFQELQRVLHKLTTLHVYE
j	1		EDPREAVRLHSPQTHWKTVREERKKPTEEEIRKICRDEKEALGQ
) !	1		NEESPKQGSGSEGEDGFQVELELVELTVGTLDLCESEVLPKRRR
	1		RKRNKKEKSRDQEAGAHRTLLQQTQEEEPSTQSSQAVAAPLGPL
			LDEAKAPGQPELWNALLAACRAGDVGVLKLQLAPSPADPRVLSL
7097			LSAPLGSGGFTLLHAAAAAGRGSVVRLLLEAGADPTVQCQDH
	256	1228	IRTKSAATWEAWPQCGREGSRIITEPCEANAGSRQELQTERISS
'**'			FLAAQGDQAFHSGLETNNSNSELPLRVGLKVAQGSPLMGGQVSA

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine.
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine.
i	residue of	residue of	S=Serine, T=Threonine, V=Valine,
1	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
}	sequence	sequence	Codon, /=possible nucleotide deletion,
	Bodgence		\=possible nucleotide insertion)
į.			SNSFSRLHCRNANEDWMSALCPRLWDVPLHHLSIPGSHDTMTYC
			LNKKSPISHEESRLLQLLNKALPCITRPVVLKWSVTQALDVTEQ
		•	LDAGVRYLDLRIAHMLEGSEKNLHFVHMVYTTALVEDTLTEISE
i	•]	WLERHPREVVILACRNFEGLSEDLHEYLVACIKNIFGDMLCPRG EVPTLRQLWSRGQQVIVSYEDESSLRRHHBLWPGVPYWWGNRVK
1			TEALIRYLETMKSCGR
7098	82	956	SSFLKRCRKVLGCWGIPSEQSLFSTLEEPRDKEIDNYCVMRLQT
	1		EARSGFWAPNRFPVNICRMTAVDGDRGGSSRETCRCHFHPSLEA
1	1		LVLLLQDWQPGGVGICTSFLGISWALLDYHRALRTCLPSKPLLG
1	j		LGSSVIYFLWNLLLLWPRVLAVALFSALFPSYVALHFLGLWLVL
1			LLWVWLQGTDFMPDPSSEWLYRVTVATILYFSWFNVAEGRTRGR
1	ŀ		AIIHFAFLLSDSILLVATWVTHSSWLPSGIPLOLWLPVGCGCFF
			LGLALRLVYYHWLHPSCCWKPDPDQVD
7099	992	210	LFRLAPGFLRSLARQGYHQIWAFPFLPSGATATWPAASRSRSLA
ł			ARSLPRSPARPGPNDALLGEHDFRGQGVRAORFRFSRRPGPGAD
1			GAVLEVHVPQIGAGVSLPGILAAKCGAEVILSDSSELPHCLEVC
1			ROSCOMNNLPHLQVVGLTWGHISWDLLALPPQDIILASDVFFEP
			BDFEDILATIYFLMHKNPKVQLWSTYQVRSADWSLEALLYKWDM
7100	205	671	KCVHIPLESFDADKEDIAESTLPGRHTVEMLVISFAKDSL
		971	ANGGFWEAAPGSEVSLPLWVPTASHSKTTALGIGSAPPPHLSVL
1 1			PLFSFPPQLGDPLEAPPVFKKYDRNGLNVSIECKRVSGLEPATV DWAFDLTKTNMQTMYEQSEWGWKDREKREEMTDDRAWYLIAWEN
L			SSVPVAFSHFFFDVERGDEVLYW
7101	2	503	WRGGPRRAKRLAGGAVGWVLLVRGVHSVRAGGGRPPRAADMKKD
]			VRILLVGEPRVGKTSLIMSLVSEEFPEEVPPRAEEITIPADVTP
1			ERVPTHIVDYSEAEQSDEQLHQEISQANVICIVYAVNNKHSIDK
			VTSRWIPLINERTDKDSRLPLILGGNKSDLVRYSR
7102	2	503	WRGGPRRAKRLAGGAVGWVLLVRGVHSVRAGGGRPPRAADMKKD
1	1		VRILLVGEPRVGKTSLIMSLVSEEFPEEVPPRAKEITIPADUTD
1 1			ERVPTHIVDYSEAEQSDEQLHQEISQANVICIVYAVNNKHSIDK
7103	119		VTSRWIPLINERTDKDSRLPLILGGNKSDLVEYSR
1 /203	119	438	GSQSSVAVNIRSGTDEESMDLMNGQASSVNIAATASEKSSSES
1	f		LSDKGSELKKSFDAVVFDVLKVTPBEYAGQITLMDVPVFKAIQP
7104	1670	795	DELSSCGWNKKEKYSSAP
1		, , , ,	RLWEHRSVSAGASGWGLSSPGCLLLHPSLPEEERVDYLINNAGV MRCPHWTTEDGFEMQFGVNHLGEAWAGAAPWVQAILPRRPPKVL
1	1		GF*V*VKSDLFIILNPGHFLLTNLLLDKLKASAPSRIINLSSLA
			HVAGHIDFDDLNWQTRKYNTKAAYCQS\KLAIVLFTKELSRRLQ
	J		GSGVTVNALHPGVARTELGRHTGIHGSTFLQHHN\WAHLLAAWS
			KSPRSWPAPAQHNTLAVAEELA\VISGKYFDGLKQKAPAPEAED
7.5			EEVARRLWAESARLVGLEAPSVREOPLPR
7105	765	143	GQMCRRPSPKSTSCLSMTCDLP/RGLQDPQCLALFRVAVDKHOA
	i i	ļ	LLKAAMSGQGVDRHLFALYIVSRFLHLQSPFLTOVHSEOWOLST
1	İ	ļ	SQIPVQQMHLFDVHNYPDYVSSGGGFGPADDHGYGVSYIFMGDG
ł	1	l	MITFHISSKKSSTKTDSHRLGQHIEDALLDVASLFOAGOHFKRR
7106	14		FRGSGKENSRHRCGFLSRQTGASKASMTSTDF
	**	1064	GLQAGHPHPRSASRIPEADTH\YSKLQRAFDSIVNKDHKRMFGT
	ļ	ļ	YFRVGFFGSKFGDLDEQEFVYKEPAITKLPEISHRLEAFYGQCF
]	ļ	GAEFVEVIKDSTPVDKTKLDPNKAYIQITFVEPYFDEYEMKDRV
	j	1	TYFEKNFNLRRFMYTTPFTLEGRPRGELHEQYRRNTVLTTMHAF
		İ	PYTKTRISVIQKEEFVLTPIEVAIEDMKKKTLQLAVAINQEPPD
l		}	AKMLQMVLQGSVGATVNQGPLEVAQVFLAEIPADPKLYRHINKL RLCFKEFIMRCGEAVEKNKRLITADQREYQQBLKKNYNKLKBNL
		[RPMIERKIPELYKPIFRVESQKRDSFHRSSFRKCETQLSQGS
7107	1145	591	*I*WLQTGKKK
			

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, P-Phenylalanine, G-Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
İ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
}	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
}	sequence	,	\=possible nucleotide insertion)
7108	1	942	VKVALLLTNLEQPRTESEWENSFTLKMFLFQFVNLNSSTFYIAF
			FLGRFTGHPGAYLRLINRWRLEECHPSGCLIDLCMQMGIIMVLK
			QTWNNFMELGYPLIQNWWTRRKVRQEHGPERKISFPQWEKDYNL
1		ł	QPMNAYGLFDEYLEMILQFGFTTIFVAAFPLAPLLALLNNIIEI
1			RLDAYKFVTQWRRPLASRAKDIGIWYGILEGIGILSVITNAFVI
J	}		AITSDFIPRLVYAYKYGPCAGQGEAGQKCMVGYVNASLSVFRIS
J)	ĺ	DFENRSEPESDGSEFSGTPLKYCRYRDYRDPPHSLVPYGYTLQF
ļ	ļ		WHVLAW
7109	964	102	WDQRKRNSLVPGPAHGPAQEEPWEKKESLGAAQEALSIQLQPKE
1	1		TQPFPKSEQVYLHFLSVVTEDGPEPKDKGSLPQPPITEVESQVF
	1		SEKLATDTSTFEATSEGTLELQQRNPKAERLRWSPAQEESFROM
	1		VVIHKEIPTGKKDHECSECGKTFIYNSHLVVHQRVHSGEKPYKC
			SDCGKTFKQSSNLGQHQRIHTGEKPFECNECGKAFRWGAHLVQH
ł			QRIHSGEKPYECNECGKAFSQSSYLSQHRRIHSGEKPFICKECG
	1		KAYGWCSBLIRHRRVHARKEPSH
7110	96	697	RLDNFSGFLVEVTKEERHIVKPLYDRYRLVKQMLTRASITPVLG
1			SPSTKRRGQMLQPI1EGETAHFFEE1KEEEEDGVNLSSELGDML
1			KTAVQVQSSLKNSESDVEENQEKLALDLRLSSSRAASMPELLEQ
1.	j		LWKARAEKKKLRKTLREFEEAFYQQNGRNAQKEDRVPVLEEYRE
1			YKKIKAKLEVLISKODSSKSI
7111	2	414	GSGLYRGPTPGGQCIWKPNSMPPDHERNFGFTQFALELNELTAE
1	, i		LKRSLPSTDTRLRPDQRYLEEGNIQAAEAQKRRIEQLQRDRRKV
ì			MEENNIVHQARFFRRQTDSSGKEWWVTNNTYWRLRAEPGYGNMD
1	1		GAVLW
7112	103	495	PRCFPVADRGRLIGGLPDVVTIMEGKTLNLTCTVFGNPDPEVIW
]		FKNDQDIQLSEHFSVKVEQAKYVSMTIKGVTSEDSGKYSINIKN
			KYGGEKIDVTVSVYKHGEKIPDMAPPQQAKPKLIPASASAAGQ
7113	1	824	KCLRQAWHEAPSSLAFTRWCSREERAEGGGNLHRSITRDPKPPG
1			LRPSQRPMDDKKKKRSPKPCLAQPAQAPGTLRRVPVPTSHSGSL
1 '			ALGLPHLPSPKQRAKFKRVGKEKCRPVLAGGGSGSAGTPLOHSF
		•	LTEVTDVYEMEGGLLNLLNDFHSGRLQAFGKECSFEOLEHVREM
	•		QEKLARLHFSLDVCGEEEDDEEEEDGVTEGLPEEQKKTMADRNL
1			DQLLSNLGSCLGALVPGGMRGGEGTYSQSHSWALGEKVGVHGSK
			SSGPLNLPRR
7114	3	1492	VWEVDEQIDHYKESQDKFLWQAAFIGKETLKDESGQECKICRKI
	1		IYLNTDFVSVKQRLPKYYSWERCSKHHLNFLGQNRSYVRKKDDG
	1		CKAYWKVCLHYNLHKAQPAERFFDPNQRGKALHQKQALRKSQRS
; l			QTGEKLYKCTECGKVFIQKANLVVHQRTHTGEKPYECCECAKAF
			SQKSTLIAHQRTHTGEKPYECSECGKTFIQKSTLIKHQRTHTGE
.	Ì		KPFVCDKCPKAFKSSYHLIRHEKTHIRQAFYKGIKCTTSSLIYQ
[· .		RIHTSEKPQCSEHGKASDEKPSPTKHWRTHTKENIYECSKCGKS
į l			FRGKSHLSVHQRIHTGEKPYECSICGKTFSGKSHLSVHHRTHTG
İ			EKPYECRRCGKAFGEKSTLIVHQRMHTGEKPYKCNECGKAFSEK
	1	İ	SPLIKHORIHTGERPYECTDCKKAFSRKSTLIKHORIHTGEKPY
			KCSECGKAFSVKSTLIVHHRTHTGEKPYECRDCGKAFSGKSTLI
<u> </u>			KHQRSHTGDKNL
7115	1	947	NAAHGYNWGLWCMYIIPPQDWLDRGDESAPIRTPAMIGCSPVVD
			REYFGDIGLLDPGMEVYGGENVKLGMRVWQCGGSMEVLPCSRVA
1	}		HIERTRKPYNNDIDYYAKRNALRAAEVWMDDFKSHVYMAWNIPM
1	1	.	SNPGVDFGDVSERLALRQRLKCRSFKWYLENVYPEMRVYNNTLT
1			YGEVRNSKASAYCLDQGAEDGDRAILYPCHGMSSQLVRYSADGL
]	LQLGPLGSTAFLPDSKCLVDDGTGRMPTLKKCEDVARPTQRLWD
			FTQSGPIVSRATGRCLEVEMSKDANFGLRLVVQRCSGQKWMIRN
			WIKHARH
7116	866	95	RVRMRRNAEVIEEKLSMKSWAKFRPGEPWKGYPNIDPETDPYVT
]	•	PGSVINNLSINTVREVDHLRDRNSGSSSSLNTTLPSTSAWSSIR
			TOTOMOST TOT

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F-Phenylalanine, G-Glycine,
i	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
i	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ł	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ŀ	amino acid	sequence	Codon, /=possible nucleotide deletion,
ł	sequence	_	\=possible nucleotide insertion)
			ASNYNVPLSSTAQSTSARNSDSKLTWSPGSVTNTSLAHELWKVP
ļ			LPPKNITAPSRPPPGLTGQKPPLSTWDNSPLRIGGGWGNSDARY
1	1		TPGSSWGESSSGRITNWLVLKNLTPQIDGSTLRTLCMQHGPLIT
1		}	FHLNLPHGNALVRYSSKEEVVKAQKSLHISDLFLLTL
7117	695	1261	LLISTPGGCHPPPSSIEFTYTGAWGKALPAPHMPCAPGALPQGA
1			FVSQAARAIPLLQPSQAAQAEGLSQPARACGALCSLPWPLRNWG
1			SPILRLPGGLRTPTNDRKTRTRSAMACWARAQWDTLGPLKLSHR
[Í	ļ	GKVCLRHPRPTGVRGGPGAAGRQGGMGTRRRGTFTSGARDPGGL
			RVKHRCOPTGHLP
7118	49	1863	PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLOPQVE
1			ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHEDLR
			LLLETHLPSKKKKVLLGVGDPKIGAAIQEBLGYNCQTGGVIAEI
	1	1	LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD
			NMIIQSISLLDQLDKDINTFSMRVREWYGYHFPELVKIINDNAT
ľ	ì		YCRLAQFIGNRRELNEDKLEKLEELTMDGAKAKAILDASRSSMG
			MDISAIDLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAPSLS
	ŀ		ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT
l	}		RGNTPKYGLIFHSTFIGRAAAKNKGRISRYLANKCSIASRIDCF
1			SEVPTSVFGEKLREQVEERLSFYETGEIPRKNLDVMKEAMVQAE
i i	ł		EAAAEITRKLEKQEKKRLKKEKKRLAALALASSENSSSTPEECE
]	ļ		EMSEKPKKKKKQKPQEVPQENGMEDPSISFSKPKKKKSFSKEEL
			MSSDLEETAGSTSIPKRKKSTPKEETVNDPEEAGHRSGSKKKRK
			FSKEEPVSSGPEEAAGKSSSKKKKKFHKASQED
7119	49	1863	PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE
1			ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHEDLR
			LLLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEI
			LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD
			NMIIQSISLLDQLDKDINTFSMRVREWYGYHFPELVKIINDNAT
l i	,		YCRLAQFIGNRRELNEDKLEKLEELTMDGAKAKAILDASRSSMG
1 1			MDISAIDLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAPSLS
1 1		:	ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT
			RGNTPKYGLIFHSTFIGRAAAKNKGRISRYLANKCSIASRIDCF
		•	SEVPTSVFGEKLREQVBERLSFYETGEIPRKNLDVMKEAMVOAE
1 1			EAAAEITRKLEKQEKKRLKKEKKRLAALALASSENSSSTPEECE
] }			EMSEKPKKKKKQKPQEVPQENGMEDPSISFSKPKKKKSPSKEEL
[1	Ï	MSSDLEETAGSTSIPKRKKSTPKEETVNDPEEAGHRSGSKKKRK
7120			FSKBEPVSSGPEEAAGKSSSKKKKKFHKASQED
'-20	1991	64	QLGTRRCLRGDKVTNAMQDFLVTNLEPRFIEPQTANLSVVFKDS
	1		NSTTPLIFVLSPGTDPAADLYKFAEEMKFSKKLSAISLGQGQGP
	1		RAEAMMRSSIERGKWVFFQNCHLAPSWMPALERLIEHINPDKVH
i f	1	· ·	RDFRLWLTSLPSNKFPVSILQNGSKMTIEPPRGVRANLLKSYSS
	į	·	LGEDFLNSCHKVMEFKSLLLSLCLFHGNALERRKFGPLGFNIPY
	[EFTDGDLRICISQLKMFLDEYDDIPYKVLKYTAGEINYGGRVTD
'	ļ		DWDRRCIMNILEDFYNPDVLSPEHSYSASGIYHQIPPTYDLHGY
}	ľ	1	LSYIKSLPLNDMPEIFGLHDNANITFAQNETFALLGTIIQLQPK
	ł	1	SSSAGSQGREEIVEDVTQNILLKVPEPINLQWVMAKYPVLYEES
j		ŀ	MNTVLVQEVIRYNRLLQVITQTLQDLLKALKGLVVMSSQLELMA
		,	ASLYNNTVPELWSAKAYPSLKPLSSWVMDLLQRLDFLQAWIQDG
		j	IPAVFWISGFFFPQAFLTGTLQNFARKFVISIDTISFDFKVMFE
			APSELTQRPQVGCYIHGLPLEGARWDPEAFQLAESQPKELYTEM
1	ľ	ļ	AVIWLLPTPNRKAQDQDFYLCPIYKTLTRAGTLSTTGHSTNYVI
7121			AVEIPTHQPQRHWIKRGVALICALDY
1121	2	546	RPLRPWVLSLGSMVGLMTYGRRQFQSLDTTMRRLIPPFREASAK
1]	LTTLVDADABAFTAYLEAMRLPKNTPEEKDRRTAALQEGLRRAV
ĺ	1	ĺ	SVPLTLAETVASLWPALQELARCGNLACRSDLQVAAKALEMGVF
			GAYFNVLINLRDITDEAFKDQIHHRVSSLLQEAKTQAALVLDCL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A-Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
Į.	residue of	amino acid	Warmantenham V manage
İ	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	bequence	Codon, /=possible nucleotide deletion,
	-		\=possible nucleotide insertion) ETROE
7122	2	546	
1 '	-	540	RPLRPWVLSLGSMVGLMTYGRRQFQSLDTTMRRLIPPFREASAK
1		ł	LTTLVDADAEAFTAYLEAMRLPKNTPEEKDRRTAALQEGLRRAV
ł		}	SVPLTLAETVASLWPALQELARCGNLACRSDLQVAAKALEMGVP
1	1		GAYFNVLINLRDITDEAFKDQIHHRVSSLLQEAKTQAALVLDCL
7123			ETRQE
/123	1	1092	KPAVPEARSAGTSEAGRSGAEEVSCGSVSGDGAAMRLTPRALCS
ľ	1		AAQAAWRENFPLCGRDVARWFPGHMAKGLKKMOSSLKLVDCIIE
ì	ł .		VHDARIPLSGRNPLFQETLGLKPHLLVLNKMDLADLTROOKIMO
		•	HLEGEGLKNVIFTNCVKDENVKQIIPMVTELIGRSHRYHRKENI.
ł			BYCIMVIGVPNVGKSSLINSLRROHLRKGKATRVGGRPGTTRAV
1	1		MSKIQVSERPLMFLLDTPGVLAPRIESVETGLKLALCGTVLDHT.
			VGBETMADYLLYTLNKHQRFGYVQHYGLGSACDMVERVLKSVAV
1			KLGKTQKVKVLTGTGNVNVIQPNYPAAARDFLQTFRRGLLGSVM
			LDLDVLRGHPRV
7124	2	382	LPLTLLLAAPFAHLLLPPGHDQSPCWHPGPALSPGTLGPLSWAM
			ANSGLQLLGYFLALGGWVGIIASTALPOWKOSSYAGDASIOLRS
			KVFVLESEWGGDSLGLPRDCGWSCLLHSAVRSEKGFWS
7125	166	1127	NCISEKRNYSFSMQKGKGRTSRIRRRKLCGSSESRGVNESHKSE
			FIELRKWLKARKFQDSNLAPACFPGTGRGLMSOTSLOEGOMITS
		•	LPESCLLT\RDTVIRSYLGAYITKWKPPPSPLLALCTFLVSRKH
1			AGHRSLLEA\YLEILPKAYTCPVCLEPEVVNLLPKSLKAKAEEO
·			RAHVQEFFASSRDFFSSLQPLFAEAVDSIFSYSALLWAWCTVNT
1			RAVYL\SPGSGNAFLQSRTPVQLAPYLDLLNHSPHVQVKAAFNE
			ETHSYEIRTTSRWRKHEEVFICYGPHDNQRLFLEYGFVSVHNPH
			ACVYVSRGWNQLCS
7126	1	733	CRDMAAFIVPSPARRCSQKGSLGHLPTQPWLWAAMSPRGQERGT
1			SHSQAREPORPGRWLLGSLQSSPGTLGQAGTASRRRGCMVORWV
1 1			QVATGRRAVQVPKGALGLALGETSPGASRGMSGGAGGCWALGWA
1 1			PSPVLPSWLLEGPPPWLSIISDSGTORPSPRRCPARPSPWGPOC
1 1			WRGGRIASAEASST*TPGSGSRARSGRRSPGSRRRSASAPSPTP
			PTDACA*SCVARPAGSRSSRPAAA
7127	1311	277	GLPAMCST*KAGYYEETEGDCIPKDR*IEKRPFKEI*RRIPRIF
1			AKQKQI*S*NSQKIGASEIDRGRKEADCSDAPAAARIGAVSVFR
1 1		1	RSTQEARVSPRSNAKSANLRAVRAD*WEHFVLI.FHTPEOFLARC
]		•	ICRST**K*WHQLC*PLSSL*TGLKRKLLL*VLFRI*WLKDCDV
			*FCQKIFATNFCNWQNLIQ*EE*KPVEYSVEN*HIMNLLLPM*I.
j j	ł		CQSSLRDQTIVTWRM*RNYSMFRINMISSL*DGSIHIPLKLHFY
[ſ		PALIFTLTVPINSCCQRPLPLFAHOSIKTLASSGSPMLACLRFL
1-9125			LVKKRAFIHTPRSPGCSV*CKHVLVKDNKNNCVGSEV
7128	2	5228	GRVDLWTILLGRSALRELSQIEAELNKHWRRLLEGLSYYKPPSP
		ĺ	SSAEKVKANKDVASPLKELGLRISKFLGLDEEOSVOLLOCYLOE
ľ			DYRGTRDSVKTVLQDERQSQALILKIADYYYEERTCILRCVI.HI.
]		i	LTYFQDERHPYRVEYADCVDKLEKELVSKYRQOFEELYKTRAPT
	ĺ	1	WETHGNLMTERQVSRWFVQCLREQSMLLEIIPLYYAYFEMAPSD
[.]	İ	!	LLVLTKMFKEQGFGSRQTNRHLVDETMDPFVDRIGYFSALILVE
1		į	GMDIESLHKCALDDRRELHQFAQDGLICODMDCLMLTFGDIPHH
[. [1	Į.	APVLLAWALLRHTLNPEETSSVVRKIGGTAIOLNVFOYLTRLLO
1 1	ĺ	1	SLASGGNDCTTSTACMCVYGLLSFVLTSLELHTLGNOODTIDTA
[İ	[CEVLADPSLPELFWGTEPTSGLGIILDSVCGMFPHLLSPLLQLL
		1	RALVSGKSTAKKVYSFLDKMSFYNELYKHKPHDVISHEDGTLWR
			RQTPKLLYPLGGQTNLRIPQGTVGQVMLDDRAYLVRWEYSYSSW
1	1		TLFTCEIEMLLHVVSTADVIQHCQRVKPIIDLVHKVISTDLSIA
			DCLLPITSRIYMLLQRLTTVISPPVDVIASCVNCLTVLAARNPA
			KVWTDLRHTGFLPFVAHPVSSLSQMISAEGMNAGGYGNLLMNSE
<u> </u>		1	QPQGEYGVTIAFLRLITTLVKGQLGSTQSQGLVPCVMFVLKEML

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, FaPhenylalanine, G=Glycine,
ĺ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ļ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine.
- 1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion.
	sequence		\=possible nucleotide insertion)
1	ļ		PSYHKWRYNSHGVREQIGCLILELIHAILNLCHETDLHSSHTPS
- I		}	LQFLCICSLAYTEAGQTVINIMGIGVDTIDMVMAAOPRSDGAEG
		}	QGQGQLLIKTVKLAFSVTNNVIRLKPPSNVVSPLEOALSOHGAH
1			GNNLIAVLAKYIYHKHDPALPRLAIOLLKRLATVAPMSVYACLG
1			NDAAAIRDAFLTRLQSK\IE\DMRIK\VMIL\EFLTVA\VETQP
]			GLIELFLNLEVKDG\SDGSKEFSLGMW\SCLHAV/VWELTDSOO
ł	į į		QDRYWCPPLLHRAAIAFLHALWQDRRDSAMLVLRTKPKFWENLT
			SPLFGTLSPPSETSEPSILETCALIMKIICLEIYYVVKGSLDQP
i	1		LKDTLKKFSIEKRFAYWSGYVKSLAVHVAETEGSSCTSLLEYQM
ļ	}		LVSAWRMLLIIATTHADIMHLTDSVVRRQLFLDVLDGTKALLLV
1	1		PASVNCLRLGSMKCTLLLILLRQWKRELGSVDEILGPLTEILEG
1			VLQADQQLMEKTKAKVFSAFITVLQMKEMKVSDIPQYSQLVLNV
			CETLQEEVIALFDQTRHSLALGSATEDKDSMETDDCSRSRHRDQ
1	ľ		RDGVCVLGLHLAKELCEVDEDGDSWLQVTRRLPILPTLLTTLEV SLRMKQNLHFTEATLHLLLTLARTQQGATAVAGAGITQSICLPL
			LSVYQLSTNGTAQTPSASRKSLDAPSWPGVYRLSMSLMEQLLKT
	}		LRYNFLPEALDFVGVHQERTLQCLNAVRTVQSLACLEEADHTVG
1			FILQLSNFMKEWHFHLPQLMRDIQVNLGYLCQACTSFLHSRKML
1			QHYLQNKNGDGLPSAV\AQRV\QRPPSAASAAPSSSKQPAADTE
1			ASEQQALHTVQYGLLKILSKTLAALRHFTPDVCQILLDQSLDLA
	:		EYNFLFALSFTTPTFDSEVAPSFGTLLATVNVALNMLGELDKKK
			EPLTQAVGLSTQAEGTRTLKSLLMFTMENCFYLLISOAMRYLRD
1			PAVHPRDKQRMKQELSSELSTLLSSLSRYFRRGAPSSPATGVLP
7130			SPQGKSTSLSKASPESQEPLIQLVQAFVRHMOR
7129	1	1054	FRRFRWRRRLH*AGPASSAGGSPGEASGTMSGELPPNINIKEPR
			WDQSTFIGRANHFFTVTDPRNILLTNEQLESARKIVHDYRQGIV
1	İ		PPGLTENELWRAKYIYDSAFHPDTGEKMILIGRMSAQVPMNMTI
1			TGCMMTFYRTTPAVLFWQWINQSFNAVVNYTNRSGDAPLTVNEL
			GTAYVSATTGAVATALGLNALTKHVSPLIGRFVPFAAVAAANCI
1 1			NIPLMRQRELKVGIPVTDENGNRLGESANAAKQAITQVVVSRIL
1			MAAPGMAIPPFIMNTLEKKAFLKRFPWMSAPIQVGLVGFCLVFA
7130	2	780	TPLCCALFPQKSSMSVTSLEABLQAKIQESHPELRRVYFNKGL HEVPSLQTSDPLPGSVQRCSVVVSQPNKENWCQDHLYNSLGRKG
1 1			ISAKSQPYHRSQSSSSVLINKSMDSINYPSDVGKQQLLSLHRSS
li	Í		RCESHQDLLPDIADSHQQGTEKLSDLTLQDSQKVVVVNRNLPLN
	ł		AQIATQNYFSNFKETDGDEDDYVEIKSEEDESELELSHNRRRKS
			DSKFVDADFSDNVCSGNTLHSLNSPRTPKKPVNSKLGLSPYLTP
			YNDSDKLNDYLWRGPSPNQQNIVQSLREKFOCLSSSSFA
7131	805	573	AAAEGHIEVVKFLIEACKVNPFAKDRWGNIPLDDAVOFNHLEVV
1 2122			KLLQDYQDSYTLSETQAEAAAEALSKENLESMV
7132	1420	1087	IDMLLLSGALVSGPYTLITTAVSADLGTHKSLKGNAHALSTVTA
1	Ì		IIDGTGSVGAALGPLLAGLLSPSGWSNVFYMLMFADACALLFLT
7133	2		RLIHKELSCPGSATGDQVPFKEQ
,	2	3648	QQIPGLLPAHGESGDALRKPRLQKPITGHLDDLFFTLYPSLEKF
1 1	Ì	,	EEELLELHVQDHFQEGCGPLDGGALEILERRLRVGVHNGLGFVQ
1	ĺ	ſ	RPQVVVLVPEMDVALTRSASFSRKVVSSSKTSSGSQALVLRSRL
[. [[RLPEMVGHPAFAVIFQLEYVFSSPAGVDGNAASVTSLSNLACMH
		ł	MVRWAVWNPLLEADSGRVTLPLQGGIQPNPSHCLVYKVPSASMS
1 1		1	SEEVKQVESGTLRFQFSLGSEEHLDAPTEPVSGPKVERRPSRKP
1 1		į	PTSPSSPPAPVPRVLAAPQNSPVGPGLSISQLAASPRSPTQHCL
			ARPTSQLPHGSQASPAQAQEFPLEAGISHLEADLSQTSLVLETS
Į į			IAEQLQELPFTPLHAPIVVGTQTRSSAGQPSRASMVLLQSSGFP
			EILDANKQPAEAVSATEPVTFNPQKEESDCLQSNEMVLQFLAFS
			RVAQDCRGTSWPKTVYFTFQFYRFPPATTPRLQLVQLDEAGQPS SGALTHILVPVSRDGTFDAGSPGFQLRYMVGFGFLKPGERRCFA
			RYLAVQTLQIDVWDGDSLLLIGSAAVQMKHLLRQGRPAVQASHE
			THE THE THE THE THE THE THE THE THE THE

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ĺ	location	corresponding	Glutamic Acid, F-Phenylalanine, G-Glycine, H-Histidine, I-Isoleucine, K-Lysine,
J	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
Į	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown +-Chan
1	amino acid	sequence	Codon, /=possible nucleotide deletion
	sequence		\=possible nucleotide insertion)
			LEVVATBYEQDNMVVSGDMLGFGRVKPIGVHSVVKGRLHLTLAN
1			VGHPCEQKVRGCSTLPPSRSRVISNDGASRFSGGSLLTTGSGDD
i	l	1	KHVVQAQKLADVDSELAAMLLTHAROGKGPODVSRRSDATTDDDV
1			LERMRSVRLQEAGGDLGRRGTSVLAOOSVRTOHLRDLOVIAAVP
İ	İ	{	ERTKAESIASLLSLAITTEHTLHATLGVAEFPEFVLKNPHNTOH
i			TVTVEIDNPELSVIVDSQEWRDPKGAAGLHTPVEEDMFHLRGSL
		ł	APQLYLRPHETAHVPFKPQSFSAGQLAMVQASPGLSNEKGMDAV
			SPWKSSAVPTKHAKVLFRASGGKPIAVLCLTVELQPHVVDQVFR
Í			FYHPELSFLKKAIRLPPWHTFPGAPVGMLGEDPPVHVRCSDPNV ICETONVGPGEPRDIFLKVASGPSPEIKDFFVIIYSDRWLATPT
			QTWQVYLHSLQRVDVSCVAGQLTRLSLVLRGTQTVRKVRAFTSH
ĺ	1		PQELKTDPKGVFVLPPRGVQDLHVGVRPLRAGSRFVHLNLVDVD
			CHQLVASWLVCLCCRQPLISKAFEIMLAAGEGKGVNKRITYTNP
İ	1		YPSRRTFHLHSDHPELLRFREDSFOVGGGETYTIGLOFAPSORY
			GEEEILIYINDHEDKNEEAFCVKVIYO
7134	2115	1111	GGEGFSYPPHVGLSLGTPLDPHYVLLEVHYDNPTYEEGLIDNSG
ŀ	<u> </u>		LRLFYTMDIRKYDAGVIEAGLWVSLFHTIPPGMPEFOSEGHCTL
			ECLEEALEAEKPSGIHVFAVLLHAHLAGRGIRLRHFRKGKEMKT.
	i	ı	LAYDDDFDFNFQEFQYLKEEQTILPGDNLITECRYNTKDRAEMT
,			WGGLSTRSEMCLSYLLYYPRINLTRCASIPDIMEQLQFIGVKEI
			YRPVTTWPFIIKSPKQYKNLSFMDAMNKFKWTKKEGLSFNKLVL
•			SLPVNVRCSKTDNAEWSIQGMTALPPDIERPYKAEPLVCGTSSS SSLHRDFSINLLVCLLLLSCTLSTKSL
7135	2	2072	FVPRVTPRSLSLQGPKGBSVGSITQPLPSSYLIFRAASESDGRC
			WLDALELALRCSSLLRLGTCKPGRDGEPGTSPDASPSSLCGLPA
			SATVHPDQDLFPLNGSSLENDAFSDKSERENPEESDTETQDHSR
			KTESGSDQSETPGAPVRRGTTYVEOVOEELGELGRASOVETVSE
			ENKSLMWTLLKQLRPGMDLSRVVLPTFVLEPRSFLNKLSDVVVU
			ADLLSRAAVEEDAYSRMKLVLRWYLSGFYKKPKGTKKDYNDTIG
			ETFRCCWFHPQTDSRTFYIAEOVSHHPPVSAPHVSNRKDGFCTS
1			GSITAKSRFYGNSLSALLDGKATLTFLNRAEDYTLTMPYAHCKG
	ĺ		ILYGTMTLELGGKVTIECAKNNFQAQLEFKLKPFFGGSTSINQI
	ł		SGKITSGEEVLASLSGHWDRDVFIKEEGSGSSALFWTPSGEVRR
	į	,	QRLRQHTVPLEEQTELESERLWQHVTRAISKGDQHRATQEKFAL EEAQRQRARERQESLMPWKPQLFHLDPITQEWHYRYEDHSPWDP
1	ł		LKDIAQFEQDGILRTLQQBAVARQTTFLGSPGPRHERSGPDQRL
1			RKASDQPSGHSQATESSGSTPESCPELSDEEQDGDFVPGGESPC
	1	•	PRCRKEARRLQALHEAILSIREAQQBLHRHLSAMLSSTARAAQA
			PTPGLLQSPRSWFLLCVFLACOLFINHILK
7136	2	418	DFVPSFRRPSGNTSQTVWLLRAATLEKEVAGLREKIHHLDDMI.K
ļ	1	ļ	SQQRKVRQMIEQLQNSKAVIQSKDATIOELKEKIAYLEAENTEM
	1		HDRMEHLIEKQISHGNFSTQARAKTENPGSIRISKPPSPKPMPV
7137	2		IRVVET
, ,	•	466	WASGMSTVPGGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA
1	1		GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELORLDCAT
ļ	ļ		PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT
7138	2	466	RMEQLSDKESYKLSCQLEPENP
1		300	WASGMSTVPCGSRHSLGIQVRGGWGVTGGEEESLTVPVADTWQA
]	į]	GSFKVATQERNPQRAQMRLRRQKKGVVPFLGDFLTELQRLDSAI
	ļ	f	PDDLDGNTNKRSKEVRVLQEMQLLQVAAMNYRLRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP
7139	1	357	SLRNSARGLKMAASAARGAAALRRSINQPVAFVRRIPWTAASSQ
1			LKEHFAQFGHVRRCILPFDKETGFHRGLGWVQFSSEEGLRNALQ
		l	QENHI I DGVKVQVHTRRPKLPQTSDDEKKDF
7140	1401	1957	RASSLQVLKANGGLIPSSFOOOHTGOYALEELFDLKVVDCRCSF
			NMNVSLEKQLRPSQPWPRGKCRKTPGWEEARPKAQDLRGDLGKT

SEQ	Predicted	Predicted end	The state of the s
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
ĺ	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
i i	amino acid		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	sequence	Codon, /=possible nucleotide deletion,
<u> </u>	bequence		\=possible nucleotide insertion)
İ			QAGPAEAHTRGPPRLPAATGCPPHLPGLLSGISVDIDPTGLQSQ
1	1	ł	WTPKGQDPPLMFSEDYQKSLLEQYHLGLDQKLRKYVVGELIWNF
7141	124		ADFMINGCG
/ + 4 + 1	124	1073	LDSRSCWLDMEDLEEDVRFIVDETLDFGGLSPSDSREEEDITVL
			VTPEKPLRRGLSHRSDPNAVAPAPQGVRLSLGPLSPEKLEETLD
1	j		EANRLAAQLEQCALQDRESAGEGLGPRRVKPSPRRETEVI.KDSp
1	1		VRDLLPTVNSLTRSTPS/LKQPDASTPE***EGVSOGSPGVTWK
1			EALQHEEGVTHLQSVPCIQKPSIFSS\SRSTPPVRGRAGDSGDA
1	1		AASEETRAAKLRGAAAKSSCOLPIPSAIPRPASRMPI.TSPSVDD
ł	1		GRGALPPDSLSTRKGLPRPSTAGHRVRESGHKVPVSQRLNLPVM
7142			GATRSNLQPP
/142	658	839	LIFLMLHMELKMLSSVTLHIRAFLYWICLKPTSCLIFQNVLNLL
	1 1		KK*SRAVGVVVVMCRT/YSSDLQVGVIKPWLLLGSQDAAHDLDT
			LKKNKVTHILNVAYGVENAFLSDFTYKSISILDLPETNILSYFP
7143		<u></u>	ECFEFIEEAKRKDGVVLVHCNA
/143	3	773	SLEMSSDGEPLSRMDSEDSISSTIMDVDSTISSGRSTPAMMNGQ
1	:		GSTTSSSKNIAYNCCWDQCQACFNSSPDLADHIRSIHVDGQRGG
1			VFVCLWKGCKVYNTPSTSQSWLQRHMLTHSGDKPFKCVVGGCNA
1	1		SFASQGGLARHVPTHFSQQNSSKVSSQPKAKEESPSKAGMNKRR
l			KLKNKRRRSLARPHDFFDAQTLDAIRHRAICFNLSAHIESLGKG
			HSVVFHSTVSILLFFQIKYKTLQKNISTIISKSLKI
7144	1	988	FRVNMQDGGPSPAEHSKAEESAGMEARFLGLPDAAGSSGPTPAR
1			RCPAPRPAGVSYVIRDEVEKYNRNGVNALQLDPALNRLFTAGRD
			SIIRIWSVNQHKQDPYIASMEHHTDWVNDIVLCCNGKTLISASS
	1		DTTVKVWNAHKGFCMSTLRTHKDYVKALAYAKDKELVASAGLDR
1	[!	QIFLWDVNTLTALTASNNTVTTSSLSGNKDSIYSLAMNQLGTII
j 1]		VSGSTEKVLRVWDPRTCAKLMKLKGHTDNVKALLLNRDGTQCLS
	ĺ		GSSDGTIRLWSLGQQRCIATYRVHDEGVWALQVNDAFTHVYSGG
L		. [RDRKIYCTDLRNPDIRVLICE

TRADOCS:1416260.1(%CSK011.DOC)

WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NO:1-1786 and 3573-5358, a mature protein coding portion of SEQ ID NO:1-1786 and 3573-5358, an active domain of SEQ ID NO:1-1786 and 3573-5358, and complementary sequences thereof.

- 2. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide hybridizes to the polynucleotide of claim 1 under stringent hybridization conditions.
- 3. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide has greater than about 90% sequence identity with the polynucleotide of claim 1.
- The polynucleotide of claim 1 wherein said polynucleotide is DNA.
- 5. An isolated polynucleotide of claim 1 wherein said polynucleotide comprises the complementary sequences.
- 6. A vector comprising the polynucleotide of claim 1.
- 7. An expression vector comprising the polynucleotide of claim 1.
- 8. A host cell genetically engineered to comprise the polynucleotide of claim 1.
- 9. A host cell genetically engineered to comprise the polynucleotide of claim 1 operatively associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell.
- 10. An isolated polypeptide, wherein the polypeptide is selected from the group consisting of:

(a) a polypeptide encoded by any one of the polynucleotides of claim 1; and

- (b) a polypeptide encoded by a polynucleotide hybridizing under stringent conditions with any one of SEQ ID NO:1-1786 and 3573-5358.
- 11. A composition comprising the polypeptide of claim 10 and a carrier.
- 12. An antibody directed against the polypeptide of claim 10.
- 13. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
- a) contacting the sample with a compound that binds to and forms a complex with the polynucleotide of claim 1 for a period sufficient to form the complex; and
- b) detecting the complex, so that if a complex is detected, the polynucleotide of claim 1 is detected.
- 14. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
- a) contacting the sample under stringent hybridization conditions with nucleic acid primers that anneal to the polynucleotide of claim 1 under such conditions;
- b) amplifying a product comprising at least a portion of the polynucleotide of claim 1; and
- c) detecting said product and thereby the polynucleotide of claim 1 in the sample.
- 15. The method of claim 14, wherein the polynucleotide is an RNA molecule and the method further comprises reverse transcribing an annealed RNA molecule into a cDNA polynucleotide.
- 16. A method for detecting the polypeptide of claim 10 in a sample, comprising:

a) contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex; and

- b) detecting formation of the complex, so that if a complex formation is detected, the polypeptide of claim 10 is detected.
- 17. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:
- a) contacting the compound with the polypeptide of claim 10 under conditions sufficient to form a polypeptide/compound complex; and
- b) detecting the complex, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.
- 18. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:
- a) contacting the compound with the polypeptide of claim 10, in a cell, under conditions sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and
- b) detecting the complex by detecting reporter gene sequence expression, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.
- 19. A method of producing the polypeptide of claim 10, comprising,
- a) culturing a host cell comprising a polynucleotide sequence selected from the group consisting of a polynucleotide sequence of SEQ ID NO:1-1786 and 3573-5358, a mature protein coding portion of SEQ ID NO:1-1786 and 3573-5358, an active domain of SEQ ID NO:1-1786 and 3573-5358, complementary sequences thereof and a polynucleotide sequence hybridizing under stringent conditions to SEQ ID NO:1-1786 and 3573-5358, under conditions sufficient to express the polypeptide in said cell; and
 - b) isolating the polypeptide from the cell culture or cells of step (a).

20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of any one of the polypeptides SEQ ID NO:1787 -3572 and 5359-7144, the mature protein portion thereof, or the active domain thereof.

- 21. The polypeptide of claim 20 wherein the polypeptide is provided on a polypeptide array.
- 22. A collection of polynucleotides, wherein the collection comprising the sequence information of at least one of SEQ ID NO:1-1786 and 3573-5358.
- 23. The collection of claim 22, wherein the collection is provided on a nucleic acid array.
- 24. The collection of claim 23, wherein the array detects full-matches to any one of the polynucleotides in the collection.
- 25. The collection of claim 23, wherein the array detects mismatches to any one of the polynucleotides in the collection.
- 26. The collection of claim 22, wherein the collection is provided in a computerreadable format.
- 27. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.
- 28. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising an antibody that specifically binds to a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US00/34263

IPC(7) : C07H 21/04; C12N 15/11, 15/63, 15/70, 15/82, 15/85; C07K 14/00 US CL : 536/23.1; 435/320.1, 455, 468, 530/300, 350				
	According to International Patent Classification (IPC) or to both national classification and IPC			
	DS SEARCHED			
	cumentation searched (classification system followed 36/23.1; 435/320.1, 455, 468, 530/300, 350	by classification symbols)		
Documentation	Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched			
Electronic da MEDLINE,	ata base consulted during the international search (name EAST	ne of data base and, where practicable, sea	rch terms used)	
	UMENTS CONSIDERED TO BE RELEVANT			
Category *	Citation of document, with indication, where	appropriate, of the relevant passages	Relevant to claim No.	
A	WAJIMA et al. The cDNA cloning and transient exhibition hydroxysteroid dehydrogenase of chickens. Gene. I		1-11, 13-16, and 19-26	
A	US 5,175,095 A (MARTINEAU et al) 29 December columns 3-18.	er 1992 (29.12.1992), see especially	1-11, 13-16, and 19-26	
A	Database PubMed, ID No. 2393392, FREUDENSTEIN et al. mRNA of bovine tissue inhibitor of metalloproteinase: sequence and expression in bovine ovarian tissue. Biochem. Biophys. Res. Commun. August 1990. Vol.171. No. 1. pages 250-256, see Abstract.		1-11, 13-16, and 19-26	
A,P	Database PubMed, ID No. 10919256, HENNEBO generation and characterization of an ovary-selectiv library. Endocrinology. August 2000, Vol.141, No.	e complementary deoxyribonucleic acid	1-11, 13-16, and 19-26	
A	Database PubMed, ID No. 2760883, BEIL et al. Sy the baboon (Papio anubis). J. Reprod. Fertil. July l Abstract.	onthesis of polypeptides by the cervix of 989, Vol.86. No.2. pages 535-544, see	1-11, 13-16, and 19-26	
A,P Database PubMed, ID No. 10830289, HINSHELW upstream of the human CYP19 (aromatase) gene me transgenic mice. Endocrinology. June 2000. Vol.14		diates ovary-specific expression in	1-11, 13-16, and 19-26	
	documents are listed in the continuation of Box C.	See patent family annex.		
"A" document	defining the general state of the art which is not considered to be arrelevance	"T" later document published after the inter date and not in conflict with the applicate principle or theory underlying the inver-	ation but cited to understand the	
"E" earlier app	olication or patent published on or after the international filing date	"X" document of particular relevance; the c considered novel or cannot be consider when the document is taken alone		
'L' document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)		"Y" document of particular relevance; the c considered to involve an inventive step	when the document is	
"O" document referring to an oral disclosure, use, exhibition or other means		combined with one or more other such being obvious '2 a person skilled in the		
"P" document published prior to the international filing date but later than the priority date claimed		"&" document member of the same patent for	amily	
Date of the actual completion of the international search		Date of mailing of the international searc	h report	
Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT		Authorizesbofficer Alli Wassel Michael Woodward	Idlan for	
Washington, D.C. 20231 Facsimile No. (703)305-3230		Telephone No. (703) 308-0196	/)	

Form PCT/ISA/210 (second sheet) (July 1998)

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US00/34263

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)			
This	internat	ional report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:	
1.		Claim Nos.: because they relate to subject matter not required to be searched by this Authority, namely:	
2.		Claim Nos.: because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:	
3.		Claim Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).	
Box	II Ob	servations where unity of invention is lacking (Continuation of Item 2 of first sheet)	
This This	Internati includes	ional Searching Authority found multiple inventions in this international application, as follows: 4 invention Groups and 3572 sequence species	
	_		
1.	\boxtimes	As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.	
2.		As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.	
3.		As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:	
4.		No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:	
Rema	rk on P	rotest The additional search fees were accompanied by the applicant's protest.	
		No protest accompanied the payment of additional search fees.	

Form PCT/ISA/210 (continuation of first sheet(1)) (July 1998)

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US00/34263

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional serch fees must be paid. Group I, claims 1-11, 13-16, and 19-26, drawn to nucleic acid molecules, vector molecules and host cells containing said nucleic acids, polypeptides, methods of making said polypeptides and method of detection using said nucleic acids and polypeptides. Group II, claim 12 and 28, drawn to antibodies and method of treatment using composition comprising said antibodies. Group III, claims 17-18, drawn to methods of indentifying a binding partner to a polypeptides. Group IV, claim 27, drawn to method of treatment using composition comprising polypeptides.

The inventions listed as Groups I-IV do not relate to a single inventive concept under PCT Rule 13.1 because, udner PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: Group I encompasses nucleic acids, polypeptides expressed thereby, vectors and host cells containg same, respectively, and methods of making as well as the first method of use of this jubject matter. Groups II-V all are directed to different special technical features as summarized as follows: Group II is directed to an antibody and method of treatment using same, which antibody undergoes recognition and binding reactions wherein what is bound is different from what is bound by the compositions of Group I. For example, the polypeptides of Group I do not bind the polypeptides of Group I as the antibody of Group II does. Identification of binding partner and treatment are clearly different special technical features from detection. Group II is directed to the identification of a binding partner of a polypeptide, which is not identified in any of the other Groups and thus clearly contains its own special technical feature. Group IV is directed to treatment, which is a clearly different methods than the methods in the other Groups. Thus, in summary, each of Groups I-IV are directed to different special technical features and thus support this lack of unity.

Additionally, each of the claims is directed to more than one species of the generic invention. These species are deemed to lack unity of invention because they are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for more than one species to be searched, the appropriate additional search fees must be paid. The species are as follows: The claims include a series of polynucleotides and the polypeptides encoded thereby as represented by the sequences of SEQ ID Nos: 1-1786, and 3573-5358. Each of these polynucleotide sequences encodes a separate polypeptide and thus represent a separate gene. Therefore, each of these genes defines its own special technical feature. In summary, one species is a gene represented by one polynucleotide sequence and one polypeptide sequence encoded thereby.